
WAPESRA
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Sun Sep 13 07:26:01 1998; MasPar time 4580.90 Seconds
Tabular output not generated. 1340.595 Million cell updates/sec

Title: >US-08-554-424-7
Description: (1-6513) from US08554424.seq
Perfect Score: 6513
N.A. Sequence: 1 TCTAGACGTTGGCGCATAG.....ACGCGAGTATTAGCTCTAGA 6513
Comp: AGATCTGCAACCGCGTATC.....TGGCTCATATCGAGATCT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1460335 seqs, 471452172 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-pending
1:P9 2:U6000 3:U6001 4:U6002 5:U6003 6:U6004 7:U6005
8:U6006 9:U6007 10:U6008 11:U7 12:U80 13:U81 14:U82
15:U83 16:U84A 17:U84B 18:U85 19:U86 20:U87 21:U88
22:U89 23:U90A 24:U90B 25:U91 26:NEWP 27:NEWU8 28:NEWU9

Statistics: Mean 11.841; Variance 4.073; scale 2.907

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	6513	100.0	6513	18	US-08-554- Sequence 7, Applicatio	0.00e+00
2	5500	84.4	6519	21	US-08-808- Sequence 24, Applicati	0.00e+00
3	4374	67.2	5461	11	US-07-998- Sequence 7, Applicatio	0.00e+00
4	4374	67.2	5461	11	US-07-998- Sequence 7, Applicatio	0.00e+00
5	3676	56.4	6318	21	US-08-808- Sequence 1, Applicatio	0.00e+00
6	3676	56.4	6318	20	US-08-772- Sequence 1, Applicatio	0.00e+00
7	3676	56.4	6318	1	PCR-US97-2 Sequence 1, Applicatio	0.00e+00
8	3664	56.3	6315	1	PCR-US97-2 Sequence 2, Applicatio	0.00e+00
9	3664	56.3	6315	20	US-08-772- Sequence 2, Applicatio	0.00e+00
10	3664	56.3	6315	21	US-08-808- Sequence 2, Applicatio	0.00e+00
11	3662	56.2	6318	19	US-08-608- Sequence 1, Applicatio	0.00e+00
12	3660	56.2	6318	19	US-08-608- Sequence 2, Applicatio	0.00e+00
13	472	7.2	1237	21	US-08-808- Sequence 26, Applicati	0.00e+00
14	356	5.5	5977	23	US-09-024- Sequence 1, Applicatio	0.00e+00
15	356	5.5	6007	23	US-09-024- Sequence 2, Applicatio	0.00e+00
16	356	5.5	6556	23	US-09-024- Sequence 7, Applicatio	0.00e+00
17	354	5.4	6826	23	US-09-024- Sequence 8, Applicatio	0.00e+00

18	320	4.9	6048	19	US-08-682- Sequence 1, Applicatio	0.00e+00
19	316	4.9	6452	21	US-08-836- Sequence 9, Applicatio	0.00e+00
20	312	4.8	3033	15	US-08-334- Sequence 1, Applicatio	0.00e+00
21	312	4.8	3033	21	US-08-836- Sequence 1, Applicatio	0.00e+00
22	308	4.7	6371	21	US-08-836- Sequence 13, Applicati	0.00e+00
23	308	4.7	6404	21	US-08-836- Sequence 14, Applicati	0.00e+00
24	298	4.6	6344	18	US-08-511- Sequence 1, Applicatio	0.00e+00
25	298	4.6	6344	21	US-08-843- Sequence 1, Applicatio	0.00e+00
26	296	4.5	6524	20	US-08-775- Sequence 1, Applicatio	0.00e+00
27	296	4.5	6524	19	US-08-669- Sequence 1, Applicatio	0.00e+00
28	296	4.5	6527	19	US-08-669- Sequence 7, Applicatio	0.00e+00
29	296	4.5	6527	20	US-08-775- Sequence 7, Applicatio	0.00e+00
30	296	4.5	7052	20	US-08-775- Sequence 5, Applicatio	0.00e+00
31	296	4.5	7052	19	US-08-669- Sequence 5, Applicatio	0.00e+00
32	254	3.9	5874	21	US-08-843- Sequence 9, Applicatio	1.28e-256
33	231	3.5	2573	19	US-08-669- Sequence 3, Applicatio	5.85e-229
34	231	3.5	2573	20	US-08-775- Sequence 3, Applicatio	5.85e-229
35	214	3.3	930	19	US-08-605- Sequence 2, Applicatio	1.32e-208
36	204	3.1	930	19	US-08-605- Sequence 21, Applicati	1.12e-196
37	194	3.0	930	19	US-08-605- Sequence 3, Applicatio	8.85e-185
38	192	2.9	930	19	US-08-605- Sequence 1, Applicatio	2.10e-182
39	177	2.7	2279	11	US-07-998- Sequence 3, Applicatio	1.20e-164
40	177	2.7	2279	11	US-07-998- Sequence 3, Applicatio	1.20e-164
41	171	2.6	696	23	US-08-024- Sequence 5, Applicatio	1.43e-157
42	148	2.3	5482	15	US-08-346- Sequence 2, Applicatio	1.26e-130
43	134	2.1	702	18	US-08-511- Sequence 3, Applicatio	2.16e-114
44	134	2.1	702	21	US-08-843- Sequence 3, Applicatio	2.16e-114
45	119	1.8	5389	15	US-08-346- Sequence 1, Applicatio	3.57e-97

ALIGNMENTS

RESULT 1
ID US-08-554-424-7 STANDARD; DNA; UNC; 6513 BP.
AC xxxxxx

DE Sequence 7, Application US/08554424
CC Sequence 7, Application US/08554424
CC GENERAL INFORMATION:

CC APPLICANT: Wan Der Ploeg, Leonardus

CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE

CC TITLE OF INVENTION: PARA SODIUM CHANNEL

CC NUMBER OF SEQUENCES: 7

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Jack L. Tribble

CC STREET: P.O. Box 2000, 125 E. Lincoln Avenue

CC CITY: Rahway

CC STATE: New Jersey

CC COUNTRY: USA

CC ZIP: 07065-0907

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/554,424

CC FILING DATE:

CC CLASSIFICATION: 424

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Tribble, Jack L.

CC REGISTRATION NUMBER: 32,633

CC REFERENCE/DOCKET NUMBER: 19338DA

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (908) 594-5321

CC TELEFAX: (908) 594-4720

CC INFORMATION FOR SEQ ID NO: 7:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 6513 base pairs

CC TYPE: nucleic acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

mind

CC MOLECULE TYPE: cDNA
SQ SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.

Query Match 100.0%; Score 6513; DB 18; Length 6513;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TCTAGAGTTGGCCGATAGACAATGACAGAAGATTCGACTCGATATCTGAGGAAGAAC 60
Qy 1 TCTAGAGTTGGCCGATAGACAATGACAGAAGATTCGACTCGATATCTGAGGAAGAAC 60
Db 61 GCAGTTTGTTCGTCCTTACCCGGAATCATTTGTCGAATCAATCAACACGCAATTGCG 120
Qy 61 GCAGTTTGTTCGTCCTTACCCGGAATCATTTGTCGAATCAATCAACACGCAATTGCG 120
Db 121 CTGAACATGAAAGCAGAGAGCTGGAAAGAAAGAGAGCCGAGGAGAGGTGCCCGCAT 180
Qy 121 CTGAACATGAAAGCAGAGAGCTGGAAAGAAAGAGAGCCGAGGAGAGGTGCCCGCAT 180
Db 181 ATGGTCGCAAGAAAACAAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGTC 240
Qy 181 ATGGTCGCAAGAAAACAAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGTC 240
Db 241 CACACCGGATCCTACACTTGACAGGGTGTCCCAATACCTTTCGATTGCAGGCAGCT 300
Qy 241 CACACCGGATCCTACACTTGACAGGGTGTCCCAATACCTTTCGATTGCAGGCAGCT 300
Db 301 TCCCGCGGAATTTGGCTCCACTCTCTCGAGGATATCGATCCCTACTACACCAATGTAC 360
Qy 301 TCCCGCGGAATTTGGCTCCACTCTCTCGAGGATATCGATCCCTACTACACCAATGTAC 360
Db 361 TGACATTCGTAGTTGAACAAAGAAAGATATTTTCGCTTTTCTGCAATCAAAAGCAA 420
Qy 361 TGACATTCGTAGTTGAACAAAGAAAGATATTTTCGCTTTTCTGCAATCAAAAGCAA 420
Db 421 TGTGGATGCTCGATCAATCAATCGATACGCTGCTGGGCCATTTACATTCAGTGCATC 480
Qy 421 TGTGGATGCTCGATCAATCAATCGATACGCTGCTGGGCCATTTACATTCAGTGCATC 480
Db 481 CATTAATTTCCCTATTATCATCACCACCAATTCCTCAACTGCATCTGATGATAATGC 540
Qy 481 CATTAATTTCCCTATTATCATCACCACCAATTCCTCAACTGCATCTGATGATAATGC 540
Db 541 CGAACAGCCCGAGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600
Qy 541 CGAACAGCCCGAGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600
Db 601 CAGCTGTTAAAGTGTGGCAGGAGTTTCATTTTATGCCGTTTACGTATCTTAGAGATG 660
Qy 601 CAGCTGTTAAAGTGTGGCAGGAGTTTCATTTTATGCCGTTTACGTATCTTAGAGATG 660
Db 661 CATGGAATTTGGCTGGACTTCGTAGTAAATAGCTTTAGCTTTATGTGACCATGGGTATAGATT 720
Qy 661 CATGGAATTTGGCTGGACTTCGTAGTAAATAGCTTTAGCTTTATGTGACCATGGGTATAGATT 720
Db 721 TAGGTAATCTAGAGCCCTGCGAACCTTTTAGGTGCTGCGAGCGTTAAACCGTAGCCA 780
Qy 721 TAGGTAATCTAGAGCCCTGCGAACCTTTTAGGTGCTGCGAGCGTTAAACCGTAGCCA 780
Db 781 TTGTGCCAGGCTTGAAGACCATCGTCGGCGCGCTCATCGAATCGGTGAAGAACTCTGCGG 840
Qy 781 TTGTGCCAGGCTTGAAGACCATCGTCGGCGCGCTCATCGAATCGGTGAAGAACTCTGCGG 840
Db 841 ATGTGATTAATCTGACCATGTTCTCCCTGTTCGGTGTTCGCGTTGATGGCCCTACAGATCT 900
Qy 841 ATGTGATTAATCTGACCATGTTCTCCCTGTTCGGTGTTCGCGTTGATGGCCCTACAGATCT 900
Db 901 ATATGGGCTGTCTACCGAGAGTGTGATCAAGAAGTTCCCGGTGGAGCGGTTCCGTGGGGA 960
Qy 901 ATATGGGCTGTCTACCGAGAGTGTGATCAAGAAGTTCCCGGTGGAGCGGTTCCGTGGGGA 960
Db 961 ATCTGACCGAGAGACTGGGACTATCACAATCGCAATAGCTCCCAATTTGTTCCGAGG 1020
Qy 961 ATCTGACCGAGAGACTGGGACTATCACAATCGCAATAGCTCCCAATTTGTTCCGAGG 1020

Qy 961 ATCTGACCGAGGAACTGGGACTATCACAATCGCAATAGCTCCAATTTGTTATCCGAGG 1020
Db 1021 ACGAGGCACTCTCATTTCCGTTATGCGCAATATATCCGTTGGGGCAATATGCGACGACG 1080
Qy 1021 ACGAGGCACTCTCATTTCCGTTATGCGCAATATATCCGTTGGGGCAATATGCGACGACG 1080
Db 1081 ATTACGTTGCTCGACGGGTTTGGTCCGAATCCGAATTTATGGCTACACAGCTTCGATT 1140
Qy 1081 ATTACGTTGCTCGACGGGTTTGGTCCGAATCCGAATTTATGGCTACACAGCTTCGATT 1140
Db 1141 CGTTCCGATGGCTTCTCTGTCGCCCTTCCGGCTGATGACACAGGACTTCTGGGAGGATC 1200
Qy 1141 CGTTCCGATGGCTTCTCTGTCGCCCTTCCGGCTGATGACACAGGACTTCTGGGAGGATC 1200
Db 1201 TGTACCACTGCTGTTTGGCGCCCGGACCATGGCACATGCTGCTTTTATAGTCATCA 1260
Qy 1201 TGTACCACTGCTGTTTGGCGCCCGGACCATGGCACATGCTGCTTTTATAGTCATCA 1260
Db 1261 TCTTCTAGTTCAATCTATCTTGTGAATTTGATTTTGGCCATTTGTTGCCATGTCGTATG 1320
Qy 1261 TCTTCTAGTTCAATCTATCTTGTGAATTTGATTTTGGCCATTTGTTGCCATGTCGTATG 1320
Db 1321 ACGAATTGCAAGGAAGCGCGAAGAAAGAGGCTGCCGAAGAGAGGCGGATCGTGAAG 1380
Qy 1321 ACGAATTGCAAGGAAGCGCGAAGAAAGAGGCTGCCGAAGAGAGGCGGATCGTGAAG 1380
Db 1381 CGGAAGAGCTGCCCGCCGCAAGCGGCAAGCTGGAGAGCGGCGCAATCGCAGGCTC 1440
Qy 1381 CGGAAGAGCTGCCCGCCGCAAGCGGCAAGCTGGAGAGCGGCGCAATCGCAGGCTC 1440
Db 1441 AGGACAGAGCGGATGGGCTGCCCGCAAGAGGCTGACATCGCATCCGGAATGGCCAA 1500
Qy 1441 AGGACAGAGCGGATGGGCTGCCCGCAAGAGGCTGACATCGCATCCGGAATGGCCAA 1500
Db 1501 GTCCGACATCTTCTGATCAGCTATGAGCTATTTTGGCGGCGAAGGCGCAACGATG 1560
Qy 1501 GTCCGACATCTTCTGATCAGCTATGAGCTATTTTGGCGGCGAAGGCGCAACGATG 1560
Db 1561 ACAACAAGAAAGAGATGTCCATTCGGAGCTCGAGGTGGAGTTCGGAGTCGGTAGCG 1620
Qy 1561 ACAACAAGAAAGAGATGTCCATTCGGAGCTCGAGGTGGAGTTCGGAGTCGGTAGCG 1620
Db 1621 TTATACAAGACACAGCAGCTTACCAGCAGACACCAAGCTTACCAAGTTTCGTAAGTGA 1680
Qy 1621 TTATACAAGACACAGCAGCTTACCAGCAGACACCAAGCTTACCAAGTTTCGTAAGTGA 1680
Db 1681 GCAGACATCTTCTTACCTGCTTACCGTTTAAACATACGAGGAGTACAGTAGTT 1740
Qy 1681 GCAGACATCTTCTTACCTGCTTACCGTTTAAACATACGAGGAGTACAGTAGTT 1740
Db 1741 CTCACAAGTACACATACGGAACGAGCTGGCGCTTTTGGTATACCCGGTAGCGATCGTA 1800
Qy 1741 CTCACAAGTACACATACGGAACGAGCTGGCGCTTTTGGTATACCCGGTAGCGATCGTA 1800
Db 1801 AGCCATTTGGTATGTCAACATATCAGGATGCCAGCAGCTTGCCTTATCCGACGACT 1860
Qy 1801 AGCCATTTGGTATGTCAACATATCAGGATGCCAGCAGCTTGCCTTATCCGACGACT 1860
Db 1861 CGAATGCGCTCACCCGATGTCGGAAGAGATGGGCCATCATAGTGGCCGTGACTATG 1920
Qy 1861 CGAATGCGCTCACCCGATGTCGGAAGAGATGGGCCATCATAGTGGCCGTGACTATG 1920
Db 1921 GCAATCTAGGCTCCCGACACTCATCTATACCTCGCATCAGTCCCGAATATCGTATACCT 1980
Qy 1921 GCAATCTAGGCTCCCGACACTCATCTATACCTCGCATCAGTCCCGAATATCGTATACCT 1980
Db 1981 CACATGGCGATCTACTCGCGGATGGCCGTATGGGGTTCAGCAATATGACCAAGGAGA 2040
Qy 1981 CACATGGCGATCTACTCGCGGATGGCCGTATGGGGTTCAGCAATATGACCAAGGAGA 2040
Db 2041 GCAAAATTCGCAACCGCAACACAGCAATCAATCAGTGGGCGCCCAATGGCGCACCA 2100
Qy 2041 GCAAAATTCGCAACCGCAACACAGCAATCAATCAGTGGGCGCCCAATGGCGCACCA 2100

Db 2101 CCTGCTGACACCAATACAAAGCTCGATCATCGGACTACGAAATTGGCCTGGAGTGA 2160
QY |||||
Db 2101 CCTGCTGACACCAATACAAAGCTCGATCATCGGACTACGAAATTGGCCTGGAGTGA 2160
QY |||||
Db 2161 CGGACGAAGCTGGCAAGATTAAACATCATGACAATCCTTTTATCGAGCCGCTCCAGACAC 2220
QY |||||
Db 2161 CGGACGAAGCTGGCAAGATTAAACATCATGACAATCCTTTTATCGAGCCGCTCCAGACAC 2220
QY |||||
Db 2221 AAACGGTGGTTGATATGAAGATGTGATGCTCCTGAATGACATCATCGAACAGCCGCTG 2280
QY |||||
Db 2221 AAACGGTGGTTGATATGAAGATGTGATGCTCCTGAATGACATCATCGAACAGCCGCTG 2280
QY |||||
Db 2281 GTCCGACAGTGGGCAAGCATCGCGGTGCTCGGTTTACTTATTTCCCAACAGAGGAG 2340
QY |||||
Db 2281 GTCCGACAGTGGGCAAGCATCGCGGTGCTCGGTTTACTTATTTCCCAACAGAGGAG 2340
QY |||||
Db 2341 ATGACGAGGATGGCGGAGCTTCAAGACAAGGCACCTCGAAGTGAATCCTCAAGGCGATCG 2400
QY |||||
Db 2341 ATGACGAGGATGGCGGAGCTTCAAGACAAGGCACCTCGAAGTGAATCCTCAAGGCGATCG 2400
QY |||||
Db 2401 ATGTGTTTTGTGTGGGACTGTGTGGGTTTGGTTGAAATTCAGGAGTGGGTATCGC 2460
QY |||||
Db 2401 ATGTGTTTTGTGTGGGACTGTGTGGGTTTGGTTGAAATTCAGGAGTGGGTATCGC 2460
QY |||||
Db 2461 TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATCAGCGTGTGCATTTGGTCAACACGA 2520
QY |||||
Db 2461 TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATCAGCGTGTGCATTTGGTCAACACGA 2520
QY |||||
Db 2521 TGTTCATGCAATGGATACCAAGCATATCAACAAGGAGATGNAAGCGTGTCAAGAGTG 2580
QY |||||
Db 2521 TGTTCATGCAATGGATACCAAGCATATCAACAAGGAGATGNAAGCGTGTCAAGAGTG 2580
QY |||||
Db 2581 GCAACTATTCTTCCAGCCACACTTTGCCATCGAGGCCACCATGAAGCTTAATGGCCATGA 2640
QY |||||
Db 2581 GCAACTATTCTTCCAGCCACACTTTGCCATCGAGGCCACCATGAAGCTTAATGGCCATGA 2640
QY |||||
Db 2641 GCCCAAGTACTATTTCAGAGGAGGCTGGAACATCTTCGACTTCATTTATCGTGGCCCTAT 2700
QY |||||
Db 2641 GCCCAAGTACTATTTCAGAGGAGGCTGGAACATCTTCGACTTCATTTATCGTGGCCCTAT 2700
QY |||||
Db 2701 CGCTATTGAACTGGGACTCGAGGGTGTCCAGGCTGTGCGGTATTCGCTTCTTCGAT 2760
QY |||||
Db 2701 CGCTATTGAACTGGGACTCGAGGGTGTCCAGGCTGTGCGGTATTCGCTTCTTCGAT 2760
QY |||||
Db 2761 TGTGCGTGTATTCAAACTGGCCAACTCTTGGCCACACTTAATTTACTCATTTTCGATTA 2820
QY |||||
Db 2761 TGTGCGTGTATTCAAACTGGCCAACTCTTGGCCACACTTAATTTACTCATTTTCGATTA 2820
QY |||||
Db 2821 TGGAGCGCACCATGGCGGCTTTGGGTAATCTGACATTTGTACTTTGCATTTATCTTCA 2880
QY |||||
Db 2821 TGGAGCGCACCATGGCGGCTTTGGGTAATCTGACATTTGTACTTTGCATTTATCTTCA 2880
QY |||||
Db 2881 TCTTTCCGCTGATGGGAATGCAACTGTTCCGAAAGAAATTTATCATGATCAAGAGCCGCT 2940
QY |||||
Db 2881 TCTTTCCGCTGATGGGAATGCAACTGTTCCGAAAGAAATTTATCATGATCAAGAGCCGCT 2940
QY |||||
Db 2941 TTCGGATGGCAGCTGCGCGCTGGAATTCACCGACTTTTATGCACAGCTTCATGATCG 3000
QY |||||
Db 2941 TTCGGATGGCAGCTGCGCGCTGGAATTCACCGACTTTTATGCACAGCTTCATGATCG 3000
QY |||||
Db 3001 TGTTCGCGTGTCTCGGAGATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGG 3060
QY |||||
Db 3001 TGTTCGCGTGTCTCGGAGATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGG 3060
QY |||||
Db 3061 ATGCTCGTGATTCCTTCTTGGCCACCGTGTCTCATCGGCAATCTTGGTACTTA 3120
QY |||||
Db 3061 ATGCTCGTGATTCCTTCTTGGCCACCGTGTCTCATCGGCAATCTTGGTACTTA 3120
QY |||||
Db 3121 ACCTTTCTTAGCCTTGTCTTGTGCAATTTTGGCTTCATCTAGCTTATCAGGCGCGACTG 3180
QY |||||
Db 3121 ACCTTTCTTAGCCTTGTCTTGTGCAATTTTGGCTTCATCTAGCTTATCAGGCGCGACTG 3180
QY |||||

Db 3181 CCGATAACGATACGATAAATAGCCGAGGCGCTTCAATCGAATTTGGCCGATTTAAAGTT 3240
QY |||||
Db 3181 CCGATAACGATACGATAAATAGCCGAGGCGCTTCAATCGAATTTGGCCGATTTAAAGTT 3240
QY |||||
Db 3241 GGGTTAAAGCGTAATATTCCTGATTGTTTCAAGTTAATAGTAACAAATTTGACAAATCAA 3300
QY |||||
Db 3241 GGGTTAAAGCGTAATATTCCTGATTGTTTCAAGTTAATAGTAACAAATTTGACAAATCAA 3300
QY |||||
Db 3301 TAAATGATCAACCATACGTTGAGAGGACCAACAGATCAGTTGGATTTGGAGCGAAGAGC 3360
QY |||||
Db 3301 TAAATGATCAACCATACGTTGAGAGGACCAACAGATCAGTTGGATTTGGAGCGAAGAGC 3360
QY |||||
Db 3361 ATGTGTCAACGAAGTGGAGCTGGGCCACGAGAGATCCTCGCCAGCGCCTCATCAAGA 3420
QY |||||
Db 3361 ATGTGTCAACGAAGTGGAGCTGGGCCACGAGAGATCCTCGCCAGCGCCTCATCAAGA 3420
QY |||||
Db 3421 AGGGATCAAGGAGCAGACGCAACTGGAGTGGCCATCGGATCGGATCGAATTCACGA 3480
QY |||||
Db 3421 AGGGATCAAGGAGCAGACGCAACTGGAGTGGCCATCGGATCGGATCGAATTCACGA 3480
QY |||||
Db 3481 TACACGGCGACATGAAGAACCAACAGCCGAAGAAATCCAAATATCTAAATACGCAACGA 3540
QY |||||
Db 3481 TACACGGCGACATGAAGAACCAACAGCCGAAGAAATCCAAATATCTAAATACGCAACGA 3540
QY |||||
Db 3541 TGATTTGCAACTCAATTAACCAACAGACAATAGACTGGAACACAGCTAAACCATAGAG 3600
QY |||||
Db 3541 TGATTTGCAACTCAATTAACCAACAGACAATAGACTGGAACACAGCTAAACCATAGAG 3600
QY |||||
Db 3601 GTTTCTCTTACAGGACGACGACCTGCCAGCATTAATCATATGTTAGCCATAAGAATC 3660
QY |||||
Db 3601 GTTTCTCTTACAGGACGACGACCTGCCAGCATTAATCATATGTTAGCCATAAGAATC 3660
QY |||||
Db 3661 GACCAATTCAGGACGAGACCAAGGCGCAGACGATGGAGCGGAGGCGGAGGAGAGC 3720
QY |||||
Db 3661 GACCAATTCAGGACGAGACCAAGGCGCAGACGATGGAGCGGAGGCGGAGGAGAGC 3720
QY |||||
Db 3721 GCGAGCGCAGAACGAGGATTTAGTCTCGAGAGGAACTGACAGAGGAGGCGAATCGG 3780
QY |||||
Db 3721 GCGAGCGCAGAACGAGGATTTAGTCTCGAGAGGAACTGACAGAGGAGGCGAATCGG 3780
QY |||||
Db 3781 AGGAGGCGCGCTCGACGCTGATATCATTTATTCATGCACAGCAGGATATACTCGATG 3840
QY |||||
Db 3781 AGGAGGCGCGCTCGACGCTGATATCATTTATTCATGCACAGCAGGATATACTCGATG 3840
QY |||||
Db 3841 AATATCCAGCTGATTCGCTGCCCGATTCGTACTATAAGAAATTTCCGATCTTAGCCGCTG 3900
QY |||||
Db 3841 AATATCCAGCTGATTCGCTGCCCGATTCGTACTATAAGAAATTTCCGATCTTAGCCGCTG 3900
QY |||||
Db 3901 AGGATGACTCGCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAACTTTTCAATTA 3960
QY |||||
Db 3901 AGGATGACTCGCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAACTTTTCAATTA 3960
QY |||||
Db 3961 TTGAAATTAATATTTTGAACAGCTGTTATCAGTATGATTTTATAGTAGCTTAGCTT 4020
QY |||||
Db 3961 TTGAAATTAATATTTTGAACAGCTGTTATCAGTATGATTTTATAGTAGCTTAGCTT 4020
QY |||||
Db 4021 TGGCAATTAAGAGTGTACATCTGCACAAAGACCCATCTGAGGATATTTTATATACTATA 4080
QY |||||
Db 4021 TGGCAATTAAGAGTGTACATCTGCACAAAGACCCATCTGAGGATATTTTATATACTATA 4080
QY |||||
Db 4081 TGGACAGAAATTTACGCTTATTTCTTTGGAAATGTTAATCAAGTGGTTGGGCGCTCG 4140
QY |||||
Db 4081 TGGACAGAAATTTACGCTTATTTCTTTGGAAATGTTAATCAAGTGGTTGGGCGCTCG 4140
QY |||||
Db 4141 GCTTCAAGTGTACTTACCAACGCGTGTGGCTCGATTTGCTGATTTGCTATGCTAT 4200
QY |||||
Db 4141 GCTTCAAGTGTACTTACCAACGCGTGTGGCTCGATTTGCTGATTTGCTATGCTAT 4200
QY |||||
Db 4201 CGCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTATTAAGCCTTCAAGACTA 4260
QY |||||
Db 4201 CGCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTATTAAGCCTTCAAGACTA 4260
QY |||||
Db 4261 TCCGAACGTTAAGAGCACTGAGACCACTACGTGCCATGTCCCGTATGCGGCGCATGAGG 4320

|||||
QY 4261 TGGAAAGCTTAAGACACTGAGACCCTAGCTGCGCATGTCCCGTATGCAAGGCATGAGGG 4320
Db 4321 TCGTCGTTAATCGCTGGTACAGCATATACGCTCCATCTTCATGTGCTATTGGTGTGC 4380
QY 4321 TCGTCGTTAATCGCTGGTACAGCATATACGCTCCATCTTCATGTGCTATTGGTGTGC 4380
Db 4381 TAATATTTTGGCTAAATTTTGGCCATAATGGGTGTACAGCTTTTTCGTGGAAATATATTTA 4440
QY 4381 TAATATTTTGGCTAAATTTTGGCCATAATGGGTGTACAGCTTTTTCGTGGAAATATTTA 4440
Db 4441 AGTCGAGGACATGAATGGCAGCAAGCTCAGCCACGAGATCATACCAAAATCGCAATGCCT 4500
QY 4441 AGTCGAGGACATGAATGGCAGCAAGCTCAGCCACGAGATCATACCAAAATCGCAATGCCT 4500
Db 4501 GCGAGCGGAGAACTACAGCTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAACG 4560
QY 4501 GCGAGCGGAGAACTACAGCTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAACG 4560
Db 4561 CGTATCTGTGCTTTTCCAAAGTGCCACCTTCAAAGGCTGGATACAAATCATGAACGATG 4620
QY 4561 CGTATCTGTGCTTTTCCAAAGTGCCACCTTCAAAGGCTGGATACAAATCATGAACGATG 4620
Db 4621 CTATCGATTCAGAGAGTGGACAAAGCAACCAATTCGTGAACAAATCATGTATT 4680
QY 4621 CTATCGATTCAGAGAGTGGACAAAGCAACCAATTCGTGAACAAATCATGTATT 4680
Db 4681 TATATTCGTATTCTTCATCATATTTGGATGCTTTTTCACACTCAATCTGTTCAATGGTG 4740
QY 4681 TATATTCGTATTCTTCATCATATTTGGATGCTTTTTCACACTCAATCTGTTCAATGGTG 4740
Db 4741 TTATCATTTGATAATTTTAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 4800
QY 4741 TTATCATTTGATAATTTTAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 4800
Db 4801 TGACAGAGATCAGAAAGTACTATATGCTATGAAAGAGTGGGCTCTAAAAACCAT 4860
QY 4801 TGACAGAGATCAGAAAGTACTATATGCTATGAAAGAGTGGGCTCTAAAAACCAT 4860
Db 4861 TAAAGCCATTCCAAAGCAAGTGGGACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 4920
QY 4861 TAAAGCCATTCCAAAGCAAGTGGGACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 4920
Db 4921 ATAAGAAATTCGATATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 4980
QY 4921 ATAAGAAATTCGATATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 4980
Db 4981 TCGATCGTTAGCATGCGTCGACACGATATACGGCGTCTTAGACTATCTCAATCGGATAT 5040
QY 4981 TCGATCGTTAGCATGCGTCGACACGATATACGGCGTCTTAGACTATCTCAATCGGATAT 5040
Db 5041 TCGTAGTTATTTTTCAGTTCCCAATGCTCTATTAATAATTTTCGCTTTACGATATCACTATT 5100
QY 5041 TCGTAGTTATTTTTCAGTTCCCAATGCTCTATTAATAATTTTCGCTTTACGATATCACTATT 5100
Db 5101 TTATGAGCCATGGAATTTATTTGATGAGTGTGATGATGATGATGATGATGATGATGATGATG 5160
QY 5101 TTATGAGCCATGGAATTTATTTGATGAGTGTGATGATGATGATGATGATGATGATGATGATG 5160
Db 5161 TACTTAGCGATATATCAGAAAGTACTTCGTGTCGCCACCTGCTCCGAGTGGTGGTG 5220
QY 5161 TACTTAGCGATATATCAGAAAGTACTTCGTGTCGCCACCTGCTCCGAGTGGTGGTG 5220
Db 5221 TGGCAAAAGTGGGCGGTGCTCTTCAGTTGGTGAAGGAGCAAGGCAATTCGGACACTGC 5280
QY 5221 TGGCAAAAGTGGGCGGTGCTCTTCAGTTGGTGAAGGAGCAAGGCAATTCGGACACTGC 5280
Db 5281 TCTTCGCTTGGCCATGTCGTCGGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTG 5340
QY 5281 TCTTCGCTTGGCCATGTCGTCGGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTG 5340
Db 5341 TCATGTTCTATCTTTCGCAATTTTCGCAATTTTCGCAATTTTCGCAATTTTCGCAATTTTCGCA 5400
|||||

QY 5341 TCATGTTCTATCTTTGCCATTTTTCGCAATTTTTCGCAATTTTTCGCAATTTTTCGCAATTTTTCG 5400
Db 5401 GCATTAACGACGCTTACAACTTTCAAGACCTTTGGCCAGAGCATGATCTGCTCTTTTCA 5460
QY 5401 GCATTAACGACGCTTACAACTTTCAAGACCTTTGGCCAGAGCATGATCTGCTCTTTTCA 5460
Db 5461 TGTGACGCTCAGCCGTTGGGATGCTGACGAGCCATTTAATGAGGAAGCATGCG 5520
QY 5461 TGTGACGCTCAGCCGTTGGGATGCTGACGAGCCATTTAATGAGGAAGCATGCG 5520
Db 5521 ATTCACCCACAGCAGCAAAAGGCTATCGGGCAATTTGTTGTTTCAGGACCCGTTGGAATAA 5580
QY 5521 ATTCACCCACAGCAGCAAAAGGCTATCGGGCAATTTGTTGTTTCAGGACCCGTTGGAATAA 5580
Db 5581 CGTTTCTCTCTCATACCTAGTTAAGCTTTTGTATAGTTTATTAATGTTACATTGCTG 5640
QY 5581 CGTTTCTCTCTCATACCTAGTTAAGCTTTTGTATAGTTTATTAATGTTACATTGCTG 5640
Db 5641 TCATTTCTGAGAACTATAGTCAGGCCACCGAGACGTGCAAGAGGCTCTAACCGACGCG 5700
QY 5641 TCATTTCTGAGAACTATAGTCAGGCCACCGAGACGTGCAAGAGGCTCTAACCGACGCG 5700
Db 5701 ACTACGACATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGCAACCCAGTACATAC 5760
QY 5701 ACTACGACATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGCAACCCAGTACATAC 5760
Db 5761 GCTATGATCAGCTGTCCGAAATTCCTGAGCTACTGAGGCCCGCTGCGATCCCAAAAC 5820
QY 5761 GCTATGATCAGCTGTCCGAAATTCCTGAGCTACTGAGGCCCGCTGCGATCCCAAAAC 5820
Db 5821 CGAACAAGTACAAGATCATATCGATGGACATACCCATCTGTCGCGTGACCTCATCTACT 5880
QY 5821 CGAACAAGTACAAGATCATATCGATGGACATACCCATCTGTCGCGTGACCTCATCTACT 5880
Db 5881 GCGTCACATCTCTGAGCCCTTACGAAAGACTTCTTTGCGGGGAAGGCAATCCGATAG 5940
QY 5881 GCGTCACATCTCTGAGCCCTTACGAAAGACTTCTTTGCGGGGAAGGCAATCCGATAG 5940
Db 5941 AGGAGACGGGTGAGATTGGTGAGATACGCGCCCGCCGATACGGAGGCTACGAGCCCG 6000
QY 5941 AGGAGACGGGTGAGATTGGTGAGATACGCGCCCGCCGATACGGAGGCTACGAGCCCG 6000
Db 6001 TCTCATCAACGCTGTGGCGTACGCGTACGAGTACTGCGCCCGCTAAATCCAGACGCT 6060
QY 6001 TCTCATCAACGCTGTGGCGTACGCGTACGAGTACTGCGCCCGCTAAATCCAGACGCT 6060
Db 6061 GCGAAGACACAGCGCGCGGAGGAGTGGGTCTTTGAGCCGATACGGATCATG 6120
QY 6061 GCGAAGACACAGCGCGCGGAGGAGTGGGTCTTTGAGCCGATACGGATCATG 6120
Db 6121 GCGATGCGGTGATCCGCGGACCCGCGGCGCTGATGAAGCAAGGAGCGGATG 6180
QY 6121 GCGATGCGGTGATCCGCGGACCCGCGGCGCTGATGAAGCAAGGAGCGGATG 6180
Db 6181 CGCCCGTGTGAGATGTTAGTGTAAAGTACTGAGAGGAGTGGCGGATGCGGATG 6240
QY 6181 CGCCCGTGTGAGATGTTAGTGTAAAGTACTGAGAGGAGTGGCGGATGCGGATG 6240
Db 6241 AGAGTAAATGTAATAGTCCGGGTGAGATGCAAGGAGTGGGTCTTTGAGCCGATACGGATCATG 6300
QY 6241 AGAGTAAATGTAATAGTCCGGGTGAGATGCAAGGAGTGGGTCTTTGAGCCGATACGGATCATG 6300
Db 6301 CGCGCGCGGCGGACGACGCGGAGTCCCGGAGCGGCTAGCGCGCGGCGGACAG 6360
QY 6301 CGCGCGCGGCGGACGACGCGGAGTCCCGGAGCGGCTAGCGCGCGGCGGACAG 6360
Db 6361 CGCGCGTCTCTGAGAGCGCGGTTGTTGAGAGAAAGCGGCAAGAGTGGTGTATCC 6420
QY 6361 CGCGCGTCTCTGAGAGCGCGGTTGTTGAGAGAAAGCGGCAAGAGTGGTGTATCC 6420
Db 6421 ACTCGGATCGCGAGCATCAGCTCGCGACGCGGATGTTCTGAGCGAGGAGGAGGCG 6480
QY 6421 ACTCGGATCGCGAGCATCAGCTCGCGACGCGGATGTTCTGAGCGAGGAGGAGGCG 6480

Db 6481 CCTCCTCAAGATGACGCGGAGTATTAGTCTTAGA 6513
QY 6481 CCTCCTCAAGATGACGCGGAGTATTAGTCTTAGA 6513

RESULT 2
ID US-08-808-793-24 STANDARD; DNA; UNC; 6519 BP.
AC xxxxxx

DT Sequence 24, Application US/08808793
DE Sequence 24, Application US/08808793
CC GENERAL INFORMATION:
CC APPLICANT: Soderlund, David M.
CC APPLICANT: Ingles, Patricia J.
CC TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
CC TITLE OF INVENTION: AND USE THEREOF
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
CC STREET: Clinton Square, P.O. Box 1051
CC CITY: Rochester
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 14603

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/808,793
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 60/034,361
CC FILING DATE: 24-DEC-1996
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 60/012,649
CC FILING DATE: 01-MAR-1996
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Braman, Susan J.
CC REGISTRATION NUMBER: 34,103
CC REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 716-263-1636
CC TELEFAX: 716-263-1600
CC INFORMATION FOR SEQ ID NO: 24:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6519 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC SEQUENCE 6519 BP; 1707 A; 1544 C; 1698 G; 1570 T; 0 OTHER.

Query Match 84 48; Score 5500; DB 21; Length 6519;
Best Local Similarity 97.7; Pred. No. 0.00e+00;
Matches 6337; Conservative 0; Mismatches 9; Indels 138; Gaps 3;

Db 1 ATGACAGAAGATCCCGACTCGATATCTGAGGAAGACGGCAGTTTGTTCGCTCCCTTTACC 60
QY 24 ATGACAGAAGATCCCGACTCGATATCTGAGGAAGACGGCAGTTTGTTCGCTCCCTTTACC 83

Db 61 CGCGAATCATTGGTGCATAATCGAACACGATTCGCGCTGAACATGAAAAGCAGAAGGAG 120
QY 84 CGCGAATCATTGGTGCATAATCGAACACGATTCGCGCTGAACATGAAAAGCAGAAGGAG 143

Db 121 CTGGAAGAAGAGAGCCGAGGAGAGGTCCCGCGATATGGTCGCAAGAAAAACAAAAA 180
QY 144 CTGGAAGAAGAGAGCCGAGGAGAGGTCCCGCGATATGGTCGCAAGAAAAACAAAAA 203

Db 181 GAAATCCGATATGATGACGAGGACGAGGATGAAGGTCCACAACCGGATCCTACACTTGA 240
QY 204 GAAATCCGATATGATGACGAGGACGAGGATGAAGGTCCACAACCGGATCCTACACTTGA 263

Db 241 CAGGGTGTCCCAATACCTGTTTCGATTGCGAGGAGAGTTCCCGCCGGAATGGCCTCACT 300
QY 264 CAGGGTGTCCCAATACCTGTTTCGATTGCGAGGAGAGTTCCCGCCGGAATGGCCTCACT 323

Db 301 CCTCTCGAGGATATGATCCCTACTACAGCAATGTACTGACATTCCTAGTGTGTAAGCAAA 360
QY 324 CCTCTCGAGGATATGATCCCTACTACAGCAATGTACTGACATTCCTAGTGTGTAAGCAAA 383

Db 361 GGAAGAAGATATTTTCGCTTTTCTGCAATCAAAAGCAATGTGATGCTCGATCCATCAAT 420
QY 384 GGAAGAAGATATTTTCGCTTTTCTGCAATCAAAAGCAATGTGATGCTCGATCCATCAAT 443

Db 421 CGGATACGTCGTGTGGCCATTTACATTCCTAGTGCATCCATTTATTTCCCTATTTCATCATC 480
QY 444 CGGATACGTCGTGTGGCCATTTACATTCCTAGTGCATCCATTTATTTCCCTATTTCATCATC 503

Db 481 ACCACAATTCGTCAACTGCATCCTGATGATAATCCGACACGCCCGGTTGAGTCC 540
QY 504 ACCACAATTCGTCAACTGCATCCTGATGATAATCCGACACGCCCGGTTGAGTCC 563

Db 541 ACTGAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGTAGTGGCACA 600
QY 564 ACTGAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGTAGTGGCACA 623

Db 601 GGTTCATTTTATGCGCGTTTACGATCTTAGAGATGCAATGGAATGGGTGGACTTCGTA 660
QY 624 GGTTCATTTTATGCGCGTTTACGATCTTAGAGATGCAATGGAATGGGTGGACTTCGTA 683

Db 661 GTAATAGCTTTAGCTTATCTGACCATGGTATAGATTTAGGTAATCTAGCAGCCCTGCGA 720
QY 684 GTAATAGCTTTAGCTTATCTGACCATGGTATAGATTTAGGTAATCTAGCAGCCCTGCGA 743

Db 721 AGCTTTAGGTTGCTGCGAGCGCTTAAACCGTAGCCATTTGTCAGGCTTGAAGACCATC 780
QY 744 AGCTTTAGGTTGCTGCGAGCGCTTAAACCGTAGCCATTTGTCAGGCTTGAAGACCATC 803

Db 781 GTCGCGCGCTCATCGAATCGGTGAAGAATCTGCGCGATGTGATATCTCGACCATGTTTC 840
QY 804 GTCGCGCGCTCATCGAATCGGTGAAGAATCTGCGCGATGTGATATCTCGACCATGTTTC 863

Db 841 TCCTCTCGGTGTTCCGGTTGATGGCCCTACAGATCTATATGGCGTGTCTCACCAGAGAAG 900
QY 864 TCCTCTCGGTGTTCCGGTTGATGGCCCTACAGATCTATATGGCGTGTCTCACCAGAGAAG 923

Db 901 TGCATCAAGAAGTTCCCGCTGGACGGTTCTGGGGCAATCTGACCCAGAGAACTGGGAC 960
QY 924 TGCATCAAGAAGTTCCCGCTGGACGGTTCTGGGGCAATCTGACCCAGAGAACTGGGAC 983

Db 961 TATCACAATCGCAATAGTCCCAATGGTATTCGAGGACGAGGGCATCTCATTTCCGTTA 1020
QY 984 TATCACAATCGCAATAGTCCCAATGGTATTCGAGGACGAGGGCATCTCATTTCCGTTA 1043

Db 1021 TCGGGCAATATATCCCGTGGGGGCAATCGGACGAGATTACGTGTCCCTGCAGGGGTTT 1080
QY 1044 TCGGGCAATATATCCCGTGGGGGCAATCGGACGAGATTACGTGTCCCTGCAGGGGTTT 1103

Db 1081 GGTCCGAATCCGAATTTATGGCTACACAGCTTCGATTGTTTCGGATGGGCTTTCCCTGTCC 1140
QY 1104 GGTCCGAATCCGAATTTATGGCTACACAGCTTCGATTGTTTCGGATGGGCTTTCCCTGTCC 1163

Db 1141 GCCTTCGGCTGATACACAGGACTTCTGGGAGATCTGTACCAGCTGTGTGTTCGCGCC 1200
QY 1164 GCCTTCGGCTGATACACAGGACTTCTGGGAGATCTGTACCAGCTGTGTGTTCGCGCC 1223

Db 1201 GCGGACCATGGACATGCTGTTCTTTATAGTCATCATCTTCCTAGGTTCAATTCATCTT 1260
QY 1224 GCGGACCATGGACATGCTGTTCTTTATAGTCATCATCTTCCTAGGTTCAATTCATCTT 1283

QY 3444 CTGGAGTGGCCATCGGGATCGGATGGAATTCACGATACACGGCGACATGAAGAACAC 3503
Db 3418 AAGCGAAGAAATCCAAATATCTAAATAACGCAACG----- 3453
QY 3504 AAGCGAAGAAATCCAAATATCTAAATAACGCAACGATGATTGGCAACTCAATTAACCCAC 3563
Db 3454 -----CAGCAGCAG 3462
QY 3564 CAAGACAATAGACTGGAACACGAGCTAAACCATAGAGGTTTGTCTTACAGGACGACGAC 3623
Db 3463 ACTGCCAGCAATTAACATCATATGGTAGCCATAAGAAATCGACCAATTAAGAGCAGAGACCCAC 3522
QY 3624 ACTGCCAGCAATTAACATCATATGGTAGCCATAAGAAATCGACCAATTAAGAGCAGAGACCCAC 3683
Db 3523 AAGGCGAGCGCCGAGACGATGAGGCGGAGGAGAGCGCGACGCCAGCAAGGAGGATTTA 3582
QY 3684 AAGGCGAGCGCCGAGACGATGAGGCGGAGGAGAGAGCGCGACGCCAGCAAGGAGGATTTA 3743
Db 3583 GGTCTCGAGCAGAACTGACGAGGAGGCGGAATGCGAGGAGGCGCGCTCGACGGTGAT 3642
QY 3744 GGTCTCGAGCAGAACTGACGAGGAGGCGGAATGCGAGGAGGCGCGCTCGACGGTGAT 3803
Db 3643 ATCATTAATTCAGCACACGACGAGGATATCTCGATGAATATCCAGCTGATTCGCTGCCCC 3702
QY 3804 ATCAATTAATTCAGCACACGACGAGGATATCTCGATGAATATCCAGCTGATTCGCTGCCCC 3863
Db 3703 GATTCGTACTATAAGAAATTTCCGATCTTAGCGCGGTGACGATGACTCGCGCTTCTGGCAA 3762
QY 3864 GATTCGTACTATAAGAAATTTCCGATCTTAGCGCGGTGACGATGACTCGCGCTTCTGGCAA 3923
Db 3763 GATGGGGCAATTTACGACTGAAACTTTTTCGATTAATTTGAGGATAAATATTTTGAACA 3822
QY 3924 GATGGGGCAATTTACGACTGAAACTTTTTCGATTAATTTGAAATAAATATTTTGAACA 3983
Db 3823 GCTGTTATCAGTATGATTTTATGAGTAGCTTAGCTTTGCGCATTAGAAGATGATACATCG 3882
QY 3984 GCTGTTATCAGTATGATTTTATGAGTAGCTTAGCTTTGCGCATTAGAAGATGATACATCG 4043
Db 3883 CCACAAAGACCCATAGCTGAGGATATTTTATATATATGACAGAGATATTTACGGTTATA 3942
QY 4044 CCACAAAGACCCATAGCTGAGGATATTTTATATATGACAGAGATATTTACGGTTATA 4103
Db 3943 TTCTTCTTGGAAATGTAATCAAGTGGTTGGCGCTCGGCTTCAAAGTGATCTTGACCAAC 4002
QY 4104 TTCTTCTTGGAAATGTAATCAAGTGGTTGGCGCTCGGCTTCAAAGTGATCTTGACCAAC 4163
Db 4003 GCGTGGTGTGGCTCGATTCGATTTGATGTCATGGTATCCGTTATCAACTTCGTTGCTTCA 4062
QY 4164 GCGTGGTGTGGCTCGATTTGCGATTTGATGGTATCGCTTATCAACTTCGTTGCTTCA 4223
Db 4063 CTGTTGGAGCTGGTGGTATTCAGGCTTCAAGACTATCGCAACGTTAAGAGCACTGAGA 4122
QY 4224 CTGTTGGAGCTGGTGGTATTCAGGCTTCAAGACTATCGCAACGTTAAGAGCACTGAGA 4283
Db 4123 CCACACTAGTGCCATGTCGCTATGACGGCATGAGGCTCGCTTAATCGCTGCTGATCAA 4182
QY 4284 CCACACTAGTGCCATGTCGCTATGACGGCATGAGGCTCGCTTAATCGCTGCTGATCAA 4343
Db 4183 GCTATACCTGCATCTTCAATGTGCTATTTGGTGTGCTAATATTTGGCTAATTTTGGC 4242
QY 4344 GCTATACCTGCATCTTCAATGTGCTATTTGGTGTGCTAATATTTTGGCTAATTTTGGC 4403
Db 4243 ATAAATGGGTGATACAGCTTTTGTGGAATAATTTTAAAGTCGAGGACATGAATGCGACG 4302
QY 4404 ATAAATGGGTGATACAGCTTTTGTGGAATAATTTTAAAGTCGAGGACATGAATGCGACG 4463
Db 4303 AAGCTCAGCCACGAGATCATACCAATTCGCAATGCTTGCAGAGCGAGAACTACACGTGG 4362
QY 4464 AAGCTCAGCCACGAGATCATACCAATTCGCAATGCTTGCAGAGCGAGAACTACACGTGG 4523
Db 4363 GTCAATTCAGCAATGAATTCGATCATATGAGTAACGCGTATCTGTCCCTTTTCCAAAGTG 4422
QY 4524 GTCAATTCAGCAATGAATTCGATCATATGAGTAACGCGTATCTGTGCCTTTTCCAAAGTG 4583

Db 4423 GCCACCTTCAAAGGCTGGATACAAATCATGAACGATGCTATCGATTACGAGAGGTGGAC 4482
QY 4584 GCCACCTTCAAAGGCTGGATACAAATCATGAACGATGCTATCGATTACGAGAGGTGGAC 4643
Db 4483 AAGCAACCAATTCGTAACAGNACATCTACATGATATTTATATTTCGTATCTTCAATCATA 4542
QY 4644 AAGCAACCAATTCGTAACAGNACATCTACATGATATTTATATTTCGTATCTTCAATCATA 4703
Db 4543 TTTGGATCATTTTCCACACTCAATCTGTTTCAATGTGTTTATCATTTGATAATTTTAAATGAG 4602
QY 4704 TTTGGATCTTTTCCACACTCAATCTGTTTCAATGTGTTTATCATTTGATAATTTTAAATGAG 4763
Db 4603 CAAAAGAAAAAGCAGGTGGATCATTTAGAAATTTTCATGACAGAAAGATCAGAAAAAGTAC 4662
QY 4764 CAAAAGAAAAAGCAGGTGGATCATTTAGAAATTTTCATGACAGAAAGATCAGAAAAAGTAC 4823
Db 4663 TATAGTGTCTATGAAAAAGATGGGCTCTAAAAACCATTAAAGCCATTCCCAAGACCAAGG 4722
QY 4824 TATAATGTCTATGAAAAAGATGGGCTCTAAAAACCATTAAAGCCATTCCCAAGACCAAGG 4883
Db 4723 TGGCCACACAGCAATAGTCTTTGAAATAGTAACCGATAGAAATTCGATATATCATTT 4782
QY 4884 TGGCCACACAGCAATAGTCTTTGAAATAGTAACCGATAGAAATTCGATATATCATTT 4943
Db 4783 ATGTTATTCAATTTGGTCTGAACATGTTCCACCATGACCCCTCGATCGTTACGATCGCTCGGAC 4842
QY 4944 ATGTTATTCAATTTGGTCTGAACATGTTCCACCATGACCCCTCGATCGTTACGATCGCTCGGAC 5003
Db 4843 AGGTATAACGGGCTCCTAGACTATCTCAATGCGATATTCGTAGTTATTTTCAGTTCCGAAA 4902
QY 5004 AGGTATAACGGGCTCCTAGACTATCTCAATGCGATATTCGTAGTTATTTTCAGTTCCGAAA 5063
Db 4903 TGTCTATTAAAAAATATCGCTTTAGCATATCACTATTTATTAGCCCATGGATTTATTT 4962
QY 5064 TGTCTATTAAAAAATATCGCTTTAGCATATCACTATTTATTAGCCCATGGATTTATTT 5123
Db 4963 GATGTAGTAGTTGTCTATTTTATCCATCTTAGTCTTTGACTTTAGCGATATTTATCGAAGAG 5022
QY 5124 GATGTAGTAGTTGTCTATTTTATCCATCTTAGTCTTTGACTTTAGCGATATTTATCGAAGAG 5183
Db 5023 TACTTCGTGTCGCCGACCCCTGCTCCGAGTGGTGGTGGCGGAGAAAGTGGGCGGTGCTCCT 5082
QY 5184 TACTTCGTGTCGCCGACCCCTGCTCCGAGTGGTGGTGGCGGAGAAAGTGGGCGGTGCTCCT 5243
Db 5083 CGACTGTTGAAGGGAGCCCAAGGGCATTCGGACACTGCTCTTCGCGTTGGCCATGTCGCTG 5142
QY 5244 CGACTGTTGAAGGGAGCCCAAGGGCATTCGGACACTGCTCTTCGCGTTGGCCATGTCGCTG 5303
Db 5143 CGGCGCCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5202
QY 5304 CGGCGCCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5363
Db 5203 GGCATGTCGTTCTTCATGCACTGAAGGAGAGAGCGGCAATTAAGCACTCTACAACTTC 5262
QY 5364 GGCATGTCGTTCTTCATGCACTGAAGGAGAGAGCGGCAATTAAGCACTCTACAACTTC 5423
Db 5263 AAGACCTTTGGCCAGCAGCATGATCTGCTCTTTTCAAGTGTGACGTGACGCGGTTGGGAT 5322
QY 5424 AAGACCTTTGGCCAGCAGCATGATCTGCTCTTTTCAAGTGTGACGTGACGCGGTTGGGAT 5483
Db 5323 GGTGTACTGGAGCCCATTTATCAATGAGGAAGCATGCGATCCACCCGACACCAACAAGGC 5382
QY 5484 GGTGTACTGGAGCCCATTTATCAATGAGGAAGCATGCGATCCACCCGACACCAACAAGGC 5543
Db 5383 TATCCGGGCAATTTGGTTTACGCGCGGTTGGAATAACGTTTCTCTCTCATACCTAGTT 5442
QY 5544 TATCCGGGCAATTTGGTTTACGCGCGGTTGGAATAACGTTTCTCTCTCATACCTAGTT 5603
Db 5443 ATAAAGCTTTTGTATAGTTATTAATATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5502
QY 5604 ATAAAGCTTTTGTATAGTTATTAATATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5663

QY 2724 GGTGTCCAGGGTGTGTCCGTATGGCTTCTCCATTCGATTCGCTGTATTCATAAACTGGCC 2783
Db 2698 AGTCTTGGCCACACTTAATTTACTTCATTCGATTTATGGAGCAGCACCATGGCGCTTTG 2757
QY 2784 AGTCTTGGCCACACTTAATTTACTTCATTCGATTTATGGAGCAGCACCATGGCGCTTTG 2843
Db 2758 GGTAACTCTGACATTTGACTTTTGCAATTCATCTTCATCTTTGCGGTGATGGGAATGCAA 2817
QY 2844 GGTAACTCTGACATTTGACTTTTGCAATTCATCTTCATCTTTGCGGTGATGGGAATGCAA 2903
Db 2818 CTGTTGGAAAGAAATATCATGATACACAGGACCGCTTTCCGGATGGCGACCTGGCGGC 2877
QY 2904 CTGTTGGAAAGAAATATCATGATACACAGGACCGCTTTCCGGATGGCGACCTGGCGGC 2963
Db 2878 TGGAACTTCACCCGACCTTATGACACAGCTTCATGATCGTGTCCGGGTGCTCTCGGAGAA 2937
QY 2964 TGGAACTTCACCCGACCTTATGACACAGCTTCATGATCGTGTCCGGGTGCTCTCGGAGAA 3023
Db 2938 TGGATCGAGTCCATGTGGGACTGCATGTAGTGGGCGGATGTCTCGTGCAATCCCTTCCTC 2997
QY 3024 TGGATCGAGTCCATGTGGGACTGCATGTAGTGGGCGGATGTCTCGTGCAATCCCTTCCTC 3083
Db 2998 TTGGCCACCGTTGTCATCGGCAATCTTGGGTACTTTAACTTTTCTTAGCCTTGTCTTTG 3057
QY 3084 TTGGCCACCGTTGTCATCGGCAATCTTGGGTACTTTAACTTTTCTTAGCCTTGTCTTTG 3143
Db 3058 TCCAAATTTTGGCTCATCTAGCTTATCAGCGCGACTGCCGATAAACGATACGAAATAAATA 3117
QY 3144 TCCAAATTTTGGCTCATCTAGCTTATCAGCGCGACTGCCGATAAACGATACGAAATAAATA 3203
Db 3118 GCGAGGCTTCAATCGAAATTTGCCGANTTTAAAGTTGGGTTAAGCGTAAATATTTGCTGAT 3177
QY 3204 GCGAGGCTTCAATCGAAATTTGCCGANTTTAAAGTTGGGTTAAGCGTAAATATTTGCTGAT 3263
Db 3178 TGTTCAGTTAATACGTAACAATTTGACAAATGACAAATGATCAACCCATCAG----- 3232
QY 3264 TGTTCAGTTAATACGTAACAATTTGACAAATGACAAATGATCAACCCATCAGGTGAG 3323
Db 3233 -----AGCATGGTGACACGAACCTGGAGCTG 3258
QY 3324 AGGACCAACAGATCAGTTGGATTTGGAGCGAAGAGCATGGTGACAACTGGAGCTG 3383
Db 3259 GGCCACAGAGATCTCTCGCGAGCGGCTCATCAGAGAGGGGATCAGAGAGAGCGCAA 3318
QY 3384 GGCCACAGAGATCTCTCGCGAGCGGCTCATCAAGAAGGGGATCAAGAGAGAGCGCAA 3443
Db 3319 CTGAGGTGGCCATCGGGGATGGCATGGAATTCACGATACACGGCGACATGAAGAACAAC 3378
QY 3444 CTGAGGTGGCCATCGGGGATCGGATGGAATTCACGATACACGGCGACATGAAGAACAAC 3503
Db 3379 AAGCCGAAGAAATCCAAATATCTTAATAACGCAACG----- 3414
QY 3504 AAGCCGAAGAAATCCAAATATCTTAATAACGCAACGATATGGCAACTCAATTAACCAAC 3563
Db 3415 -----GACGAGAC 3423
QY 3564 CAAGACAATAGACTGGAAACAGAGCTAAACCATAGAGGTTTGTCTTACAGGAGCAGCAC 3623
Db 3424 ACTGCCAGCATTAATCTCATATGTTAGCCATGAAGAAATCGACCATTCAGAGGACGAGCCAC 3483
QY 3624 ACTGCCAGCATTAATCTCATATGTTAGCCATGAAGAAATCGACCATTCAGAGGACGAGCCAC 3683
Db 3484 AAGGCGAGCGCGAGAGATGGAGGGGAGAGAGGAGCGGACCGCAGCAGAGGAGATTTA 3543
QY 3684 AAGGCGAGCGCGAGAGATGGAGGGGAGAGAGGAGCGGACCGCAGCAGAGGAGATTTA 3743
Db 3544 GGTCTCGACGAGGAACCTGGACGAGGAGGCGGAATGCGAGGAGGCGCGCTCGACGGTGTAT 3603
QY 3744 GGTCTCGACGAGGAACCTGGACGAGGAGGCGGAATGCGAGGAGGCGCGCTCGACGGTGTAT 3803
Db 3604 ATCATTTATTCACGACGAGGAGATATCTCGATGAATATCCAGCTGATTTGCTGCCCC 3663
QY 3804 ATCATTTATTCACGACGAGGAGATATCTCGATGAATATCCAGCTGATTTGCTGCCCC 3863

Db 3664 GATTCTGACTATAAGAAATTTCCGATCTTAGCCGGTGACGATGACTCGCGCTTCTTGCAA 3723
QY 3864 GATTCTGACTATAAGAAATTTCCGATCTTAGCCGGTGACGATGACTCGCGCTTCTTGCAA 3923
Db 3724 GGATGGGGCAATTTACGACGTGAAGAACTTTTCGATTAATTTGAGGATAAATATTTTGAACA 3793
QY 3924 GGATGGGGCAATTTACGACGTGAAGAACTTTTCGATTAATTTGAGGATAAATATTTTGAACA 3983
Db 3784 GCTGTATACATATGATTTTAAATGAGTAGCTTAGCTTTGGCATTAGAGATGTACATCTG 3843
QY 3984 GCTGTATACATATGATTTTAAATGAGTAGCTTAGCTTTGGCATTAGAGATGTACATCTG 4043
Db 3844 CCACAAAGACCCATACGTACGAGGATATTTTAACTATATATGACAGAAATTTTACGGTTATA 3903
QY 4044 CCACAAAGACCCATACGTACGAGGATATTTTAACTATATATGACAGAAATTTTACGGTTATA 4103
Db 3904 TTCCTCTTGGAAATGTTAAATCAAGTGGTTGGCGCTCGGCTTCAAGATGTACTTACCACAA 3963
QY 4104 TTCCTCTTGGAAATGTTAAATCAAGTGGTTGGCGCTCGGCTTCAAGATGTACTTACCACAA 4163
Db 3964 GCGTGGTGTGGCTCGATTTTCTGATTCATGCTATGCTATCGCTTATCAACTTCGTTGCTTCA 4023
QY 4164 GCGTGGTGTGGCTCGATTTTCTGATTCATGCTATGCTATCGCTTATCAACTTCGTTGCTTCA 4223
Db 4024 CTTGTTGGAGCTGGTGGTATTCAAGCCCTTCAAGACTATGCGAAGCTTTAAGACACTGAGA 4083
QY 4224 CTTGTTGGAGCTGGTGGTATTCAAGCCCTTCAAGACTATGCGAAGCTTTAAGACACTGAGA 4283
Db 4084 CCACCTACCTGGCATGTCCTGATGCGGCGATGAGGGTGGCTTAAATGCGCTGGTCAAA 4143
QY 4284 CCACCTACCTGGCATGTCCTGATGCGGCGATGAGGGTGGCTTAAATGCGCTGGTCAAA 4343
Db 4144 GCTATACCTGGCTCATCTTCAATGTGCTATTGGTGTCTCTAAATATTTTGGCTAAATTTTGGC 4203
QY 4344 GCTATACCTGGCTCATCTTCAATGTGCTATTGGTGTCTCTAAATATTTTGGCTAAATTTTGGC 4403
Db 4204 ATAATGGGTGTACACCTTTTTCGTTGGGAAATATTTTAACTGGGAGGACATGAATGGCAG 4263
QY 4404 ATAATGGGTGTACACCTTTTTCGTTGGGAAATATTTTAACTGGGAGGACATGAATGGCAG 4463
Db 4264 AAGCTCAGCCAGAGATCATACCAATCGCAATGCTCGGAGAGCGAAGCTTACACGTGG 4323
QY 4464 AAGCTCAGCCAGAGATCATACCAATCGCAATGCTCGGAGAGCGAAGCTTACACGTGG 4523
Db 4324 GTGAATTCAGCAATGAATTTTCGATCATGTAGTAACGGTATCTGTGCTTTTCCAAGTG 4383
QY 4524 GTGAATTCAGCAATGAATTTTCGATCATGTAGTAACGGTATCTGTGCTTTTCCAAGTG 4583
Db 4384 GCCACCTTCAAGGCTGGATCAAAATCATGACGATGCTATCGATTTCAGAGAGGTGAC 4443
QY 4584 GCCACCTTCAAGGCTGGATCAAAATCATGACGATGCTATCGATTTCAGAGAGGTGAC 4643
Db 4444 AAGCAACCAATTCGTGAAGCAACATCTACATGTATTATATTTTCGTATTTCTTCATCATA 4503
QY 4644 AAGCAACCAATTCGTGAAGCAACATCTACATGTATTATATTTTCGTATTTCTTCATCATA 4703
Db 4504 TTTGGATCAATTTTTCACACTCAATCTGTTTCATTTGGTGTATCATTTGATAATTTTAAATGAG 4563
QY 4704 TTTGGATCAATTTTTCACACTCAATCTGTTTCATTTGGTGTATCATTTGATAATTTTAAATGAG 4763
Db 4564 CAAAGAAAAGAGAGGTGATCATTAGAAATGTTTCATGACAGAAAGATCAGAAAAGTAC 4623
QY 4764 CAAAGAAAAGAGAGGTGATCATTAGAAATGTTTCATGACAGAAAGATCAGAAAAGTAC 4823
Db 4624 TATAGTGTCTATGAAGAAAGATGGGCTCTTAAAGAAACCATTTAAAGGCCATTCCAGACCAAGG 4683
QY 4824 TATAGTGTCTATGAAGAAAGATGGGCTCTTAAAGAAACCATTTAAAGGCCATTCCAGACCAAGG 4883
Db 4684 TGGCGACACAGCAATAGTCTTTGAAATAGTAACCGGATAAGAAATTCGATATATCATTT 4743
QY 4884 TGGCGACACAGCAATAGTCTTTGAAATAGTAACCGGATAAGAAATTCGATATATCATTT 4943

||||| 2904 CTGTCGGAAGAAATTATCATGATCACAGGACCGCTTCCGGATGGCGACCTGCGCGCG 2963
Db 2878 TGAACCTTACCAGCTTTATGACAGCTTTCATGATCGTGTTCGGGTGCTCTCGGAGAA 2937
QY 2964 TGAACCTTACCAGCTTTATGACAGCTTTCATGATCGTGTTCGGGTGCTCTCGGAGAA 3023
Db 2938 TGCATCGAGTCCATGTGGGACTGCATGTAGTGGGCGATGCTCGTGCATTCCTTCTTC 2997
QY 3024 TGCATCGAGTCCATGTGGGACTGCATGTAGTGGGCGATGCTCGTGCATTCCTTCTTC 3083
Db 2998 TTGCCACCGCTTGCATCGGCAATCTGTGCTACTTAACTTTCTTCTAGCTTGCCTTTTG 3057
QY 3084 TTGCCACCGCTTGCATCGGCAATCTGTGCTACTTAACTTTCTTCTAGCTTGCCTTTTG 3143
Db 3058 TCCAAATTTGGCTCACTAGCTTATCAGCGCCGACTGCCGATAACGATAGGAATAAATA 3117
QY 3144 TCCAAATTTGGCTCACTAGCTTATCAGCGCCGACTGCCGATAACGATAGGAATAAATA 3203
Db 3118 GCCAGGCGCTTCAATCGAATTTGCCGATTTAAAGTTGGGTTAAGCGTAATATGCTGAT 3177
QY 3204 GCCAGGCGCTTCAATCGAATTTGCCGATTTAAAGTTGGGTTAAGCGTAATATGCTGAT 3263
Db 3178 TGTTCGAAGTTAATACGTAACAAATTGACAAATCAAAATAGTATGATCAACCATCAG---- 3232
QY 3264 TGTTCGAAGTTAATACGTAACAAATTGACAAATCAAAATAGTATGATCAACCATCAGGTGAG 3223
Db 3233 -----AGCATGGTGACAAACGAACTGGAGCTG 3258
QY 3324 AGGACCAACAGATCAGTTGGATTTGGAGCGAAGAGCATGCTGACAACTGGAGCTG 3383
Db 3259 GGCACGACGAGATCTCGCCGAGCGGCTCATCAAGAGGGGATCAAGGAGCAGAGCAAA 3318
QY 3384 GGCACGACGAGATCTCGCCGAGCGGCTCATCAAGAGGGGATCAAGGAGCAGAGCAAA 3443
Db 3319 CTGAGGTGCCATCGGGGATGCGATGGAATTCAGCATACACGCGACATGAGAACAAAC 3378
QY 3444 CTGAGGTGCCATCGGGGATGCGATGGAATTCAGCATACACGCGGACATGGAACAAAC 3503
Db 3379 AAGCCGAAGAAATCCAAATATCTAAATAACGCAACG----- 3414
QY 3504 AAGCCGAAGAAATCCAAATATCTAAATAACGCAACGATGATTGGCACTCAANTTAACCAC 3563
Db 3415 -----GACGAGAC 3423
QY 3564 CAAGACAATAGACTGGAAACAGCAGCTAAACCATAGAGGTTTGTCTTTACAGGACGACGAC 3623
Db 3424 ACTGCCAGCATTAACCTCATATGTTAGCCATAAGAAATCGACCATTCAGGAGCAGAGCCAC 3483
QY 3624 ACTGCCAGCATTAACCTCATATGTTAGCCATAAGAAATCGACCATTCAGGAGCAGAGCCAC 3683
Db 3484 AAGGCGACGCCGAGAGCGATGGAGGGCGAGGAAGCGCGACGCCAGCAAGGAGGATTTA 3543
QY 3684 AAGGCGACGCCGAGAGCGATGGAGGGCGAGGAGAGCGCGACGCCAGCAGGAGGATTTA 3743
Db 3544 GGTCTCGACGAGGAACGTGAGAGGAGGGCGAATGCGAGGAGGGCGCGCTCGACGCTGAT 3603
QY 3744 GGTCTCGACGAGGAACGTGAGAGGAGGGCGAATGCGAGGAGGGCGCGCTCGACGCTGAT 3803
Db 3604 ATCAATTTATCATGCACGACGAGGATATACTCGATGAATATCCAGCTGATGCTGCCCC 3663
QY 3804 ATCAATTTATCATGCACGACGAGGATATACTCGATGAATATCCAGCTGATGCTGCCCC 3863
Db 3664 GATTCGTACTATAAGAAATTTCCGATCTTAGCCGCTGACGATGACTCGCGCTTCTGSCAA 3723
QY 3864 GATTCGTACTATAAGAAATTTCCGATCTTAGCCGCTGACGATGACTCGCGCTTCTGSCAA 3823
Db 3724 GGATGGGCAATTTACGACTGAAACCTTTTCGATTAATTTAGGATTAATATTTTGAACA 3783
QY 3924 GGATGGGCAATTTACGACTGAAACCTTTTCGATTAATTTAGGATTAATATTTTGAACA 3983
Db 3784 GCTGTTATCACTATGATTTAATGAGTAGCTTGGATTTGGATTTAGAAATGATACATCTG 3843
|||||

QY 3984 GCTGTTATCACTATGATTTTAATGAGTAGCTTAGCTTTGGCATTAGAAGATGTACATCTG 4043
Db 3844 CCACAAGACCCACTACTGCAAGGATATTTTATACTATATGACAGAAATATTTACGGTTATA 3903
QY 4044 CCACAAGACCCACTACTGCAAGGATATTTTATACTATATGACAGAAATATTTACGGTTATA 4103
Db 3904 TTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCGGCTTCAAAGTGTACTTGACCAAC 3963
QY 4104 TTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCGGCTTCAAAGTGTACTTGACCAAC 4163
Db 3964 GGTGTGTTGGCTCGATTTTCGTTGATTCATGGTATCGCTTATCAACTTCGTTGCTTCA 4023
QY 4164 GGTGTGTTGGCTCGATTTTCGTTGATTCATGGTATCGCTTATCAACTTCGTTGCTTCA 4223
Db 4024 CTTGTTGGAGCTGGTGGTATTCGAAGCTTCAAGACTATCGAAGCTTAAAGAGCACTGAGA 4083
QY 4224 CTTGTTGGAGCTGGTGGTATTCGAAGCTTCAAGACTATCGAAGCTTAAAGAGCACTGAGA 4283
Db 4084 CCACCTACGTGCCATGTCCTGATTCAGGCGATGAGGGTCTGCTTAATGGCTGGTACAA 4143
QY 4284 CCACCTACGTGCCATGTCCTGATTCAGGCGATGAGGGTCTGCTTAATGGCTGGTACAA 4343
Db 4144 GCTATACCGTCCCATCTTCAATGTGCTATTGGTGTCTAATATTTTGGCTAAATTTTGGC 4203
QY 4344 GCTATACCGTCCCATCTTCAATGTGCTATTGGTGTCTAATATTTTGGCTAAATTTTGGC 4403
Db 4204 ATAATGGGTGTACAGCTTTTTCGTGAAATATTTTAAAGTGGAGGACATGAATGGCAG 4263
QY 4404 ATAATGGGTGTACAGCTTTTTCGTGAAATATTTTAAAGTGGAGGACATGAATGGCAG 4463
Db 4264 AGCTCAGCCACGAGATCATACAAATCGCAATGCCATGGCGAGAGCAGAACTACAGTGG 4323
QY 4464 AGCTCAGCCACGAGATCATACAAATCGCAATGCCATGGCGAGAGCAGAACTACAGTGG 4523
Db 4324 GTGAATTCAGCAATGAATTCGATCATGTAGGTAAAGCGCTATCTGCTGCTTTTCCAAAGT 4383
QY 4524 GTGAATTCAGCAATGAATTCGATCATGTAGGTAAAGCGCTATCTGCTGCTTTTCCAAAGT 4583
Db 4384 GCCACCTTCAAAGGCTGGATACAAATCATGAAGCTGCTATCGATTTCAGGAGAGTGGAC 4443
QY 4584 GCCACCTTCAAAGGCTGGATACAAATCATGAAGCTGCTATCGATTTCAGGAGAGTGGAC 4643
Db 4444 AAGCAACCAATTCGTGAAAGCAACATCTACATGATTTTATTTTCGTATTCCTTCATCAT 4503
QY 4644 AAGCAACCAATTCGTGAAAGCAACATCTACATGATTTTATTTTCGTATTCCTTCATCAT 4703
Db 4504 TTTGGATCATTTTTCACATCATCTGTTCAATGCTGTTTATCATTTATTTATGAG 4563
QY 4704 TTTGGATCATTTTTCACATCATCTGTTCAATGCTGTTTATCATTTATTTATGAG 4763
Db 4564 CAAAAGAAAAAGCAGGTGGATCATTTAGAAATGTTTCATGACAGAAGATCAGAAAAAGTAC 4623
QY 4764 CAAAAGAAAAAGCAGGTGGATCATTTAGAAATGTTTCATGACAGAAGATCAGAAAAAGTAC 4823
Db 4624 TATAGTGTATGAAAAAGATGGCTCTAAAAAACCATTTAAAAAGCCATTTCCAGACCAAGG 4683
QY 4824 TATAATGCTATGAAAAAGATGGCTCTAAAAAACCATTTAAAAAGCCATTTCCAGACCAAGG 4883
Db 4684 TGGCGACCACAACCAATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATTAATCAT 4743
QY 4884 TGGCGACCACAACCAATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATTAATCAT 4943
Db 4744 ATGTTATTCATTCGCTGAAACATGTTCCACCATGACCTCGATCGTTACGATCGCTGGAC 4803
QY 4944 ATGTTATTCATTCGCTGAAACATGTTCCACCATGACCTCGATCGTTACGATCGCTGGAC 5003
Db 4804 ACGTATAACCGCGTCTAGACTATCTCAATTCGATATTCGTAGTTATTTTCAGTTCCGAA 4863
QY 5004 ACGTATAACCGCGTCTAGACTATCTCAATTCGATATTCGTAGTTATTTTCAGTTCCGAA 5063
Db 4864 TGTCTATTAATAATATTCGTTTACGATATCACTATTTTATGAGCCATGGAATTTATTT 4923
QY 5064 TGTCTATTAATAATATTCGTTTACGATATCACTATTTTATGAGCCATGGAATTTATTT 5123
|||||

Db	5245	ATCTTTGCTATCTTTGGCATGTCCTTCTTCATGCATGTCAAGAGAGAGACGGCATAAAT	5304
QY	5349	ATCTTTGGCCATTTTGGCATGTCGTCTTCATGCACTGGAAGGAGAGACGGCATTAAC	5408
Db	5305	GCTGCTATAAATTTTAAAGACATTTGGCCAAAGTATGATATGCTGTTTCAGATGCTACC	5364
QY	5409	GACGCTACAACCTTCAAGACCTTTGGCCAGAGCATGATCTGCTTTCAGATGCTCAGC	5468
Db	5365	TCAGCCGGTTGGATGGTGTGTAGATGCCATTATCAATAGGAAGATTTGGCATCCACC	5424
QY	5469	TCAGCCGGTTGGATGGTGTACTGGACGCCATTATCAATAGGAAGCATGCGATCCACC	5528
Db	5425	GACAACGACAAAGGCTATCCGGGCAATTTGTGTTTCAGCGACTGTTGGAATTAACGTTTCTC	5484
QY	5529	GACAGCGACAAAGGCTATCCGGGCAATTTGTGTTTCAGCGACCGTTGGAATTAACGTTTCTC	5588
Db	5485	CTTTTCATATCTAGTTATAAGCTTTTGTAGTATTAAATATGTACATTTGCTCATTTCTC	5544
QY	5589	CTCTCATACCTAGTTATAAGCTTTTGTAGTATTAAATATGTACATTTGCTGTCAATTC	5648
Db	5545	GACAACATAGCCAGCTACGGAGCATGTACAGGAGGCTCTCACCGACGAGATTACGAT	5604
QY	5649	GAGACTATAGTCAGGCCACCGAGGACGTGCAAGAGGCTCTAACCGAGGAGCTAGCAC	5708
Db	5605	ATGTACTACGAGATTTGGCAACAATTCGATCCGGAGGCGACCCAGTACATACGCTAGCAC	5664
QY	5709	ATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGCGACCCAGTACATACGCTATGAT	5768
Db	5665	CAGCTGTCGAGTTTCTGGACGTGTGGAGCGCCGCTGCGAGATCCACAACCGCAACAAG	5724
QY	5769	CAGCTGTCGAAATTCCTGGACGTACTGGAGCCCCGCTGCGAGATCCACAACCGCAACAAG	5828
Db	5725	TACAAAATCATATCGATGACATGCCGATATGTCGGGCGGACATGATCTACTGTGTGGAT	5784
QY	5829	TACAAGATCATATCGATGACATACCCATCTCTCCGGTGACCTCATGTACTGCGTCGAC	5888
Db	5785	ATATTGGATGCCCTGACCAAGGACTTCTTTTGGCGCAAGGGTAAATCCGATCGAGGAGACG	5844
QY	5889	ATCCTCGAGCGCCCTTACGAAAGACTTCTTTGCGCGGAAGGGCAATCCGATAGAGGAGACG	5948
Db	5845	GGTGAATTTGGTGAATAGCGGGGACCGGACCGAGGCGCTATGATCGGTCGCTCTCA	5904
QY	5949	GGTGAGATTTGGTGAATAGCGGCCCGCCGGATACGGAGGGCTACGAGCCCGTCTCATCA	6008
Db	5905	ACACTGTGCGCCACCGTGAAGGAGTACTGCGCCAAAGCTGATACAGAATTCGCTGGCG	5960
QY	6009	ACGCTGTGCGCTCAGCGTGAGGAGTACTGCGCCCGGCTTAATCCAGACGCGCTGGCG	6064

RESULT 6
ID US-08-772-512A-1 STANDARD; DNA; UNC; 6318 BP.
AC xxxxxx
DT
Sequence 1, Application US/08772512A
DE
Sequence 1, Application US/08772512A
CC
GENERAL INFORMATION:
CC
APPLICANT: Soderlund, David M.
CC
APPLICANT: Knipples, Douglas C.
CC
APPLICANT: Ingles, Patricia J.
CC
TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
CC
TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
CC
TITLE OF INVENTION: FLIES
CC
NUMBER OF SEQUENCES: 19
CC
CORRESPONDENCE ADDRESS:
CC
ADDRESS: NIXON, HARGRAVE, DEVANS & DOYLE LLP
CC
STREET: P.O. Box 1051, Clinton Square
CC
CITY: Rochester
CC
STATE: New York
CC
COUNTRY: USA
CC
ZIP: 14603
CC
COMPUTER READABLE FORM:
CC
MEDIUM TYPE: Floppy disk
CC
COMPUTER: IBM PC compatible
CC

```

CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/772,512A
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/608,618
CC FILING DATE: 01-MAR-1996
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Braham, Susan J.
CC REGISTRATION NUMBER: 34,103
CC REFERENCE/DOCKET NUMBER: 19603/601(CRED-1657)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 716-263-1636
CC TELEFAX: 716-263-1600
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6318 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: CDNA
CC SEQUENCE 6318 BP: 1713 A; 1341 C; 1597 G; 1667 T; 0 OTHER.

Query Match 56.48; Score 3676; DB 20; Length 6318;
Best Local Similarity 84.98; Pred. No. 0.00e+00;
Matches 4986; Conservative 0; Mismatches 806; Indels 84;

```

Db 811 CTGTCGGTTCGCGCTGATGGCCCTACAAATCTATATGGTGTCTTAACACAAAAGTGC 870
 QY 867 CUGTCGGTTCGCGTGTGATGGCCCTACAGATCTATATGGGCGTCTCACCGAGAGTGC 926
 Db 871 ATTAACAGATTCCTCCCTGGAGCGCATGTGGGCAATCTGACGATGAAATGGTTCCTA 930
 QY 927 ATCAAGAAGTTCCTCCCTGGAGCGCATGTGGGCAATCTGACGAGAGAACTGGGACTAT 986
 Db 931 CACATAGCAACAGTTCCTCAATTTGGTTACGGAGAGAGATGGGAGTCTATCCGGTGTGC 990
 QY 987 CACAATCGCAATAGTCTCAATTTGGTATTCGGAGAGAGGAGATCTCATTTCCGTTATGC 1046
 Db 991 GGAATGTATTCGGTTCGGGCAATTCGGCGAGGATTAGCTGTGCTGACAGGCTTCGCG 1050
 QY 1047 GCAATATATTCGGTTCGGGCAATTCGGCGAGGATTAGCTGTGCTGACAGGCTTCGCG 1106
 Db 1051 CCAATTCCTCAATAGACTACACCAATTTGCTGATTCATTCGTTGGGCTTCCTGTGCGCG 1110
 QY 1107 CCGAATCCGAATTTATGGCTACACCAAGTTCCTGGAGGATCTGACAGCTGGTGTGGCGCGCC 1166
 Db 1111 TTTCGCTCATGACCAAGATTTCTGGGAGGATCTGTATCAGCAGCTGCTGCAACGACT 1170
 QY 1167 TTCGGCTCATGACAGAGACTTCTGGGAGGATCTGTACAGCTGGTGTGGCGCGCC 1226
 Db 1171 GGACCTGCGACATGTGTCTTATAGTATCATCTTCTAGGTTTCATCTATCTTGTG 1230
 QY 1227 GGACATGGACATGTGTCTTATAGTATCATCTTCTAGGTTTCATCTATCTTGTG 1286
 Db 1231 AATTTGATTTGGCCATGTGTGCCATCTTATAGCAATTCGAAAGAGCCCGAAGAA 1290
 QY 1287 AATTTGATTTGGCCATGTGTGCCATCTGATGACGAATTCGAAAGAGCCCGAAGAA 1346
 Db 1291 GAGAGCTGCCGAGGAGGCGATACGAGAGCTGAGAGAGCTGAGAGAGGCGCAGCAGCGG 1350
 QY 1347 GAGAGGCTGCCGAGGAGGCGATACGAGAGCTGAGAGAGCTGAGAGAGGCGCAGCAGCG 1406
 Db 1351 GCCAACTGGAGGAGGCGCAATGTAGAGCTCAAGCGGCTCAGGATGACGCGATGCC 1410
 QY 1407 GCCAACTGGAGGAGGCGCAATGTAGAGCTCAAGCGGCTCAGGATGACGCGATGCC 1466
 Db 1411 GCTGGCGAGCTCTGATCCGAGATGGCAAGAGTCCACGACTCTTTCGATTAAGTAT 1470
 QY 1467 GAAGAGGCTCACTGCTATCGGAAATGGCCAGAGTCCGACGCTATTTTCGATCACTAT 1526
 Db 1471 GAATGTTTCTGGCGGAGAGGCGCAAGTACAAACAAAGAGAGATGTCCTA 1530
 QY 1527 GAGTATTTCTGGCGGAGAGGCGCAAGTACAAACAAAGAGAGATGTCCTA 1586
 Db 1531 CGCAGCTCGAAGTGGAAATCGGAGTCCGTTAGCGTTTATACAAAGACACAGCAGCTACC 1590
 QY 1587 CGGAGCTCGAGGTGGAGTCCGAGTCCGTTAGCGTTTATACAAAGACACAGCAGCTACC 1646
 Db 1591 ACAGCAC-CC-GCTACTAAGTCCGTAAGTTAGCAGGACTCTCTTATCTTACTCTGT 1647
 QY 1647 ACAGCACCAAGCTACCAAGTTCGTAAGTGGAGCAGGACTCTTATCTTACTCTGT 1706
 Db 1648 TCACCAATTAACCTACCGCGGATACAGTACAGTTCACAAAGTACACAAATACGAAATGG 1707
 QY 1707 TCACCGTTTAACTACACGAGGAGTACAGTACAGTTCACAAAGTACAGTACGAGAGGA 1766
 Db 1708 CGTGGAGCTTTTGGTATACAGGTAGGATCGGAGGATTCGAGGATTCGAAACATATCAG 1767
 QY 1767 CGTGGCGCTTTGGTATACCGGTAGGATCGGATTCGAGGATTCGAAACATATCAG 1826
 Db 1768 GATGCCAGCAGCATTTTCCCTATGCGGATGACTTCGAAATCGGCTACACCAATGTCGAA 1827
 QY 1827 GATGCCAGCAGCAGCTTTCCCTATGCGGAGGACTTCGAAATCGGCTACCCGATGTCGAA 1886
 Db 1828 GAGATGGTGCATATATAGCAGGCTACTATTTGTAATTTAGGTTCTAGACATTTCTCA 1887
 QY 1887 GAGAAATGGGCGCATATAGTGGCGGTGTACTATGGCAATCTAGGCTCCCGCAGCAGTATC 1946
 Db 1888 TATACCTCGCATCAATCAAGAAATCTGATACATCATCGTATTTATTTGGGTGGCATG 1947

QY 1947 TATACCTCGCATCAGTCCGGAATATCGTATACCTACATGGGATCTACTCGCGGCATG 2006
 Db 1948 CGCGCATGGTCCAGCAGCAATGACAAAGAGAGCAAAATGGGAGTGGCAACACACCG 2007
 QY 2007 GCGTCTATGGGCTGACGCAATGACAAAGAGAGCAAAATGGGAGTGGCAACACACCG 2066
 Db 2008 AATCAATCAATCTGCTGCAACCAATGGTGGCAGTAGTACGGCTGGTGGTGTATCC 2067
 QY 2067 AATCAATCACT-GG-GC-GCCACCAATGGCGCACCA--C--CTG-TC-TGGACA--CC 2114
 Db 2068 GATGCCAATCACAAAGAACAAAGGATATGAAATGGGTCCAGGATATACAGACGAAGT 2127
 QY 2115 AATCACAAAGCTC--GATCATCGGACTAGCAAAATGGGCTGGAGTCCAGGACGAAGT 2171
 Db 2128 GGCNAATTAACACACGACGACAAATCTTTTATCGAGCCGCTCCAAACTCAAAACAGTGGTA 2187
 QY 2172 GGCNAATTAACACATCATGACAAATCTTTTATCGAGCCGCTCCAGACAAACGGTGGT 2231
 Db 2188 GACATGAAAGATGTATGTCTTAAATGATATCATTTGAACAGCGCTGTCGCGCATAGT 2247
 QY 2232 GATATGAAAGATGTATGTCTTAAATGATATCATTTGAACAGCGCGCTGTCGCGCATAGT 2291
 Db 2248 CGTCTAGTGAACGAGGTG-----AGGACGATGACGAGAT 2283
 QY 2292 CGGCAAGCGATCGCGTGTCTCGTTTACTATTTCCAAACAGAGGACGATGACGAGAT 2351
 Db 2284 GGTCCACATTCAGGACATCGCCCTCGAATACATCTTAAAGGCATCGAAATCTTTGT 2343
 QY 2352 GGGCGAGCTTCAAGACAAAGGACATCGAAGTATCTTCAAGGCAATCGATGTGTGT 2411
 Db 2344 GTATGGGAGCTGTTGTTGGGTGTGTTAAATTTCAAGAAATGGGTGTCCTTTATTTGTTC 2403
 QY 2412 GTGTGGGAGCTGTTGTTGGGTGTGTTAAATTTCAAGAAATGGGTGTCCTTTATTTGTTC 2471
 Db 2404 GATCCATTCGTGGAGCTCTTCATTTACCTCTGTATTTGTTGTCATAGGATTTATGCGC 2463
 QY 2472 GATCCCTTCGTGAGCTCTTCATCACGCTGTGATTTGTTGTCATAGGATTTATGCGC 2531
 Db 2464 ATGATCATCATACGACATGAATTCGGAATTTAGAGAGTGTCTGAAAAGTGTGAATTTTC 2523
 QY 2532 ATGATCACAGATGATGACAGAGATGGAAGCGCTGTCTAAGATGGCACTATTTTC 2591
 Db 2524 TTCAGCGGCACTTTTGAATTTGAAGCAGCATGAATGATGCGCCATGAGCCGCAAGTAC 2583
 QY 2592 TTCAGCGGCACTTTGCAATTCGAGCCACCATGAAGCTAATGCGCCATGAGCCCAAGTAC 2651
 Db 2584 TACTTCCAGGAGGCTGGAACATTTTCGATTTTCATTTGTTGCGCTTGTCTCTGCTGAA 2643
 QY 2652 TATTTCAGGAGGCTGGAACATTTTCGATTTTCATTTGTTGCGGCTTATCGCTATTGAA 2711
 Db 2644 TTGGCTTGGAGGCTGTCAGGCGCTGTGCGTGTGAGAAAGTTCGTTTTCGTTCTGCTGTA 2703
 QY 2712 CTGGAGCTGAGGCTGTCAGGCTGTGCGGTATTCGTTCTTCGATTTGCTCGGTGA 2771
 Db 2704 TTCAAATTTGCAAAATCATGCGCCACACTCAATTTACTTCATTTTCGATTTATGCGCGGACA 2763
 QY 2772 TTCAAATTTGCAAAAGTCTTGGCCACACTTAAATTTACTTCATTTTCGATTTATGCGAGCACC 2831
 Db 2764 ATGGTGTATTTGGTAACTCTGACATTTGATTTGCAATTCATCTCATCTTTTCCGCTG 2823
 QY 2832 ATGGGCGCTTTGGGTAATCTGACATTTGATTTGCAATTCATCTCATCTTTTCCGCTG 2891
 Db 2824 ATGGGAATGCAACTTTTCGAAAGAACTATATGACCACAAAGGATCGTTTCAAGGACCAT 2883
 QY 2892 ATGGGAATGCAACTTTTCGAAAGAACTATATGATGATCACAAGGACCGCTTTCCGAGTGC 2951
 Db 2884 GAATTTACCGCGTGAAGTTCACCGACTTCATGACAGCTTCATGATTTGTTCTCGAGTGC 2943
 QY 2952 GACCTTCGCGCGTGAAGTTCACCGACTTTATGACAGCTTCATGATTTGTTCTCGGCTG 3011
 Db 2944 CTGTGCGGAGAGTGGATCGAGTCCCATGTGGGACTGATGTATGTGGGCGATGTCACTGT 3003

QY 3012 CTCTGGGAGNATGGATCGATCCATGTGGACTGCAATGACGTGGCGGATGTCCTGTCG 3071
Db 3004 ATACCCTTCTTTGGCCACGGTCGTGATAGGCAATCTTGTGTTCTTAATCTTTTCTTA 3063
QY 3072 ATCCCTTCTTCTTGGCCACGGTTGTGTCATCGGCAATCTTGTGGTACTTAACCTTTTCTTA 3131
Db 3064 GCATTGCTTTTGCCAACTTTCGGTTCAATCTAGTTTATACAGCCGGGACTGCGGACAATGAT 3123
QY 3132 GCCTTGCTTTTGTCCAAATTTGGCTCATCTAGCTTATACAGCGCGGACTGCGGATAACGAT 3191
Db 3124 ACCAATAAATAGCAGAGCCCTTCAATCGTATTCCTCGTTTAAAGAACTGGGTGAACGCT 3183
QY 3192 ACGAATAAATAGCCGAGGCTTCAATCGAATTTGGCCGATTTAAAGCTTGGGTAAACGCT 3251
Db 3184 AATATTCCGATTTGTTTAAAGTTAAATCGAAATAAATTTGACAAATCAAAATAAGTGACAA 3243
QY 3252 AATATTGCTGATTTGTTCAAGTTAATACGTAACAAATTTGACAAATCAAAATAAGTGACAA 3311
Db 3244 CCATCAG-----A-CA-----TGG--CGAT-A--ATG----- 3265
QY 3312 CCATCAGGTGAGAGGACCAACAGATCAGTTGGATTTGGAGCGAAGAGCATGTTGTGACAAC 3371
Db 3266 -AAGTGGAGTTGGGTGATGAGGAATCATGGCGATGCTTGATCAAAAAGGGTATCAAG 3324
QY 3372 GAATGGAGCTGGCCACGACGAGATCCTCGCCAGCGCTCATCAAGAAAGGGATCAAG 3431
Db 3325 GGCAGACCCAGCTGGAGGTGGCCATTGGCGATGGCATGGATTTACGATACATGCGGAT 3384
QY 3432 GAGCAGACGCACTGGAGGTGGCCATCGGGATCGGATGGAATTCACGATACAGCGGAC 3491
Db 3385 ATGAAAACAACAGCCGAGAAATCAAAATTCATGAACAAACACAGCATGATTGGAAAC 3444
QY 3492 ATGAAGAACACAACGCGAAGAAATCCAAATATCTAAATACGCAACGATGATTGGCAAC 3551
Db 3445 TCAATAAACCAACCAAGACAATAGACTGGAACATGAGCTAAACCATAGAGTTTGTCCATA 3504
QY 3552 TCAATTACCCCAAGACAATAGACTGGAACACGAGCTAAACCATAGAGTTTGTCCATA 3611
Db 3505 CAGGACGATGACACTGCCAGCATTAACATCATATGTTAGCCATAAGAATCGACCAATTCAG 3564
QY 3612 CAGGACGACGACACTGCCAGCATTAACATCATATGTTAGCCATAAGAATCGACCAATTCAG 3671
Db 3565 GACGAGACCAACAGGGAGCGCCGAGACCATCGAGGGCGAGGAAACGCGAGCTCAGC 3624
QY 3672 GACGAGACCAACAGGGAGCGCCGAGACCATCGAGGGCGAGGAAACGCGAGCTCAGC 3731
Db 3625 AAAGAGACCTCGCCCTCGACGAGAACTGGACGAGAGCGCGGCGATGAGGGCCAG 3684
QY 3732 AAGGAGGATTTAGGTCTCGACGAGAACTGGACGAGGAGGCGGAATCGGAGGAGGCGCCG 3791
Db 3685 CTGGATGTTGACATTAATCATTCATCGCGCAAAACGACGACGAGATAATCGACGACTATCCG 3744
QY 3792 CTCACGGTGATATCATTTATCATGACACA---CGACGAGGATATCTCGATGATATCCA 3848
Db 3745 GCCGACTGTTTCCCGGACTCGTACTACAAGAAATTTCCGATCTTTGGCCGCGCAGGAGAC 3804
QY 3849 GCTGATGCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCGGGTGACGATGAC 3908
Db 3805 TCGCCGTTCTGGCAAGATGGGCAATTTAGCACTGAAACTTTTCAATTAATTTGAAAT 3864
QY 3909 TCGCCGTTCTGGCAAGATGGGCAATTTAGCACTGAAACTTTTCAATTAATTTGAAAT 3968
Db 3865 AAATATTTGAAACCGGAGTTATCACTATGATTTTAAATGAGTAGCTTAGCTTTGGCCCTTA 3924
QY 3969 AAATATTTGAAACAGCTGTATCACTATGATTTTAAATGAGTAGCTTAGCTTTGGCATTA 4028
Db 3925 GAAGATGTTTACCCGATCGACCTGTCATGCGAGGATFACGTACTACATGGACAGG 3984
QY 4029 GAAGATGTACATCTGCCACAAAGACCCATCTGCAGGATATTTTATACTATATGGACAGA 4088
Db 3985 ATATTACGGTGATTTCTTTTGGAGATGTTGATCAAAATGGTTGGCCCTGGGCTTTAAG 4044
QY 4089 ATATTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGGCTCGGCTTCAAA 4148

Db 4045 GTTTACTTACCAGTCCCTGGTGTGGCTGGATTTCTGATTTCTCATGCTATCGCTTATA 4104
QY 4149 GTGTACTTACCAGCGGTGGTGTGGCTGGATTTCTGATTTCTCATGCTATCGCTTATC 4208
Db 4105 AATTGGTTGGCTTTGGTGGGCTTAAATGATATAGCCGTGTTAGATCAATGCGGCACA 4164
QY 4209 AACTTGGTGGCTTCACTTGTGGAGCTGGTGGTATTCAAGCCTTCAAGACTATGCGAAGC 4268
Db 4165 CTGGGCGCCCTAAGGCATTCGCTGCTCTAGATGGAGGATGATGAAGTTGTCGTG 4224
QY 4269 TTAAGAGCACTGAGACCACTACGTGCCATGTCCTGATGACAGGCATGAGGGTGCCTG 4328
Db 4225 AATGCGCTGGTTCAAGCTATACCGTCCATCTTCAATGTCTTATTTGGTGTCTGATATTT 4284
QY 4329 AATGCGCTGGTACAAGCTATACCGTCCATCTTCAATGTCTATTTGGTGTCTGATATTT 4388
Db 4285 TGGCTATTTTTCCTATATGAGGATGACAGCTTTTGTGCGGAAATATTTTAAGTGTAAA 4344
QY 4389 TGGCTAATTTTTCCTAATGAGTGGTGTACAGCTTTTGTGCGAATAATTTTAAGTGTGAG 4448
Db 4345 GATGGTAATGACACTGTGCTGAGCCATGAATCATACCGAATCGTAAATGCTCTCAAAAGT 4404
QY 4449 GACATGAATGGCAGAGCTGACCCAGAGATCATCAAAATCGCAATGCTGCGGAGGC 4508
Db 4405 GAAACTTACACTTGGGAAATTCGCAATGAATTCGATCATGTAGTAAATGGGTATCTC 4464
QY 4509 GAGAACTTACAGTGGTGAATTCAGCAATGAATTCGATCATGTAGTAAATGCGGTATCTG 4568
Db 4465 TGTCTATTTCAAGTGGCCACCTTTAAGGGCTGGATCAGATTTAAGCATGCGCATTTGAT 4524
QY 4569 TGGCTTTTCCAGTGGCCACCTTCAAGGGCTGGATCAAAATCATGACAGTATGATATTC 4628
Db 4525 TCACGAGAGTGGACAGAGCGATCCGAGAAACCAATATCTACATGATTTATATATTC 4584
QY 4629 TCACGAGAGTGGACAGAGCAACCAATTCGTGAAACGCAATCTACATGATTTATATTC 4688
Db 4585 GTATTCTTCAATATTTGGATCATTTTTCACACTCAATCTGTTCAATGGTGTATCATTT 4644
QY 4689 GTATTCTTCAATATTTGGATCATTTTTCACACTCAATCTGTTCAATGGTGTATCATTT 4748
Db 4645 GATAATTTTAAAGCAAAAGAAAGAGCTGGTGGATCATTTAGAAATGTTTCATGACAGAA 4704
QY 4749 GATAATTTTAAAGCAAAAGAAAGAGCTGGTGGATCATTTAGAAATGTTTCATGACAGAA 4808
Db 4705 GATCAGAAAAGTACTATATGCTATGAAAAGATGGCTCTAANAACCATTAANAAGCC 4764
QY 4809 GATCAGAAAAGTACTATATGCTATGAAAAGATGGCTCTAANAACCATTAANAAGCC 4868
Db 4765 ATTCCAGACCGAGGTGGCGACCAAGCAATAGTATTCGAAATAGTTACAGATAAANA 4824
QY 4869 ATTCCAGACCAAGGTGGCGACCAAGCAATAGTCTTTGAAATAGTAAACGATAAGAA 4928
Db 4825 TTGATATAATCATATATGTTGTTCAATGGCTTAAACATGTTTACCATGACCCCTGATCGG 4884
QY 4929 TTGATATAATCATATATGTTTATTCATTTGTTGCTGAACATGTTTACCATGACCCCTGATCGT 4988
Db 4885 TAGCAGCCCTCCGAGGCTACACAACTGCTCTGACAAAACCTCAATGGGATATTCGTAGTT 4944
QY 4989 TAGCAGCCCTCCGAGGCTACACAACTGCTCTGACAAAACCTCAATGGGATATTCGTAGTT 5048
Db 4945 ATTTTCAGTGGCAATGCTTATTAANAATATTCGCTTTAGCATATCACTATTTTCAAAAGAG 5004
QY 5049 ATTTTCAGTTCGCAATGCTTATTAANAATATTCGCTTTAGCATATCACTATTTTATGAG 5108
Db 5005 CCATGGAATTTATTTGATGATGATGTTGTCATTTTATCCATCTTAGTCTTGTACTCAGC 5064
QY 5109 CCATGGAATTTATTTGATGATGATGTTGTCATTTTATCCATCTTAGTCTTGTACTTAGC 5168
Db 5065 GACATCATTTGAGAGTATTTTCGTATCGCCGACACTGCTCCGTGGTGGTGGAGTGGCCAAA 5124
QY 5169 GATATTATCAGAGATGACTTTCGTGTCGCCGACCCCTGCTCCGAGTGGTGGTGGCGAAA 5228

QY 747 TTTAGGTCGTCGAGCGCTTAAACCGTAGCCATTGTGCCAGCTTGAAGACCATCGTC 806
Db 751 GGTGCTGTCATTGAATCTGTAAAAATCTACGCGATGTGATAATTTTGACAAATGTTTCC 810
QY 807 GCGCGCTCATCGAATCGGTGAAGAATCTCGCGATGTGATTTATCCTGACCAATGTTCTCC 866
Db 811 CTGTCGGTGTCCGCGTGTAGTGGCCCTACAAATCTATATGGGTGTTCTACACAAAGTGC 870
QY 867 CTGTCGGTGTCCGCGTGTAGTGGCCCTACAGATCTATATGGCGGTGCTACCGGAGAGTGC 926
Db 871 ATTAAGAGTATCCCTCCCTGGACGCGAGTTGGGCAATCTGACCCGATGAAGAACTGGTTCTA 930
QY 927 ATCAAGAGTTCCCGCTGGACGCTTCTGGGGCAATCTGACCCAGCAGAACTGGGACTAT 986
Db 931 CACAATAGCAACAGTGTCCAAATTTGGTTTACGGAGAAGCATGGCGAGTCAATCCGGTGTGC 990
QY 987 CACAATCGCAATAGTCCAAATTTGGTATTCGAGGACGAGGCATCATTTCCGTTTATGC 1046
Db 991 GGAATGTATCCGGTGGGGGACAAATGGGGGAGGATTTACGTCGTGCTGAGGCGTTCGGC 1050
QY 1047 GGAATATATCCGGTGGGGGCAATGCGACGAGATTTACGTCGTGCTGAGGCGTTCGGT 1106
Db 1051 CCCAATCCCAACTACGACTACACAGTTTCGATTTCGATTTCGTTGGGCTTTCCTGTGCGG 1110
QY 1107 CCGAATCCGAATATGGCTACACAGCTTCGATTCGATTCGGATGGGCTTTCCTGTCCGCC 1166
Db 1111 TTTCTGCTCATGACCCAAAGATTTCTGGAGGATCTGTATCAGCACGCTGCTGCAAGCAGCT 1170
QY 1167 TTCGGCTGATGACACAGGACTTCTGGAGGATCTGTACCAGTGGTGTGCGCGCGCC 1226
Db 1171 GGACCTGGCACATGTTGTTCTTTATAGTCATCATCTTCCTAGGTTCAATTCATCTTTGTG 1230
QY 1227 GGACCATGGCACATGCTGTTCTTTATAGTCATCATCTTCCTAGGTTCAATTCATCTTTGT 1286
Db 1231 AATTGATTTTGGCCATGTTGTCATGCTCTTATGACGAATGCAAAAGAGCGCGAAGAA 1290
QY 1287 AATTGATTTTGGCCATGTTGTCATGCTCTGATGACGAATGCAAAAGAGCGCGAAGAA 1346
Db 1291 GAAGAGGCTGCCAGGAGGAGGCGATACGAGAAGCTGAAGAAGCGGACGAGCAAGGCG 1350
QY 1347 GAAGAGGCTGCCAGGAGGAGGCGATACGTGAAGCGGAAGACTGCCCGCGCAAGCG 1406
Db 1351 GCCAACTGGAGAGGCGGCGAATGTAGCAGCTCAAGCGGCTCAGGATGACGGGATGCC 1410
QY 1407 GCCAAGCTGGAGAGGCGGCGAATGCGCAGGCTCAGGACGAGCGGATGCGGCTGCCGCC 1466
Db 1411 GCTGCGGACGCTCTGCATCCGAGATGGCAAGAGTCCACGCTACTCTTCGATTAAGCTAT 1470
QY 1467 GAAGAGGCTGCATGCTGCATCCGGAATGGCCAAAGTCCGACGCTATTCTTCGATCAGCTAT 1526
Db 1471 GAACATGTTTGTGGCGCGAGAAGGCGAACGATGACAAACAAGAGAGAGATGTCCATA 1530
QY 1527 GAGCTATTTGTTGGCGCGAGAGGCGAACGATGACAAACAAGAGAGATGTCCATT 1586
Db 1531 CGCAGGCTCGAAGTGGAAATCGGAGTCGGTGAAGGTTATACAAAGACAAACGACACCTACC 1590
QY 1587 CGCAGGCTCGAGTGGAGTCGGAGTCGGTGAAGGTTATACAAAGACAAACGACACCTACC 1646
Db 1591 ACAGCAC-CC-GCTACTAAGTCCGTAAAGTTAGCAGGACTTCCTTATTCCTTACCTGGT 1647
QY 1647 ACAGCACCAAGCTACCAAGTTCGTTAAAGTAGCAGCAGACATCCTTATCTTACCTGGT 1706
Db 1648 TCACCATTTAACTACCGCGGGATCAGTAGTTCACACAAGTACACAATACGAAATGGG 1707
QY 1707 TCACCGTTTAACTACCGAGGGATCAGTAGTTCACACAAGTACAGATACCGAAGCGGA 1766
Db 1708 CGTGAGGCTTTGGTATACAGGTAGGATCGCAAGCCATTGGTACTGCAAAATATACAG 1767
QY 1767 CGTGCGGCTTTGGTATACCGGTAGGATCGTAAGCCATTGGTATGTCAACATATCAG 1826
Db 1768 GATGCCAGCAGCAGATTTGGCCCTATGCGGATGACTCGAATGCCGTACACCAATGTCGGAA 1827
QY 1827 GATGCCAGCAGCAGTTCGCCCTATGCGGAGACTCGAATGCCGTACACCCCGATGTCGAA 1886

Db 1828 GGAATGGTGCCATTATAGTACCAGCCTACTATTGTAATTTAGGTTCTAGACATTTCTCA 1887
QY 1887 GGAATGGGCCCATCATAGTATGCCGTGTACTATGGCAATCTAGGCTCCCGACACTCATCG 1946
Db 1888 TATACCTCCGATCAATCAAGAAATCTCGTATACATCATCATGTTGTTATTTGGTGGCATG 1947
QY 1947 TATACCTCCGATCAAGTCCGCAATATCGTATACCTCATCATGGCATCTACTCGGCGCATG 2006
Db 1948 GGGCCCATGGTGCCAGACCAATGACCAAGAGAGCAAAATTCGCGAGTGCACACACAGC 2007
QY 2007 GCGTCATCGGCGTCAGCAATATGACCAAGAGAGCAAAATTCGCGAACCGCAACACAGC 2066
Db 2008 AATCAATCAATCGGTGCTGCAACCAATGTGGCAGTAGTACGGCTGGTGGTGGCTATGCC 2067
QY 2067 AATCAATCAGT-GG-GC-GCCACCAATGCGGCACCA---C-CTG-TC-TGGACA--CC 2114
Db 2068 GATGCCAATCAAGGAACAAGGATTTATGAATGGGTGAGGATTTATACAGACGAAGCT 2127
QY 2115 AATCAACAAGCTC---GATCATCGGACTACGAATTTGGCTGGAGTGCAGGACGAAGCT 2171
Db 2128 GGCAAAATAAAACACACGACCAATCCTTTATCGAGCGCTCCAACTCAACAGTGGTA 2187
QY 2172 GGCAGATTTAAACATCATGACAATCCTTTATCGAGCGCTCCAGACAAACGGTGGTT 2231
Db 2188 GACATGAAGATGTTATGTCTTAAATGATATCATTTGAACAGCCGCTGCTCGGATAGT 2247
QY 2232 GATATGAAGATGTGATGCTCTGATGACATCATGACAGCGCGCTGCTCGGACAGT 2291
Db 2248 CGTGTAGTGAACGAGGTG-----AGGACGATGACGAAGAT 2283
QY 2292 CCGGCAAGCGATCGGCGTCTCCGTTTACTATTTCCCAACAGAGGACGATGACGAGAT 2351
Db 2284 GGTCCACATTTCAAGGACATCGCCCTCGAATACATCTTAAAGGCTCAAAATCTTTGT 2343
QY 2352 GGGCCGACGTTCAAGACAAAGGACCTCGAAGTGAATCCTCAAGGCTCATGTTGTTGT 2411
Db 2344 GTATGGACTGTTGTTGGTGTGTTTAAATTTTCAAGAAATGGGTGCTCTTATTTGTTTC 2403
QY 2412 GTGTGGACTGTTGCTGGCTTTGGTTGAATTTTCAAGAGTGGGTATCGCTCATCGTTC 2471
Db 2404 GATCCATTCGTGGAGCTTTCATTAACCTGTGTATTTGGTCAATACGATGTTTATGGCC 2463
QY 2472 GATCCCTTCGTGGAGCTTTCATACGCTGTGCTATGTTGGTCAACAGATGTTTCATGGCA 2531
Db 2464 ATGGATCATCAGACATGAATCCGGAATTAGAGAAGTCTGTAAGAGTGGTACTATTTC 2523
QY 2532 ATGGATCACACGATATGAACAAGGAGATGGAAACGCGTGTCTCAAGAGTGGCACTATTTC 2591
Db 2524 TTCACGGCCACTTTTGAATTTGAAGCCAGCATGAACACTGATGCCCATGAGCCCGAAGTAC 2583
QY 2592 TTCACGGCCACTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGAGCCCAAGTAC 2651
Db 2584 TACTTCCAGAAAGCTGGAAACATTTTCGATTTTCAATTTATTTGGGCTGTCTCTGTGGAA 2643
QY 2652 TATTTCCAGAGGGCTGGAAACATCTTCGACTTCATATCGTGGCCCTATCGCTATTGGAA 2711
Db 2644 TTGGGCTCGAGGGTCTCAGGCGCTGTCGGTGTTCAGAAAGTTTCGTTGTTCTGTGTA 2703
QY 2712 CTGGGACTCGAGGGTCTCAGGCTGTCGCTGTTTCGCTTCCTTCGATTGTCGCTGTA 2771
Db 2704 TTCAAATTTGGCAAAATCATGGCCACACATTAATTTACTCATTTTCGATTATGGCCCGGACA 2763
QY 2772 TTCAACTGGCCAAAGTCTTGGCCACACATTAATTTACTCATTTTCGATTATGGGACGACC 2831
Db 2764 ATGGGTGCATTTGGGTAACTGTGACATTTGTACTTTTGATTTATCATCTTCATCTTTGCCGTG 2823
QY 2832 ATGGGCGCTTTGGGTAATCTGACATTTGACITTTGCAATTATCATCTTCATCTTTGGCGTG 2891
Db 2824 ATGGGAATGCACATTTTTCGGAAGAAGACTATATTGACCACAAGGATCGCTTCAAGGACCAT 2883
QY 2892 ATGGGAATGCACATTTTCGGAAGAAGATTTATCATGATCACAAGGACCGCTTTCGGATGTC 2951

Dbb 631 ATAGCTTTAGCTTATGTGACCATGGGCATAGATTTAGTGAATATCTCGCAGCTTTGAGAAACA 690
QY 687 ATAGCTTTAGCTTATGTGACCATGGGTATAGATTTAGTGAATATCTAGCAGCCTTCGGAACG 746
Dbb 691 TTTAGGTTACTCGAGCTCTGAAACCCGTAGCCATTTGTGCCAGGTCTAAACACCATTTGC 750
QY 747 TTTAGGGTGTCTGCGAGCGCTTAAACCCGTAGCCATTTGTGCCAGGTCTGAAACCATCTGC 806
Dbb 751 GGTGTCTCATTAATCTGTAATAAATCTACCGCATGTGATAATTTTGACAAATGTTTTCC 810
QY 807 GCGCGCTCATCATCGTGAAGATCTGCGGATGTGATATCTGACCATGTTCTCC 866
Dbb 811 CTGTGCGTGTTCGCGCTGATGGCCCTACAAATCTATATGGTGTCTTAACACAAAAGTGC 870
QY 867 CTGTGCGTGTTCGCGTGTATGGCCCTACAGATCTATATGGGCGTCTCACCGAAGAAGTGC 926
Dbb 871 ATTAACAGATTTCCCTTGACCGCAGTTGGGCAATCTGACCGATGAACACTGGTTCTTA 930
QY 927 ATCAAGAAGTTCCCGTGGACCGTTCCTGGGGCAATCTGACCGAGGAATGGGACTAT 986
Dbb 931 CACAATAGCAACAGTTCCAATTTGGTTTACGGAGAACGATGGCGAGTCTATATCCGCTGTGC 990
QY 987 CACAATCGCAATAGTCCAATTTGGTATTCGAGGAGCGGGCATCTCATTTCCGTTATGC 1046
Dbb 991 GGAATGTATCCGTCGCGGGACAATCGCGCGAAGATTAGTCTGCTCGCCTGCGAGGCTTCCGC 1050
QY 1047 GGCAATATATCCGGTTCGCGGGCAATCGCAGACGATAGTGTGCTGCGCTGCGAGGGTTTGGT 1106
Dbb 1051 CCCAATCCCAACTAGCACTACACCACTTTCGACTCATTCGCTGGGTTCCTCTGTCGCGC 1110
QY 1107 CCGAATCCGAATTTGGCTTACACCACTTCGATTCGTTCCGATGGGCTTCTGTCCGCC 1166
Dbb 1111 TTTCTGTCTCATGCCAAAGATTTCTGGAGGATCTGTATFCAGCACGTGCTGCAAGCAGCT 1170
QY 1167 TTTCCGCTCATGACACAGCACTTCTGGAGGATCTGTACCAGCTGGTGTGTGCGCGCGCC 1226
Dbb 1171 GGACCTTGGCAATGTTGTTCTTTATAGTCATCATCTTCTAGGTTCATCTATCTTGTG 1230
QY 1227 GGACCATGACATGCTGTCTTTATAGTCATCATCTTCTAGGTTCATCTATCTTGTG 1286
Dbb 1231 AATTTTCATTTTGGCAATTTGTCATGCTTATGAGCAATTCGAAAGAACGCCGAAGAA 1290
QY 1287 AATTTTCATTTTGGCCATTTGTCATGCTGATGAGCAATTTGCAAGAGGAGGCCGAAGNA 1346
Dbb 1291 GAAGAGGCTGCCGAGGAGGCGGATCCGAGAGCTGGAAGAGCGGACGCGCAGCAGCGG 1350
QY 1347 GAAGAGGCTGCCGAGGAGGCGGATACGTGAAGCGGAAGAGCTGCCCGCCGCCAAAGCG 1406
Dbb 1351 GCCAACTGGAGGAGCGGCCAATGTAGCAGCTCAAGCGGCTCAGGATCGAGGGATGCC 1410
QY 1407 GCCAAGCTGGAGGAGCGGCCAATGGCAGGCTCAGGCAAGCGGATCGGCTGCCGCC 1466
Dbb 1411 GCTGCGGCACTCTGCATCCCGAGATGGCAAGAGTCCCAAGCTACTTCTTGCATTAAGCTAT 1470
QY 1467 GAAGAGGCTGCATGCTCGGAAATGGCCAGAGTCCGACGATTTCTTGCATCAGCTAT 1526
Dbb 1471 GAAGCTGTTTGGCGCGAGAGGCGAAGCATGACAAACAAGAGGAGAGATGTGATA 1530
QY 1527 GAGCTATTTTGGCGCGAGAGGCGAAGCATGACAAACAAGAGAGATGTCCAT 1586
Dbb 1531 CGCAGCGTGAAGTGGNATCGGAGTGGGTAGCGGTTATACAAGACAACCGACCTACC 1590
QY 1587 CGGAGGCTCGAGGTGGAGTGGGAGTGGGTAGCGGTTATACAAGACAACCGACCTACC 1646
Dbb 1591 ACAGCAC-CC--GCTACTAAAGTCCGTAAGTTAGCAGCACTTCTTATCCTTACCTGGT 1647
QY 1647 ACAGCACCAAGCTACCAAGTTCTGAAGTGGACGACGACATCTTATCCTTACCTGGT 1706
Dbb 1648 TCACCATTTAACCTACCGCGGGGATCAGCTAGTGTTCACAAAGTACACATACGAATGGG 1707
QY 1707 TCACCGTTTAAACATACGACGAGGATACGCTAGTGTTCACAAAGTACACATACGAACGGA 1766
Dbb 1708 CGTGGAGCTTTTGGTATACCAAGTAGGATCGGACCGCAATGGTACTGCAAAACATATCAG 1767

QY 1767 CGTGGCGCTTTTGGTATACCCGATGCGATCGTAAGCCATTTGGTATGTCAACATATCAG 1826
Dbb 1768 GATGCCCAGCAGCATTTGGCCCTATGCGGATGACTCGAATGCCCTTAACCAATGTCCGAA 1827
QY 1827 GATGCCCAGCAGCATTTGGCCCTATGCGGATGACTCGAATGCCCTTAACCAATGTCCGAA 1886
Dbb 1828 GAGAATGGTCCCATTTAGTACGAGCCTACTATTGTAATTTAGGTTCTTAGACATTTCTCA 1887
QY 1887 GAGAATGGGCCATCATAGTGGCGGTACTATGGCAATCTAGGCTCCCGACACATCATCG 1946
Dbb 1888 TATACCTCGCATCAATCAAGAATCTCGTATACATCAGATGGTGTATTTATTTGGTGGCATG 1947
QY 1947 TATACCTCGCATCAGTCCGATATCGTATACCTACATGGCATCTACTCGCGCATG 2006
Dbb 1948 GCGGCCATGGTGCAGCAATGACCAAGAGAGCAAAATTCGCGAGTCCCAACACACGC 2007
QY 2007 GCGGTATGGGCTCAGCACAAATGACCAAGAGAGCAAAATTCGCGAGTCCCAACACACGC 2066
Dbb 2008 AATCAATCAATCGGTGCTGCAACAATGTTGGCAGTGTACGGCCGGTGTGGCTATPCC 2067
QY 2067 AATCAATCAGT-GG-GC-GCCACCAATGGCGCACAC--CTGTC--TGGA--C-A--CC 2114
Dbb 2068 GATCCCAATCACAGGAACAAGGATTTAATGGTGGTCTAGGATTTATACAGACGAAGCT 2127
QY 2115 AATCACAGCTC---GATCATCGCGACTAGCAAAATGGCTGGAGTGCACGGACGAAGCT 2171
Dbb 2128 GGCAAAATAAACACCAACCAATCCCTTTATCGAGCCCGTCCAAACTCAACAGTGGTA 2187
QY 2172 GGCAAGATTAACATCATGACAACTCTTTATCGAGCCCGTCCAGACACAACGCTGTT 2231
Dbb 2188 GACATGAAGATGTTATGGTCTTAAATGATCATTTGAACAAGCCGCTGGTTCGCATAGT 2247
QY 2232 GATATGAAGATGTGTGTTGGTCTGATGATCATCATCGAACAAGCCGCTGGTTCGCACAGT 2291
Dbb 2248 CGTCTAGTGAACAGGTG-----AGGACGATGACGAAGAT 2283
QY 2292 CGGCAAGCATCGCGGTGCTCCGTTTACTATTTCCTCCACAGAGGACGATGACGAAGAT 2351
Dbb 2284 GGTCCCACTTCAAGGACATCGCCCTCGAATATATCTTAAAGGACATCGAAATCTTTGT 2343
QY 2352 GGGCGAGTTTCAAGACAGGCACTCGAAGTATCTCAAGGCACTGATGTTGT 2411
Dbb 2344 GTATGGGACTGTTGTTGGTGTGTTAAATTTTCAAGAAATGGGTCTCTTTATTTGTTCT 2403
QY 2412 GTGTGGGACTGTTGCTGGGTTTGGTTGAAATTTTCAAGAGTGGGTATCGCTCATCTCT 2471
Dbb 2404 GATCATTTCTGGAGCTCTTCTATACCTGTGTTATTTGGTCAATAACAATTTCTATGCC 2463
QY 2472 GATCCCTTCGTCGAGCTCTTCTATCAGCTGTGCAATTTGGTCAACACAGATGTTCTATGCA 2531
Dbb 2464 ATGGATCATCAGCATGAATCCGGAATTTGGAGAAGTGTCTGAAAGTGTGAATTTCT 2523
QY 2532 ATGGATCACCATGATATGAACAAGAGATGGAACGCGTGTCTCAAGAGTGGCAACTATTTCT 2591
Dbb 2524 TTCAGGCGCACTTTTGAATTTAGCCGAGCATGAACACTGATGGCCATCAGCCCCAAGTAC 2583
QY 2592 TTCAGGCGCACTTTGCCATCGAGGCACTGAAGCTTAATGGCCATGAGCCCCAAGTAC 2651
Dbb 2584 TACTTCCAGGAGGCTGGAACATTTTCATTTTATTTGGCTTCTCTCTCTGCGAA 2643
QY 2652 TATTTCCAGGAGGCTGGAACATTTCTGACTTCTATCTGTCGCTCTATCTATGGA 2711
Dbb 2644 TTGGGCTGGAGGTTCCAGGGCTGTGCGGTGTGAGAAGTGTTCGTTTCTCTGCGTGA 2703
QY 2712 CTGGGACTCGAGGTTCTCAGGCTGTGCGTATTTGCGTTCTCTCTCTGCTGCTGTA 2771
Dbb 2704 TTCAATTTGGCAAAATCATGCCCCACACTGAATTTACTCATTTTCGATTTATGGCCGGA 2763
QY 2772 TTCAAACTGGCCAGTCTTTGGCCACACTTAATTTACTCATTTTCGATTTATGGGACAC 2831
Dbb 2764 ATGGGTGATTTGGGTAATCTGACATTTTGTACTTTGCAATTTATCTCTTCTCTGCGCTG 2823

QY 2832 ATGGCGCTTTGGGTAATCTGACATTTGTAATTTGCAATTTATCACTTCATCTTTGCGGTG 2891
Db 2824 ATGGAATGCAACTTTTCGGAAGAACTATATATGACCAAGAGTCGCTTCAAGGACCAT 2893
QY 2892 ATGGAATGCAACTTTTCGGAAGAAATTTATCATGATCAAGAGGACCGCTTTCCGGATGGC 2951
Db 2884 GAAATACCGCGCTGGAATTTACCGACCTTCATGACAGCTTCATGATGCTGTCGAGTG 2943
QY 2952 GACCTGCCGCGCTGGAATTTACCGACCTTTATGACACAGCTTCATGATGCTGTCGCGGTG 3011
Db 2944 CTGTGCGGAGAGTGGATCCAGTTCAGTGTGGACCTGCATGTATGTGGGCGATGTGTCAGCTGT 3003
QY 3012 CTCTGCGGAGATGGATCCAGTTCATGTGGGCGATGTGTCAGTGTGCGGCGATGTCTCTGTCG 3071
Db 3004 ATACCTTTCTTTCTGCGCACCGGTGCTGATGCGCAATTTTGGTTCCTTTAACTTTTCTTA 3063
QY 3072 ATTCCCTTCTTTCTGCGCACCGGTGCTATCGCAATCTGTGGTACTTAACTTTTCTTA 3131
Db 3064 GCTTTGCTTTTGTCCAACTTCCGTTTCATCTAGTTTATCAGCCCGGCTGCGGACAAATGAT 3123
QY 3132 GCTTTGCTTTTGTCCAAATTTTGGCTTCATCTAGCTTATCAGCGCGGACTGCGGATAACGAT 3191
Db 3124 ACCAATAAATAGCAGAGCGCTTCAATCGTATGTCTGTTTTTAAAGACTGGGTGAAACGT 3183
QY 3192 ACGAATAAATAGCGAGCGCTTCAATCGAATGGCCGATTTAAAGTTGGTTAAAGCGT 3251
Db 3184 AATATTGCGGATTTGTTTAAAGTTAATTCGAATAAATGACAAATCAATAAAGTGACCAA 3243
QY 3252 AATATTGCTGATTTTCAAGTTAATACGTAAACAAATTTGACAAATCAATAAAGTGACAA 3311
Db 3244 CCATCAG-----A-CA-----TGG--CGAT-A--ATG----- 3265
QY 3312 CCATCAGTGGAGGAGGACCAACAGATCATAGTTGGATTTGGAGCGAAGCATGGTGACAAAC 3371
Db 3266 -AACTGGAGTTGGGTCATGAGCAATCATGGCGATGGCTTGATCAAAAGGATATGAG 3324
QY 3372 GAATGGAGCTGGGCCAGCAGATGCTCGCCGAGCGCTCATCAAGAGGATCAAG 3431
Db 3325 GCGGAGACCCAGCTGGAGGTGGCCATTTGGCGATGGCATGGAGTTTCACGATACATGGCGAT 3384
QY 3432 GAGCAGACGCAACTGGAGGTGGCCATCGGGATCGATGGAATTCACGATACACGGCGAC 3491
Db 3385 ATGAAAAACACAGCCCAAGAAATCAAAATTCATAAACACACACAGATGATGGAAAC 3444
QY 3492 ATGAAGAACAAACAGCCCAAGAAATCCAAATATCTAAATTAACGCAACGATGATGGCAAC 3551
Db 3445 TCAATTAACCAACCAAGACAATAGACTGGAACATGAGCTAAACCATAGAGTTTGTCCATA 3504
QY 3552 TCAATTAACCAACCAAGACAATAGACTGGAACACAGCTAAACCATAGAGTTTGTCCATA 3611
Db 3505 CAGGACGATGACACTGCCAGCATTAACATCATATGTTAGCCATAGAATTCGACCATTTCAAG 3564
QY 3612 CAGGACGACGACTGCCAGCATTAACATCATATGTTAGCCATAGAATTCGACCATTTCAAG 3671
Db 3565 GACGAGCCCAAGGGGAGCGCCGAGACCATCTGAGGGCGAGGAGAAACGGCAGCTCAGC 3624
QY 3672 GACGAGCCCAAGGGGAGCGCCGAGACCATCTGAGGGCGAGGAGAAACGGCAGCCAGC 3731
Db 3625 AAAGAGGACCTCGGCTCGACGAGAACTGGACGAGAGGCGGCGGCGATGAGGGCCAG 3684
QY 3732 AAGGAGGATTTAGGTCTCGACGAGAACTGGACGAGGAGGCGGAAATCGGAGGAGGGCCG 3791
Db 3685 CTGGATGGTGACATCATCTATCCCAAAACGACGAGATTAATCGACGACTATCCG 3744
QY 3792 CTCGCGGTGATCATTAATTCATGCCACA--CGACGAGGATATACTCGATGAATATCCA 3848
Db 3745 GCCGACTGTTCCCGACTCGTACTACAGAAAGTTTCCGATCTTGGCCGCGCAGGAGAC 3804
QY 3849 GCTGATGCTGCCCCGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTGACGATGAC 3908
Db 3805 TCGCCGTTCTGCGCAGGATGGGGCAATTTACGACTGAAACATTTTCAATTAATGAAAAT 3864
QY 3909 TCGCCGTTCTGCGCAGGATGGGGCAATTTACGACTGAAACATTTTCAATTAATGAAAAT 3968

Db 3865 AAATATTTTGAACCGCAGGTTATCAGTATGATTTTAATGAGTAGCTTAGCTTTGGCCCTTA 3924
QY 3969 AAATATTTTGAACAGCGTGTATCACATGATGATTTTAATGAGTAGCTTAGCTTTGGCATTA 4028
Db 3925 GAAGATGTTCAATTTACCGCATCGACCTGTCTATCAGGATATCTGTACTACATGACGAGG 3984
QY 4029 GAAGATGATCATTCGCCAAGAACCCATATCGAGGATATTTATATCTATATGGACAGA 4088
Db 3985 ATATTTACGTTGATTTCTTTTGGAGATGTGATCAATAGTTGGCCCTGGGCTTTAAG 4044
QY 4089 ATATTTACGTTGATTTCTTTTGGAAATGTTAATCAAGTTGGCTCGGCTTCAAA 4148
Db 4045 GTCTACTTCAACAAATGCTGTGTGGCTGGATTTCTGATGTGCTATGCTATGCTTATA 4104
QY 4149 GTGTACTTCAACACGCGTGTGTGGCTGGATTTCTGATTTGTGATGCTATGCTTATC 4208
Db 4105 AATTTGTTGCGGCTTGTGTCGGGCTTAAATGATATGCCGTTTATGATCAATCGCGACA 4164
QY 4209 AACTTCGTTGCTTCACTTTGTTGGAGCTGGTGTATTCAAGCTTCAAGACTATCGGAACG 4268
Db 4165 CTGCGCGCCCTAAGCCCAATTCGCTGTCTCTAGATGGGAGGTATGAAAGTTGTCTGTG 4224
QY 4269 TTAAGACGACTGAGACCACTACGTGCCATGTCCCGTATGAGGCGCATGAGGCTGCTGTT 4328
Db 4225 AATCGCTGTGTTCAAGCTATACCGTCCATCTTCAATGCTATTTGGTGTGCTGATATTT 4284
QY 4329 AATCGCTGTGTACAAGCTATACCGTCCATCTTCAATGCTATTTGGTGTGCTAATATTT 4388
Db 4285 TGGCTTATTTTGGCATATGCGGAGTACAGCTTTTCTGCTGGAATAATTTTAAAGTGAAA 4344
QY 4389 TGGTAAATTTTGGCATAAATGGGTGTACAGCTTTTCTGCGAAATATTTTAAAGTGGAG 4448
Db 4345 GATGGTAAATGACACTGTGTGAGCATGAATCATACCGAATCGTAAATGCTGCTGCAAAAGT 4404
QY 4449 GACATGAATGGCAGCAAGCTCAGCCAGCATCATCAATCCCAATGCTGCTGAGAGC 4508
Db 4405 GAAACTACACTCGGAAAAATTCGGCAATGAACCTTCGATCATGTAGTAAATGCTATCTC 4464
QY 4509 GAGAATACAGTGGTGGATTCAGCAATGAATTTTCGATCATGTAGTAAAGCTGATCTG 4568
Db 4465 TGTCTATTTCAAGTGGCCACCTTTAAGGGTGGATCAGATATTGAACGATGCCATGAT 4524
QY 4569 TGCCTTTTCCAAAGTGGCCACCTTCAAAAGCTGGATCAAAATCATGAACGATGCTATCGAT 4628
Db 4525 TCAGGAGGTGGACAGCAGCCGATCCGAAACCAATATCTACATGTATTTATATTTTC 4584
QY 4629 TCAGGAGGTGGACAGCAACCAATTCGTGAAACGAACTCATATGATTTATATTTTC 4688
Db 4585 GTATTTCTCATTAATTTGGATCATTTTTCACACTCAATCTGTTCAITGTTGTTATCATTT 4644
QY 4689 GTATTTCTCATTAATTTGGATCCTTTTTCACACTCAATCTGTTCAITGTTGTTATCATTT 4748
Db 4645 GATAATTTTAATGAACAAAGAAAGAGGAGGATGATGATTAAGAAATGTTTCATGACAGAA 4704
QY 4749 GATAATTTTAATGACAAAGAAAGAAAGAGGATGATGATTAAGAAATGTTTCATGACAGAA 4808
Db 4705 GATCAGAAAAAGTACTAATGCTATGAAAGATGGCTCTAAAGAACCAATTTAAAGCC 4764
QY 4809 GATCAGAAAAAGTACTAATGCTATGAAAGATGGCTCTAAAGAACCAATTTAAAGCC 4868
Db 4765 ATTCCAAGACCGGCTGGCGACCAAGCAATAGTATTTCGAAATAGTTTACAGATAAAAAA 4824
QY 4869 ATTCCAAGACCAAGTGGCGACCAACAGCATAGCTTTTGAATAGTAACCGATAGNAA 4928
Db 4825 TTCGATTAATCATTAATGTTGTTTTCATTTGGCTTAAACATGTTTACCATGACCCCTCGATCGG 4884
QY 4929 TTCGATTAATCATTAATGTTTTCATTTGGCTGAACATGTTTCAACATGACCCCTCGATCGT 4988
Db 4885 TACGACCCCTCGAGGCGTACAAATGCTCCCAAACTCAATGGGATATTTGATGTT 4944
QY 4989 TACGATCGTGGCAGCGATTAACGCGTCTAGACTATCTCAATGCGATATTCGATGTT 5048

Db	4945	ATTTTCAGTGGCGAATGTCTATTAAAAAATATTCGCTTTACGATATCACTATTTTCAAGAG	5004
Qy	5049	ATTTTCAGTTCCGAATGTCTATTAAAAAATATTCGCTTTACGATATCACTATTTTATTTAG	5108
Db	5005	CCATGGAATTTATTTGATGTAGTAGTGTCTATTTTATTCACATCTTAGTGTCTGTACTACAG	5064
Qy	5109	CCATGGAATTTATTTGATGTAGTAGTGTCTATTTTATTCACATCTTAGTGTCTGTACTACG	5168
Db	5065	GACATCATTTGAGAAGTATTTCTGATGCGCGACATGCTCCGTTGFGTGGAGTGGCGAAA	5124
Qy	5169	GATATTATCGAGAAGTACTTCTGTGTCGCGACCCCTGCTCCGAGTGTGTGCTGTGGCGAAA	5228
Db	5125	GTGGTGTCTGCTCGTGTATGTCGAAGGTGCCAAGGTATCCGAGACGTTGCTGTGTCGGG	5184
Qy	5229	GTGGCGGTGCTCTCCAGCTGTGGAAGGAGCCAAAGGCATTCCGACACGTCTCTTCGGG	5288
Db	5185	TTAGCCATGTCGTTGCTGCCCTTATTTCAACATTTGTGTGTTGCTGTTCTTTGGTGATGTTTC	5244
Qy	5289	TTGGCCATGTCGTCGCGGCCCTGTTCACATCTGCCTGTCTGTGTTCTCTGTGTCATGTTTC	5348
Db	5245	ATCTTTTGCTATCTTTGCGCATGCTCTCTTCATGCAATGTCAAAGAGAAGACGCGCATAAAT	5304
Qy	5349	ATCTTTGCCATTTTTCGCGATGCTGTTCTTCATGCAAGTGAAGGAGAAGACGCGCATTAAC	5408
Db	5305	GCTGTGTATAATTTTAAGACATTTGCCCAAGTATGTATATTGCTGTGTTTCAGATGTCTTACC	5364
Qy	5409	GACGTCTACAACTTTCAAGACCTTTGGCCAGAGCATGATCTTCTCTTCAGATGTCTGACG	5468
Db	5365	TCAGCCGTTTGGCATGGTGTGTAGATGCCATATCAATAGGAGAAGATTCGATCCACACC	5424
Qy	5469	TCAGCCGTTTGGGATGGTGTACTGGACGCCATATCAATGAGGAAGCATGCGATCCACCC	5528
Db	5425	GACAACGACAAGGCTATCCGGCCAAATTTGTTTCAGCGACTGTGGAAATTAAGTTFCTC	5484
Qy	5529	GACAGCACAAGGCTATCCGGCCAAATCTGGTTTCAGCGAGCCGTTGGAATAACGTTTCTC	5588
Db	5485	CTTTCATATCTAGTTATAGCTTTTGTAGTTATTTATATGTACATTTGCTGTCTATTCTC	5544
Qy	5589	CTCTCATACCTAGTTATAGCTTTTGTAGTTATTTATATGTACATTTGCTGTCTATTCTC	5648
Db	5545	GAGAACTATAGCCAGGCTACGGAGGATGTACAGGAGGTTCTACCGGAGCAGCATATGAT	5604
Qy	5649	GAGAACTATAGTCAGGCCACCGGAGGACGTGCAAGAGGGTCTTAACCGAGCAGCATACGAC	5708
Db	5605	ATGTACTACGAGATTTGGCAACAATTCGATCCGGAGGTTACCCAGTACATAAAGATACGAC	5664
Qy	5709	ATGTACTATGAGATCTGGCAGCAATTCGATCCGAGGGCACCCAGTACATACGCTATGAT	5768
Db	5665	CAGTGTGCCGAGTTCTTGGACGTGCTGGAGCCGCCCTGCGATCCCAACGCCGAACAG	5724
Qy	5769	CAGTGTCCGAAATTCCTTGGACGTACTGGAGCCCCCGCTCGATCCAAAACCGAACAAG	5828
Db	5725	TACAAAATCATATCGATGGACATGCCGATATGTCGGGGCGACATCATCTACTGTGTGGAT	5784
Qy	5829	TACAAGATCATATCGATGGACATACCCATCTGTCCGGGTGTACTCTATCTGGTGTGAC	5888
Db	5785	ATATTGGATGCCCTGACCAAGGACTCTTTTGGCGCAAGGGTAAATCCGATCGAGGAGACG	5844
Qy	5889	ATCTCTCGACGCCCTTACGAAAGACTCTTTTGGCGCAAGGGCAATCCGATAGAGGAGACG	5948
Db	5845	GGTGAATTTGGTAGATTTGGCGCGACCGACACCGAGGCGTATGATCCGTTGCTGTCG	5904
Qy	5949	GGTAGATTTGGTAGATAGCGCCCGCCCGGATACGAGGGGTACGAGCCGCTCTATCA	6008
Db	5905	ACACTGTGGCGCCACGCTGAGGAGTACTGCGCCAAGCTGATACGAATTCGTGTGGC	5960
Qy	6009	ACGCTGTGGCGTACAGCTGAGGAGTACTGCGCCGGCTTAATCCAGACGCTGTGGC	6064

RESULT 9
ID US-08-772-512A-2 STANDARD; DNA; UNC; 6315 BP.
AC xxxxxx
DT

Sequence 2, Application US/08772512A
Sequence 2, Application US/08772512A
GENERAL INFORMATION:
CC APPLICANT: Soderlund, David M.
CC APPLICANT: Knipple, Douglas C.
CC APPLICANT: Ingles, Patricia J.
CC TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
CC TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
CC TITLE OF INVENTION: FLIES
CC NUMBER OF SEQUENCES: 19
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
CC STREET: P.O. Box 1051, Clinton Square
CC CITY: Rochester
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 14603
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/772.512A
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/608,618
CC FILING DATE: 01-MAR-1996
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Braman, Susan J.
CC REGISTRATION NUMBER: 34,103
CC REFERENCE/DOCKET NUMBER: 19603/601(CRFD-1657)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 716-263-1636
CC TELEFAX: 716-263-1600
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6315 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cdna
CC SEQUENCE 6315 BP: 1711 A: 1344 C: 1595 G: 1665 T: 0 OTHER.

1

Db	511	GAGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTAGTCGACGAGGTT	570
Qy	567	GAGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTAGTCGACGAGGTT	626
Db	571	TTCAATTTATGCCCGTTTACGTATCTTAGAGATGCATGGAATTCGCTGGACTTCGTAGTA	630
Qy	627	TTCAATTTATGCCCGTTTACGTATCTTAGAGATGCATGGAATTCGCTGGACTTCGTAGTA	686
Db	631	ATAGCTTTAGCTTTATGTGACCATGGCCATAGATTTAGTAAATCTCGCAGCTTTTGAGAA	690
Qy	687	ATAGCTTTAGCTTTATGTGACCATGGTATAGATTTAGTAAATCTAGCAGCCCTGCGAAG	746
Db	691	TTTAGGTACTGCGAGCTCTGAACACCGTAGCCATGTGCGCAGGTCTAAACACCATGTCT	750
Qy	747	TTTAGGTGCTGCGAGCGCTTAAACACCGTAGCCATGTGCGCAGGTCTGAAGACCATGCT	806
Db	751	GGTGCTGTCAATCAATCTCTAATAATCTACGCGATGTGAATTTTGACAATGTTTTC	810
Qy	807	GGCGCGCTCATCGAATCGGTGAAGAACTGCGCGATGTGATATCTCTGACCATGTTCTCC	866
Db	811	CTGTGCGGTGTTTCGCGTGTATGGCGCTTACAAATCTATATGGGTGTTCTTAAACACAAAAGT	870
Qy	867	CTGTGCGGTGTTTCGCGTGTATGGCGCTTACAGATCTATATGGCGTCTCACCGAGAAGT	926
Db	871	ATTAAAGGATTTCCCTTGACGGCGTAGTTGGGCAATCTGACCGATGAATACTGGTTTCTA	930
Qy	927	ATTAAAGGATTTCCCGTGGACGGTTCCTGGGCAATCTGACCGACGAGAATGGGACTAT	986
Db	931	CACAATAGCAACATGTTCCAATTTGGTTTACGGAGACGATGGCGATCATATCCGGTGTGC	990
Qy	987	CACAATCGCAATAGTCTCAATTTGGTATTCGGAGGACGAGGCACTCATTTCCGTTATGC	1046
Db	991	GGGAATGATATCCCGTGGGCAATTCGCGCAAGATTAAGTCTGCTGTCAGGGCTTCGGC	1050
Qy	1047	GGCAATATATCCGTCGCGGCAATCGGACGACGATTAAGTGTGCTGTCAGGGCTTTGGT	1106
Db	1051	CCCAATCCCAACTACGACTACACCAAGTTTCGACTCATTCGGTGGGCTTTCCCTGTGCGGC	1110
Qy	1107	CCGAATCCGAATTTATGGCTACACCAAGTTCGATTCGTTCCGATGGGCTTTCTGTCCGCC	1166
Db	1111	TTTCGCTCATGACCAAGATTTCTGGAGGATCTGTATCAGCAGCTGCTGCAAGCAGCT	1170
Qy	1167	TTCCGGCTGATGACACAGCACTTCGGAAGGATCTGACCAGCTGGTGTTCGCGCGCGCC	1226
Db	1171	GGACCTTGGCACATGTTGTTCTTTATAGTCATCATCTTCCTAGGTTCATTTCTATCTTGTG	1230
Qy	1227	GGACCATGGCAATGTTGTTTATAGTCATCATCTTCCCTAGGTTCATTTCTATCTTGTG	1286
Db	1231	AATTTGATTTTGCCATTTGTCATGCTTTATGACGAATTCGCAAGGCTCAGGATGACGGATGCC	1290
Qy	1287	AATTTGATTTTGCCATTTGTCATGCTTTATGACGAATTCGCAAGGCTCAGGATGACGGATGCC	1346
Db	1291	GAAGAGCTGCCGAGGAGGCGATCCGAGAGCTGAAGAGCGGCGACGACCAAGCGC	1350
Qy	1347	GAAGAGCTGCCGAGGAGGCGATGCTGAAGCGGAAGAGCTGCGCGCGCCCAAGAGC	1406
Db	1351	GCCAACTGAGGAGCGGCGCAATGTAGCAGCTCAAGCGGCTCAGGATGACGGGATGCC	1410
Qy	1407	GCCAACTGAGGAGCGGCGCAATGGCAGGCTCAGGACGACGCGGATGCGGCTCGCGCC	1466
Db	1411	GCTGCGCAGCTTCGCATCCCGAGATGGCAAGAGTCCCACTACTCTTGCAATTAGCTAT	1470
Qy	1467	GAAGAGCTGCACATGTCATCCGGAATGGCCAAAGAGTCCGACGTATTTCTTGCAATCAGCTAT	1526
Db	1471	GAACTGTTTGTTCGCGCGCAGAGGCGACGATGACACACAGGAGGAGAGATGTCGATA	1530
Qy	1527	GAGCTATTTGTCGCGCGCAGAGGCGCAACGATGACACAAAGAGAGAGATGTCGCAAT	1586
Db	1531	CGCAGCTGCAAGTGGAACTGGAGTGGGTGACGCTTATACAAAGACCAACGACCACTACC	1590
Qy	1587	CGGAGCTCGAGTGGAGTGGGAGTGGGTGACGCTTATACAAAGACCAACGACCACTACC	1646
Db	1591	ACAGCAC-CC--GCTACTAAAGTCCGTAAGTTAGCAGCACTTCCTTATCTCTACCTGGT	1647

[illegible]

QY 2712 CTGGGACTCGAGGTGTCCAGGCTCTCCGTTATTCGGTTCTCTTCGATTGCTGCGTGA 2771
Db 2704 TTCAAAATGGCAAAATCATCGCCACACACTGAATTTACTCATTTTCGATTATGGCCGGAC 2763
QY 2772 TTCAAACTGGCCAAAGTCTTGGCCACACTTAATTTACTCATTTTCGATTATGGACGCACC 2831
Db 2764 ATGGGTGCATTTGGGTAACTTGACATTTGTACTTTGGATTATCATCTTCATCTTTGCCGTG 2823
QY 2832 ATGGCGCTTTGGGTAACTTGACATTTGTACTTTGGATTATCATCTTCATCTTTGCCGTG 2891
Db 2824 ATGGGAATGCAACTTTTCGGAAGAAGTATATTGACACAAAGATCGCTTCAAGGACCAT 2883
QY 2892 ATGGGAATGCAACTTTTCGGAAGAAGTATATTGACACAAAGATCGCTTTCGGATGCG 2951
Db 2884 GAATTACCGCGCTGGATTTTACCGACTTCATCGACAGCTTCATGATGTTCGCGAGTG 2943
QY 2952 GACCTGCGCGCTGGAACTTTACCGACTTTATGCACAGCTTCATGATCGTTCCGGGTG 3011
Db 2944 CTGTCCGGAGAGTGGATCGAGTCCATGTGGGACTGCTATGTGTGGCGGATGTCAGCTGT 3003
QY 3012 CTCTGCCGAGNAATGGATCGATCCATGTGGGACTGCTATGTGTGGCGGATGTCGTCG 3071
Db 3004 ATACCTCTCTTTGGCCAGGTCGTGATCGGCAATTTTGTGTGTTCTTAATCTTTTCTTA 3063
QY 3072 ATTCCTCTCTTTGGCCAGGTCGTGATCGGCAATTTTGTGTGTTCTTAATCTTTTCTTA 3131
Db 3064 GCTTTGCTTTTGTCCAACTTTGCTTCATCTAGTTTATCAGCCCGACTGCGGCAATGAT 3123
QY 3132 GCTTTGCTTTTGTCCAACTTTTGGCTCATCTAGTTTATCAGCCCGACTGCGGCAATGAT 3191
Db 3124 ACCAATAAATPAGCAGAGGCTTCAATCGTATTGCTCGTTTTTAAAGAACTGGGTGAACGT 3183
QY 3192 ACGAATAAATPAGCAGGCTTCAATCGAATTTGGCGGATTTAAAGTTGGGTAAAGCT 3251
Db 3184 AATATTGCGGATTTGTTTAACTTAACTTGAATTAATTTGCAATCAAAATGAAGTACCAA 3243
QY 3252 AATATTGCTGATTTTCAAGTTAATACGTAAACAAATGCAAAATGAAGTATCAA 3311
Db 3244 CCATCAG-----A-CA-----TGG--CGAT-A--ATG----- 3265
QY 3312 CCATCAGGTGAGAGGACCAACCATCATGTTGGATTTTGGAGCGAAGCATGTTGACAAC 3371
Db 3266 -AATCGGATTTGGCTATGAGAAATCATGGCGGATGGCTTGATCAAAAAGGTTATGAAG 3324
QY 3372 GAATCGGAGCTGGCCAGCAGAGATCCTCGCCAGCGCTCATCAAGAAGGGGATCAAG 3431
Db 3325 GCGCAGACCCAGCTGGAGGTGGCCATTGGCGATGGCATGGATTCAGCATACATGGCGAT 3384
QY 3432 GAGCAGACGCAACTGGAGGTGGCCATCGGGGATCGGATGGAAATTCACGATACAGCGGCAC 3491
Db 3385 ATGAAAAACAACAGCCCAAGAAATCAAAATTCATAACACACACAGCATGATTGGAAC 3444
QY 3492 ATGAAGACACACAGCCGAAGAAATCCAAATATCTAATAACGCAACGATGATTGGCAAC 3551
Db 3445 TCAATAAACACCAAGACAATAGACTGGAACATGAGCTAAACCATAGAGTTTGCCTTA 3504
QY 3552 TCAATTAACCAACCAAGACAATAGACTGGAACACAGCTAAACCATAGAGTTTGCCTTA 3611
Db 3505 CAGGACGATGACCTGCCAGCATTAACCTCATATGTTAGCCATAAGATTCGACCATTTCAAG 3564
QY 3612 CAGGACGACGACCTGCCAGCATTAACCTCATATGTTAGCCATAAGATTCGACCATTTCAAG 3671
Db 3565 GACGAGACCCACAAGGGCAGCGCCAGACCATTCGAGGGCGAGGAGAAACGCGCTCAGC 3624
QY 3672 GACGAGACCCACAAGGGCAGCGCCAGACCATTCGAGGGCGAGGAGAAACGCGCGCAGC 3731
Db 3625 AAAGAGGACCTCGGCTCGACGAGAACTGGACGAGAGGCGCGGCGATGAGGGCCAG 3684
QY 3732 AAGGAGGATTTAGGTCTCGACGAGGAACTGGACGAGAGGCGGAATGCGAGGAGGGCCCG 3791
Db 3685 CTGGATTTGGATCATCATCTATCCCAAAACGACGACGAGATAATCGACGACTATCCG 3744
QY 3792 CTCGAGGTTGATATCATTTATTCATGCACA---CGACGAGGATATCTCGATGAATATCCA 3848

Db 3745 GCCGACTGTTCCCGACTCGTACTACTACAAGAGTTTCCGATCTTTGCGCGGCGACGAGAC 3804
QY 3849 GCTGATTCCTCCCGATTCTGTAATAAGAAATTCGATCTTTAGCGGGTACGATGAC 3908
Db 3805 TCGCCGTTCTGGCAAGGATGGGCAATTTAGACTGAAAACCTTTTCAATTAATTAATAAT 3864
QY 3909 TCGCCGTTCTGGCAAGGATGGGCAATTTAGACTGAAAACCTTTTCAATTAATTAATAAT 3968
Db 3865 AAATATTTTGAACCGCAGTTATCAGTATGATTTTAAAGTACGTTAGCTTTGGCCCTTA 3924
QY 3969 AAATATTTTGAACCGCAGTTATCAGTATGATTTTAAAGTACGTTAGCTTTGGCAATTA 4028
Db 3925 GAAAGTGTTCATTTACCAGATCGACCTCATCGAGGATATATCTACTACATGACGACAGG 3984
QY 4029 GAAAGTGTACATCTGCCACAAGACCCATCTGCAGGATATTTATATATATGACAGAGA 4088
Db 3985 ATATTACGGTGATATCTTTTGGAGATGTGATCAAAATGGTTGGCCCTGGGCTTTAAG 4044
QY 4089 ATATTACGGTTATATCTTCTTGGAAATGTAAATCAAGTGTGTGGCGCTGGGCTTCAA 4148
Db 4045 GTCTACTTCACAAATGCGTGTGGTGGCTGATTCGATTCGATTCATCTATCGCTTATA 4104
QY 4149 GTGTACTTCACCAACGCGTGGTGGCTCGATTTCTGTGATGTCATGATGATGCTTATC 4208
Db 4105 AATTGGTTGGCGTTTGGTTCGGCTTAAATGATATAGCCGTTTATAGATCAATGCGCACA 4164
QY 4209 AACTTCGTTGCTTACTTGTGGAGCTGGTGTATTAAGCCCTTCAAGACTATGCGAAGC 4268
Db 4165 CTGCGCGCTTAAGCCATTTGGTCTCTCTAGATGGGAGGATATGAAGTTGCTGCG 4224
QY 4269 TTAAGAGCACTGAGACCATACGTGCCATGTCCCCTATGTCAGGGCATGAGGCTCGCTT 4328
Db 4225 AATGGCTGGTTCAAGCTATACCTCCATCTTCAATGTCTATGCTGTTGCTGCTGATATT 4284
QY 4329 AATGGCTGGTACAGCTATACCTCCATCTTCAATGTGCTATGCTGCTGCTATATATT 4388
Db 4285 TGGCTTATTTTGGCCATTTAGGAGTACAGCTTTTGTCTGGAATAATTTTAAAGTGTAAA 4344
QY 4389 TGGCTAATTTTGGCCATTAATGGTGTACAGCTTTTGTCTGGAATAATTTTAAAGTGTAAA 4448
Db 4345 GATGTTAATGACACTGCTGAGCCATGAATCATACCGAATCGTAATGCCCTGCAAAAGT 4404
QY 4449 GACATGAATGGCAAGAGCTCAGCCAGAGATCATACCAATCGCAATCGCTTGCAGAGC 4508
Db 4405 GAAACTACACCTGGGAAATTCGCAATGAATTCGATCATGTAGTAAATCGCTATCTC 4464
QY 4509 GAGAATACACGTTGGTGAATTCAGCAATGAATTCGATCATGTAGTTAACCGTATCTG 4568
Db 4465 TGTCTATTTCAAGTGGCCACCTTTAAGGCTGGATCCAGATTATGAACGATGCCATGAT 4524
QY 4569 TGGCTTTTCCAAGTGGCCACCTTCAAAAGCTGGATACAAATCATGAACGATGCTATCGAT 4628
Db 4525 TCACGAGAGGTGGACAGCAGCGGATCCGAGAAACCATATCTACATGATTTATATTTTC 4584
QY 4629 TCACGAGAGGTGGACAGCAGCAACCAATTCGTGAACGAGCATCTACATGATTTATTTTC 4688
Db 4585 GTATTTCTTATATTTTGGATCATTTTTCACACTCAATCTGTTTATGTTGTTTATCATTT 4644
QY 4689 GTATTTCTTATATTTTGGATCATTTTTCACACTCAATCTGTTTATGTTGTTTATCATTT 4748
Db 4645 GATAATTTTAAAGCAAAAGAAAGCAGGTGGATCATTTAGAAATGTTTCATGACAGAA 4704
QY 4749 GATAATTTTAAAGCAAAAGAAAGCAGGTGGATCATTTAGAAATGTTTCATGACAGAA 4808
Db 4705 GATCAGAAAAGTACTATATGCTATGAAAAGATGGGCTTAAAAAACCATTTAAAGCC 4764
QY 4809 GATCAGAAAAGTACTATATGCTATGAAAAGATGGGCTTAAAAAACCATTTAAAGCC 4868
Db 4765 ATTCCAGACCGAGGTGGGACCCACCAAGCAATAGTATTCGAAATAGTTACAGATAAAAA 4824
QY 4869 ATTCCAAGACCGAGGTGGGACCCACCAAGCAATAGTATTCGAAATAGTTACAGATAAAAA 4928

387 AAAGATATTTTCGCTTTTCATCAAAAGCAATGTGGATCGTCAATCAATCGG 446
391 ATACGTCGTGTAGCCATTTATATTTTAGTGCATCCCTCTGTTTCGTTATTCATTCAC 450
447 ATACGTCGTGTGCCATTTACATTTCTAGTGCATCATTTATTTCCCTATTCATCATC 506
451 ACTATTTCTAACTAAATGTATTTTAAATGATAATGCCGACAAACGCCAGCTTGGTCC 510
507 ACAATTTCTCGTCAACTGTCATCTGTGATGATAATGCCGACAAACGCCAGCTTGGTCC 566
511 GAGGTGATATTCACCGAATCTACACATTTGAATCAGCTGTTAAAGTGAATGCACAGGT 570
567 GAGGTGATATTCACCGAATCTACACATTTGAATCAGCTGTTAAAGTGAATGCACAGGT 626
571 TTCAATTTATGCCCCGTTTACGTATCTTAGAGATGCAATGGAATGGCTGGACTTCGTAG 630
627 TTCAATTTATGCCCCGTTTACGTATCTTAGAGATGCAATGGAATGGCTGGACTTCGTAG 686
631 ATAGCTTTAGCTATGTGACCATGTGGCATAGATTTAGTGAATCTCGCAGCTTTGAGACA 690
687 ATAGCTTTAGCTATGTGACCATGGTATAGATTTAGTGAATCTAGCAGCCCTGCGAAG 746
691 TTATAGGTACTCGGAGCTCTGAAACCGTAGCCATTTGCCAGGTCTAAACCAATGTC 750
747 TTATAGGTGCTCGGAGCGCTTAAACCGTAGCCATTTGCCAGGTCTGAAAGCAATCGTC 806
751 GGTGTGTCATTTGAATCTCTAAATCTACCGATGTGATTAATTTTGACAAATGTTTCC 810
807 GCGCGCTCATGCAATCGTGAAGATCTGCGGATGTGATTTCTGACCATGTTCTCC 866
811 CTGTGCGTCTCGCGTGTATGGCCCTACAAATCTATATGGGTGTTCTTAACACAAAGTGC 870
867 CTGTGCGTCTCGCGTGTATGGCCCTACAGATCTATATGGCGTGTCTACCCGAGAAGTGC 926
871 ATTAACGATTTCCCTGTGACGCGAGTTGGGCAATCTGACCGATGAATACTGTTCTA 930
927 ATCAAGAAGTTCCCGTGTGACCGGTTCCCTGGGCAATCTGACCGAGAGAACTGGGACTAT 986
931 CACAATAGCAACAGTTCCCAATTTGGTTACGGAGCAAGTGGCGAGTCATATCCGTTGTC 990
987 CACAATCGCAATAGTCCCAATTTGGTATTCGGAGGAGGAGGATCTCATTTCCGTTATGC 1046
991 GGAATGTATCCGGTGTGCGGCAATGCGCGAAGATACGTCTGCTGCGAGGCTTCGCG 1050
1047 GGAATATATCCGGTGTGCGGCAATGCGAGCAGATTAAGTGTGCTGCGAGGCTTGGT 1106
1051 CCAATCCCACTACGACTACACGAGTTTCGACTCATTCGGTTGGCTTTCTCTGTCGGG 1110
1107 CGAATCCGAATTTAGCTTACACCGAGCTTCGATTCGTTGGATGGGCTTTCTGTCCGCG 1166
1111 TTTCTCTCATACCCCAAGATTTCTGGGAGGATCTGTATCAGCAGCTGTCTGCAAGCAGCT 1170
1167 TTTCCGCTCATGACACAGACTTCTGGGAGGATCTGTACCACTGGTGTGCGCGCGCC 1226
1171 GGACCTGCGCATGTGTTCTTTATAGTCATCATCTTCTAGGTTCAATTCATCTTGTG 1230
1227 GGACCATGCGCATGTGTTCTTTATAGTCATCATCTTCTAGGTTCAATTCATCTTGTG 1286
1231 AATTGTATTTTGGCCATTTGTCCTATGTATGACGAATTCGAAGAAGGCGCAAGAA 1290
1287 AATTGTATTTTGGCCATTTGTCCTATGTATGACGAATTCGAAGAAGGCGCAAGAA 1346
1291 GAAGAGCTTCCGAGGAGGCGATCCGAGAAGCTGAAGAAGGCGCAGCAGCCCAAGGG 1350
1347 GAAGAGCTTCCGAGGAGGCGATACGTGAAGGGAAGAGCTGCCCGCCCAAGCG 1406
1351 GCCAACTGGAGGAGGCGCAATGTAGCAGCTCAAGCGGCTCAGGATCAGCGGATGCC 1410
1407 GCCAAGCTGGAGGAGGCGGCAATGCGAGGCTCAGGAGCAGCAGGATCGCGCTGCGCG 1466
1411 GCTGGGAGCTGTCATCCCGAGATGGCAAGAGTCCCACTACTCTTGCATTAAGTAT 1470
1470 GCTGGGAGCTGTCATCCCGAGATGGCAAGAGTCCCACTACTCTTGCATTAAGTAT 1470

1467 GAAGAGGCTGCACCTGCATCCGAAATGCCAAGAGTCCGAGGTATCTTGTGCATCAGCTAT 1526
1471 GAACGTGTTTGTGGCGGAGAGGCAACGATGACAACAACAGGAAGATGTCGATA 1530
1527 GAGCTATTTGTGGCGGAGAGGCAACGATGACAACAACAGGAAGATGTCCTATT 1586
1531 GCGAGCTGCGAAGTGGAAATCGGAGTCTGGTACGCTTATACAAAGACAACACGACCTACC 1590
1587 CGGAGCTGCGAGTGGAGTCCGAGTCTGGTACGCTTATACAAAGACAACACGACCTACC 1646
1591 ACAGCAC--CC--GCTACTAAAGTCCGTAAGTACGACGACTTCTTATCTTACCTGGT 1647
1647 ACAGCACACCAAGCTTACCAAAAGTCTGTAAGTACGACGACTTCTTATCTTACCTGGT 1706
1648 TCACCATTTAACTACGCGGGGATCAGTGTTCACACAAGTACACAATACGAATGGG 1707
1707 TCACCGTTTAACTACGCGGGGATCAGTGTTCACACAAGTACACAATACGAATGGG 1766
1708 GGTGACCTTTTGGTATACGAGTACGATCGCAATGGTACTGCAACATATCAG 1767
1767 GGTGCGCTTTGGTATACCGGTAGCGATCGTAAGCCATTGGTATTGTCAACATATCAG 1826
1768 GATGCGCAGCAGCATTTGCCCTATGCCGATGACTCGAATGCCGTAACACCAATGTCGAA 1827
1827 GATGCGCAGCAGCATTTGCCCTATGCCGATGACTCGAATGCCGTAACACCAATGTCGAA 1886
1828 GAGAATGTCGCAATATAGTACCGCTACTTATCTTAATTTAGGTTCTAGACATCTTCA 1887
1887 GAGAATGGGCGCATCATAGTCCCGTACTATGCAATCTAGGCTCCCGACACTCATCG 1946
1888 TATACCTCGCATCAATCAAGAATCTCGTATACATCACATGGTGTATTATTTGGTGGCATG 1947
1947 TATACCTCGCATCAGTCCCGAATATCGTATACCTCACATGGCGATCTACTCGCGCGATG 2006
1948 GCGGCATGGTCCGAGCACAATGACCAAGAGAGCAATTTGCGCAGTCTGCAACACAGCG 2007
2007 CCGCTCATTTGGCGTGCACACAATGACCAAGAGAGCAATTTGCGCAACCGCAACACAGCG 2066
2008 AATCAATCAATCGGTGCTGCAACCAATGTCGCACTAGTACGCGCGGTGGTGGCTATCCC 2067
2067 AATCAATCAGT--GG--GCCACCAATGGCGCACCC--CTGTC--TGGG--C--A--CC 2114
2068 GATGCCAATCAAGGAACAAGGATTTGAAATGGTTCAGGATTTATACAGACGAAGCT 2127
2115 AATCAAGCTC--GATCATCGGACTACGAAATTTGGCTGGAGTGCACGAGCAAGCT 2171
2128 GCAAAATAAACACCAAGCAATCTTTATCGAGCCGCTCCAAACTCAACAGTGGTA 2187
2172 GCAAGATTAACATCATGACAAATCTTTATCGAGCCCGTCCAGACACAACCGTGGT 2231
2188 GACATGAAGATGTTATGCTTTAAATGATATCATTTGAACAAGCGCTGGTGGCATAGT 2247
2232 GATATGAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2291
2248 GGTGAGTGAACGAGGTG-----AGGACGATGACGAAGAT 2283
2292 CGGCAAGCGATCGCGGTGCTCCGTTTACTATTTCCCAACAGAGGAGCATGACGAGAT 2351
2284 GGTCCCATTTCAAGGACATCGCCCTCGAATATATCTTAAAGGATCGAATCTTTGT 2343
2352 GGGCGAGCTTTCAAGACAGGCACTCGAAGTGAATCTTCAAGGATCGATGCTGTTGT 2411
2344 GTATGGGACTGTTGTTGGTGTGTTAAATTTTCAAGGATGGTCTCTTATTTGTTTC 2403
2412 GTGTGGGACTGTTGCTGGGTTTGGTGAATTTTCAAGAGTGGTATCGCTCATCGCTTC 2471
2404 GATCATTTGCTGGAGCTCTTCAATACCTGTGTATTGTGGTCAATPACATGTTTATGCC 2463
2472 GATCCTTTGCTGAGCTCTTCAATACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2531
2464 ATGGATCATCAGCATGAATCCGGAATTTGGAAGAGTGTGAAAGTGGTAACTATTTC 2523
2532 ATGGATCACCAGATATGAACAAGGAGATGGAACCGGCTCAAGAGTGGCAACTATTTC 2591

Db	2524	TTCA	GGCCACACTTTT	TC	CAATTGAGG	CCAGCATGAA	ACTGATGG	CCATGAGCC	CAAGATAC	2583
Qy	2592	TTCA	CCGCCACACCTTT	T	CCCATCGAGG	CCACCATGA	AGCTTAATGG	CCATGAGCC	CAAGATAC	2651
Db	2584	TACT	TTCCAGGAAGGCT	GG	AAACATTTTC	GATTTTCAT	TATTATGG	CGCTTGCTCT	CGCTCGAA	2643
Qy	2652	TAT	TTCCAGGAGGCT	GG	AAACATTTTC	GATTTTCAT	TATTATGG	CGCTTGCTCT	CGCTCGAA	2711
Db	2644	TTGG	GCCTGGAGGGT	TC	CAGGCGCTG	CGGTGTTG	AGAAGTTTTC	TGTTGCTTC	GTGTTA	2703
Qy	2712	CTGG	ACTCGAGGCT	TC	CAGGCTG	TCCGCTATT	TGCGTTC	CTTTTCG	ATTGCTG	2771
Db	2704	TTCA	ATTTGGCAAAAT	CA	TGCCCCAC	ATGAATTTAC	TCTATTTTC	GATTTG	GGCCGGA	2763
Qy	2772	TTCA	AACTGGCCAAAG	TC	TTGGCCAC	ACTTAATTTAC	TCTATTTTC	GATTTG	GGCCGGA	2831
Db	2764	ATGG	GTGCATTTGGG	TAACTCG	ACATTTG	TACTTTGC	ATTATCAT	TCTTCAT	CTTTGCGGT	2823
Qy	2832	ATGG	CGCTTTGGG	TAACTCG	ACATTTG	TACTTTGC	ATTATCAT	TCTTCAT	CTTTGCGGT	2891
Db	2824	ATGG	AAATGCACTTT	TC	GGAAAGAA	CTATATG	TACCAACA	AGGATCG	CTTC	2883
Qy	2892	ATGG	AAATGCACTTT	TC	GGAAAGAA	CTATATG	TACCAACA	AGGATCG	CTTC	2951
Db	2884	GAAT	TACCGGCTG	GAATTC	ACCGAC	TTATG	GCACAC	GTTCAT	GATTTG	2943
Qy	2952	GACT	CGCGGCTGG	AACTTC	ACCGAC	TTATG	GCACAC	GTTCAT	GATTTG	3011
Db	2944	CTGT	GGGAGAGT	GG	ATCGAGT	CCATGTGG	GA	CTGATGTGG	CGATGTC	3003
Qy	3012	CTCT	GGGAGATGG	AT	CGAGTCC	ATG	TGGCG	ATGTCAG	CTGT	3071
Db	3004	ATAC	CTTCTTTGG	CCAGGTC	GTGATCGG	CAATTTT	TGTGTTCT	TAA	CTTTCTTA	3063
Qy	3072	ATT	CCCTTCTTTG	CCAC	CTGTG	TCATCGG	CAATCTGT	TGTACT	TAACTTTCTTA	3131
Db	3064	GC	TTTGTGTTG	CAACTTC	GTGTC	ATCTAG	TTTAT	CAGCC	CGACTG	3123
Qy	3132	GC	TTTGTGTTG	CAACTTT	TGGCTAT	CTAG	TTTAT	CAGCC	CGACTG	3191
Db	3124	ACCA	ATAAAATAG	CAGAG	CCCTTCA	ATCG	ATTGCTG	CTTTAA	AAGAACTGG	3183
Qy	3192	ACGA	ATAAAATAG	CCGAG	CCCTTCA	ATCG	ATTGCTG	CTTTAA	AAGAACTGG	3251
Db	3184	AA	TATGCGGATG	TTTT	AGTTT	TAGTTT	TAGTTT	TAGTTT	TAGTTT	3243
Qy	3252	AA	TATGCTGATG	TTTT	CAAGTTA	TAGTA	CAAAAT	TGACAA	ATTAAGTGATCA	3311
Db	3244	CCAT	CTAG-----	A	-CA-----	TGG--	-CGAT-A-	-ATG-----	-	3265
Qy	3312	CCAT	CAGGTGAG	AGGACCA	CCAGATCA	TGTTGG	ATTG	CGGAGG	AGCATGGTGACA	3371
Db	3266	-AA	CTGGAGTTGG	GT	CATGAC	AAATCAT	TGGCG	GATG	GTTCATCA	3324
Qy	3372	GA	CTGGAGCT	TGGCC	CACGAC	GAGATCT	TCGCC	GCGCC	TCATCA	3431
Db	3325	GGCG	AGACCAGCTG	AG	GTGGCC	ATTGCG	GATGCC	ATTG	TCACGATAC	3384
Qy	3432	GAG	CAGCGCACTG	GAG	GTGGCC	ATTGCG	GATGCC	ATTG	TCACGATAC	3491
Db	3385	ATGA	AAACAAAC	AGCC	CAAGAAAT	CAAAATTC	ATAACA	CAACA	CAAGATGATG	3444
Qy	3492	ATGA	AGNACAAAC	AGCC	CAAGAAAT	CAAAATTC	ATAACA	CAACA	CAAGATGATG	3551
Db	3445	TCA	ATAACCA	CAAG	CAAAAT	TAGCTG	GAACAT	GAGCTA	AAACCATAG	3504
Qy	3552	TCA	ATAACCA	CAAG	CAAAAT	TAGCTG	GAACAT	GAGCTA	AAACCATAG	3611
Db	3505	CAG	ACGATGAC	ACTG	CCAG	CAATTA	CTCAT	TATG	TAGCCAT	3564
Qy	3612	CAG	ACGACGAC	ACTG	CCAG	CAATTA	CTCAT	TATG	TAGCCAT	3671

Db	3565	GACGAGACCCACAAGGCGACGCCGAGACCACTCGAGGCGCAGGAGAAACGCGACGTCAGC	3626
Qy	3672	GACGAGACCCACAAGGCGACGCCGAGACCACTCGAGGCGCAGGAGAAACGCGACGTCAGC	3731
Db	3625	AAACGAGACCTCGCGCTCGACGAGGAACCTGGACGAGGAGGCGCGAGGCGGATGAGGGCCAG	3684
Qy	3732	AAGGAGGATTTAGGCTCTCGACGAGGAACCTGGACGAGGAGGCGCGAATCGCGAGGAGGGCCG	3791
Db	3685	CTGATGGTGCACATCATCTCATGCCCAAAACGACGACGAGATAATCGACGACTATTCGG	3744
Qy	3792	CTCGACGGTGATCATCTATTCATGCACA--CGACGAGGATATCTCGATGAATATCCA	3848
Db	3745	GCCGACGTGTTTCCCGACCTGCTACTACAAGAAGTTTCCGATCTTTGGCGCGCAGCAGGAC	3804
Qy	3849	GCTGATGCTGCCCGATTCGTAATAAGAAATTTCCGATCTTAGCCGGTGACGATGAC	3908
Db	3805	TCGCGGTTCTGGCAAGGATGGGCAATTTTACACATGAAACCTTTTCAATTAATTGAAAT	3864
Qy	3909	TCGCGGTTCTGGCAAGGATGGGCAATTTTACACATGAAACCTTTTCAATTAATTGAAAT	3968
Db	3865	AAATATTTTGAACCCGAGTTATCACTATGATTTTAATAGTAGTACGTTAGCTTTGGCCCTTA	3924
Qy	3969	AAATATTTTGAACACGCTGTTATCACTATGATTTTAATAGTAGTACGTTAGCTTTGGCAATTA	4028
Db	3925	GAGATGTTCAATTTACCGATCGACCTGTCTATCGAGGATATCTACTACATCGACGAGG	3984
Qy	4029	GAGATGTACATCTGCCACAAGACCCACTATGCAAGATATTTTATACTATATGACAGA	4088
Db	3985	ATATTTACGGTGATATCTTTTGGAGATGTTGATCAAAATGGTTGGCCCTGGGCTTTAAG	4044
Qy	4089	ATATTTACGGTTATATCTTTTGGAAATGTTTAACAAGTGGTTGGCGCTCGGCTTCAA	4148
Db	4045	GTCTACTTCACCAATGCTGGTGTGGCTGGATTTCTGATTTGTCATGCTATCGCTTATA	4104
Qy	4149	GTGTACTTCACCAACGCTGTTGGCTCGATTTCTGCTGATTCATGATGATTCGCTTATC	4208
Db	4105	AATTTGGTTCGGTGTGGTGGGCTTAAATGATATFAGCCGTGTTTAGATCAATCGGCACA	4164
Qy	4209	AACTTCGTTGCTTCACTTGTGGAGCTGGTGTGATCAAGCTTCAAGACTATCGCAAGC	4268
Db	4165	CTGCGCGCCCTAAGGCCATTCGGTGTCTCTAGATGGGAGGATGAAAGTTGTCTGTG	4224
Qy	4269	TTAAGACGCTGAGACCACTACGTGCCATGTCCCCTATGCAAGGCGATGAGGGTCTGCTT	4328
Db	4225	AATCGCTGGTTCAAAGCTATACCGTCCATCTTCAATGCTATGCTGTGTCATATTT	4284
Qy	4329	AATCGCTGGTACAGCTATACGTCCTCATCTTCAATGCTATGCTATGCTGTGTCATATTT	4388
Db	4285	TGGCTATTTTTCGCAATATFAGGAGTACAGCTTTTGTCTGAAATAATTTTTAAGTGTAAA	4344
Qy	4389	TGGCTATTTTTCGCAATATGTTGGTGTACAGCTTTTGTCTGAAATAATTTTTAAGTGTAAA	4448
Db	4345	GATGGTAATGACACTGTGCTGAGCCATGAAATCATACCGAATCGTAATGCCCTGCAAAAGT	4404
Qy	4449	GACATGAATGGCAGAACTCAGCCACGAGATCATACCAATTCGCAATGCCCTGGCAGAGC	4508
Db	4405	GAAACACTACACTCGGAAAATTCGGCAATGAACTTCGATCATGTAGTAATGCGCTATCTC	4464
Qy	4509	GAGAACTACAGTGGGTGTAATTCAGCAATGAATTTGATCATGTAGTAATGCGCTATCTG	4568
Db	4465	TGCTATTTTCAAGTGGCCACTTTTAAGGCGCTGGATCCAGATATGAAAGCATGCCATTTGAT	4524
Qy	4569	TGCTATTTTCAAGTGGCCACTTTCAAGGCTGGATACAAATCATGAACGATGCTATCGAT	4628
Db	4525	TCACGAGGTTGACAGCAGCGATCCGAGAAACCAATATCTACATGTTATTTATTTTC	4584
Qy	4629	TCACGAGGTTGACAGCAGCAATTCGTTGAAACGACATCTACATGTTATTTATTTTC	4688
Db	4585	GTATCTTTCATATATTTGGATCATTTTTTACACATCAATCTCTTCATTTGGTGTATCATTT	4644
Qy	4689	GTATCTTTCATATATTTGGATCATTTTTTACACATCAATCTCTTCATTTGGTGTATCATTT	4748
Db	4645	GATAATTTTATGAACAAAAGAAAGCAGGTGGATCATTTAGAAATCTTCATCAGAGAA	4704

4749 GATAATTTAATAGCAAAAGAAAAAGCAGGTGGATCATTTAGAAATGTTTCATGACGAA 4808
4705 GATCAGAAAAGTACTATAATGCTATGAAAAGATGGCTCTAAAAAACCAATTAAAAGCC 4764
4809 GATCAGAAAAGTACTATAATGCTATGAAAAGATGGCTCTAAAAAACCAATTAAAAGCC 4868
4765 ATTCCAAGACCGAGGTGGCGACCAACAATAGTATTGCAAAATAGTTTACAGATAAAAAA 4824
4869 ATTCCAAGACCAAGTGGCGACCAACAATAGTCTTTGAATAGTAACCGATAAGAA 4928
4825 TTCGATATAATCATATATGTTTCATTGGCTTAACATGTTTACCATGACCCCTCGATCGG 4884
4929 TTCGATATAATCATATGTTTTCATTGGCTGAACATGTTTACCATGACCCCTCGATCGT 4988
4885 TACGACGCTCGGAGCGGTACACAATGCTCTCGACAACCTCAATGGGATATTCGTAGTT 4944
4989 TACGATCGGTGGGACAGCTATACCGGCTCTAGACTATCTCAATGCGATATTCGTAGTT 5048
4945 ATTTTCAGTGGCGAATGCTATTAAAAATATTCGCTTTACGATATCACTATTTCAAAGAG 5004
5049 ATTTTCAGTTCGGAATGCTATTAAAAATATTCGCTTTACGATATCACTATTTATTGAG 5108
5005 CCATGGAATTTAATTTAGTAGTAGTGTGTCATTTTATCCATTTAGTCTTGTACTCAGC 5064
5109 CCATGGAATTTAATTTAGTAGTAGTGTGTCATTTTATCCATTTAGTCTTGTACTTACG 5168
5065 GACATCATTTGACAAGTATTCGTATCGCGGACACTGCTCCGTGTGTCAGAGTGCCGAAA 5124
5169 GATATTTACGGAAGTACTTCTGTGCGGCCCTGCTCCGAGTGGTGGTGGCGGAAA 5228
5125 GTGGTGTGTCCTCGTTTGTAGTCAAGGTGCCAAGGTATCCGACACTGCTGTCTCGC 5184
5229 GTGGGCGGTGCTCTCGACTGTGTGAAGGAGCGCAAGGCAATTCGGACACTGCTCTTCGC 5288
5185 TTAGCATGTCGTGCTGCTGCTTTATCAACATTTGCTGTGCTGTTCTTGGTGAATTC 5244
5289 TTGGCCATGTCGTGCTGCGGCCCTGTCAACATCTGCTGCTCTTCTGGTCAATGTTTC 5348
5245 ATCTTTGCTATCTTTGGCATGCTCTTCTTCATGATGTCAAGAGAAAGAGGCGCAATAA 5304
5349 ATCTTTGCCATTTTGGCATGCTCTTCTTCATGACAGTGAAGAGAAAGCGGCAATTAC 5408
5305 GCTGTGTATAATTTAAGACATTTTGGCCAAAGTATGATATTCGTCTGTTTCAAGATGCTACC 5364
5409 GAGCTCTACAACCTCAAGACCTTTGGCCAGACATGATCCTGCTCTTTCAGATGTCGACG 5468
5365 TCAGCCGTTGGATGGTGTAGATGCCATATCAATGAGGAAGATTCGATCCACCC 5424
5469 TCAGCCGTTGGATGGTGTAGTGGACGCCATTTATCAATGAGGAAGCATTCGATCCACCC 5528
5425 GACAAGCAAGGGCTATCCGGCAATTTGGTTACGCGACTGTTTGGAAATACGTTTCTC 5484
5529 GACAGGCAAGGGCTATCCGGCAATTTGGTTACGCGACTGTTTGGAAATACGTTTCTC 5588
5485 CTTTCATATCTAGTATAAGCTTTTGTAGTATTAAATATGATATGATGCTGCTCATCTC 5544
5589 CTCTCATACCTAGTATAAGCTTTTGTAGTATTAAATATGATATGATGCTGCTCATCTC 5648
5545 GAGAACTATAGCCAGCTACGAGGATGTACAGGAGGTCTCACCGACGACCATATGAT 5604
5649 GAGAACTATAGTCAGCCACCGAGGACGTGCAAGAGGGTCTAACCGACGACCACTACGAC 5708
5605 ATGCTACTAGGATTTTGGCAACAATTCGATCCGGAGGGTACCCAGTACATATAAGATACGAC 5664
5709 ATGCTACTAGATCTGGCAACAATTCGATCCGGAGGGCACCCAGTACATACGCTATGAT 5768
5665 CAGCTGTCCGAGTTCCTGACAGTGTGAGAGCGCCGCTGCAGATCCACAAGCGGACACAG 5724
5769 CAGCTGTCCGAAATTCCTGGACGCTACTGGAGCCCGCTGCAGATCCACAACCAACAAAG 5828
5725 TACAAAATCATATCGATGACATGCCGATATGTCGGGCGACATGATGTACGTGTGGAT 5784

5829 TACAAGATCATATCGATGGACATACCCCATCTGTGCGGGTGACCTCATGTACTGCTGCGAC 5888
5785 ATATTGGATGCTCCAGCAAGGACTTCTTTGGCGCAAGGTAATCCGATCGAGGAGACG 5844
5889 ATCTCGAGCCCTTACGAAAGACTTCTTTGCGGAAGGCAATCCGATAGGAGACG 5948
5845 GGTGAATTTGGTGTGAGATTCGGGGCGGACCGGACCGAGGGGTATGATCCGTTGTGCTG 5904
5949 GGTGAGATTTGGTGTGAGATTCGGGGCGGACCGGATACGAGGGCTTACGAGCCGCTCATCA 6008
5905 ACATGTGGCGCCAGCTGAGGAGTACTGGCCAACTGATACAGAAATGCGTGGCG 5960
6009 ACCTGTGGCGCTGAGGTGAGGAGTACTGGCCCGGCTAATCCAGCACCGCTGGCG 6064

RESULT 11
ID US-08-608-618-1 STANDARD; DNA; UNC; 6318 BP.
AC xxxxxx
DT
Sequence 1, Application US/08608618
DE Sequence 1, Application US/08608618
CC GENERAL INFORMATION:
CC APPLICANT: Soderlund, David M.
CC APPLICANT: Knipple, Douglas C.
CC APPLICANT: Ingles, Patricia J.
CC TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
CC TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT
CC TITLE OF INVENTION: HOUSE FLIES
CC NUMBER OF SEQUENCES: 19
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: Nixon, Hargrave, Devans & Doyle LLP
CC STREET: P.O. Box 1051, Clinton Square
CC CITY: Rochester
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 14603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA: US/08/608,618
CC FILING DATE:
CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Timian, Susan J.
CC REGISTRATION NUMBER: 34,103
CC REFERENCE/DOCKET NUMBER: 19603/600 (CRF D-1657)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 716-263-1636
CC TELEFAX: 716-263-1600
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6318 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
SQ SEQUENCE 6318 BP; 1712 A; 1347 C; 1597 G; 1662 T; 0 OTHER.

Query Match 56.2%; Score 3662; DB 19; Length 6318;
Best Local Similarity 84.7%; Pred. No. 0.00e+00;
Matches 4979; Conservative 0; Mismatches 813; Indels 84; Gaps 21;

Db 151 ATACGATATGATGACGAGGACGAAGTCCACAGCGGATCCACACTTGAACAG 210
Qy 207 ATCCGATATGATGACGAGGACGAGTGAAGTCCACACCGGATCTTACACTTGAACAG 266
Db 211 GGTGTGCTATACCTGTTTCGAATGACGAGGACAGTTCGCGCGGAATTGGCTCCACTCCT 270
Qy 267 GGTGTGCCAATACCTGTTTCGATTGACGAGGACAGTTCGCGCGGAATTGGCTCCACTCCT 326

Db 271 CTCGAGGATATCGATCCCTACTACAGTAATGTACTGACATTTGTAGTAATAAGTAAGGA 330
|||||
Qy 327 CTCGAGGATATCGATCCCTACTACAGCAATGTACTGATTCGTAATGTAAGCAAGGA 386
|||||
Db 331 AAGGATATTTTTCGTTTCTCGCTCAAAAGCAATGTGGCTCGATCCCAATCAATCCG 390
|||||
Qy 387 AAGGATATTTTTCGTTTCTCGATCAAAAGCAATGTGGATGCTGATCCATCAATCCG 446
|||||
Db 391 ATACGTCGTAGCCATTTATTTTATGTGATCCCTGTGTTTTCGTTATTCATATACAC 450
|||||
Qy 447 ATACGTCGTGGCCATTTACATTTAGTGCATCCATTAATTTCCCTATTATCATCATACC 506
|||||
Db 451 ACTATCTAACTAATTTGATTTAATGATATCGGCAACGCCACCGTCGAATCCACA 510
|||||
Qy 507 ACAATTCGTCACATGCTCTGATGATAATGCCGAACGCCACCGTTGAGTCCACT 566
|||||
Db 511 GAGGTGATATTACCGGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCAGAGGT 570
|||||
Qy 567 GAGGTGATATTACCGGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCAGAGGT 626
|||||
Db 571 TTCATTTATGCCGTTTACGTATCTTAGAGATGCATGGAATTTGGCTGGACTTCGTAGTA 630
|||||
Qy 627 TTCATTTATGCCGTTTACGTATCTTAGAGATGCATGGAATTTGGCTGGACTTCGTAGTA 686
|||||
Db 631 ATAGCTTTAGCTTATGTGACCATGGGCATAGATTTAGTGAATCTCGCAGCTTTGAGAACA 690
|||||
Qy 687 ATAGCTTTAGCTTATGTGACCATGGGTATAGATTTAGTGAATCTAGCAGCCTGCGAAGC 746
|||||
Db 691 TTTAGGTACTGCGAGCTCTGAAACCGTAGCCATTTGCGCAGGTCTAAAACCATTTGTC 750
|||||
Qy 747 TTTAGGTGCTGCGAGCGCTTAAACCGTAGCCATTTGCGCAGGTCTGAAGACCATGCTC 806
|||||
Db 751 GGTGCTGTCATGTAATCTGTAAAAAATCTACGCGATGTGATAATTTTGACAATGTTTTCC 810
|||||
Qy 807 GCGCGCTCATCGAATCGGTGAAGAATCTGCGCGATGTGATTATCCTGACCATGTTCTCC 866
|||||
Db 811 CTGTCGTTGTCGCTGATGGCTCAAAATCTATATGGTGTCTTAACACAAAAGTGC 870
|||||
Qy 867 CTGTCGTTGTCGCTGATGGCTCAGATCTATATGGGCGTCTCACCAGGAAGTGC 926
|||||
Db 871 ATTAACGATTCCCTCGAGCGGAGTTGGGCAATCTGACCGATGAACCTGGTTTCTA 930
|||||
Qy 927 ATCAAGATTTCCGCTGGACGGTTCTTGGGCAATCTGACCGAGCAATCGGACTAT 986
|||||
Db 931 CACAATAGCAACAGTTCAAATGGTTTACGGAGAACATGGCGAGTCTATCCGGTGTGC 990
|||||
Qy 987 CACAATCGCAATAGCTCCAATTTGTTATCCGAGGACGAGGCGATCTCATTTCCGTTATGC 1046
|||||
Db 991 GGGATGTATCCGGTGGGACAAATGCGCGGAGGATTAAGTCTGCTCGCAGGGCTTCGGC 1050
|||||
Qy 1047 GGCAATATATCCGGTGGGCGCAATGCGACGAGATTACGTGTGCTCGAGGGGTTTGGT 1106
|||||
Db 1051 CCCAATCCCACTACGACTACACCAAGTTTCGATTCATTCGGTTGGCTTTCTGTCGGCG 1110
|||||
Qy 1107 CGGAATCCGAATTTGGCTACACCAAGCTTCGATTCGTTCCGATGGCTTTCTGTCCGCC 1166
|||||
Db 1111 TTTGCTCTCATGACCAAGATTTCTGGGAGGATCTGTATCAGCAGCTGCTGCAAGCAGCT 1170
|||||
Qy 1167 TTCCGGCTGATGACACAGACTTCTGGGAGGATCTGTACCAGCTGGTGTGCGCGCCGCC 1226
|||||
Db 1171 GGACCTGGCACATGTTGCTTTATAGTCATCATCTTCCTCCTAGGTTCAATCTATCTTGTG 1230
|||||
Qy 1227 GGACCATGGCACATGCTGTTCTTTATAGTCATCATCTTCCTAGGTTCAATCTATCTTGTG 1286
|||||
Db 1231 AATTGATTTTGGCCATTGTTGCCATGCTTATGACGAATTCCTCAAAAGAGCGCGAAGAA 1290
|||||
Qy 1287 AATTGATTTTGGCCATTGTTGCCATGCTGTATGACGAATTTGCAAGGAAGCGCGAAGAA 1346
|||||
Db 1291 GAAGAGGCTGCCGAGGAGGCGCATACGAGAAGCTGAAGAGCGGCGCAGCAGCCAAAGCG 1350
|||||
Qy 1347 GAAGAGGCTGCCGAGAGAGGCGCATACGTGAAGCGGAAGAGCTGCGCGCCGCCAAAGCG 1406
|||||
Db 1351 GCCAAACTGGAGGAGCGGCCAATGTACAGCTCAAGCGGCTCAGGATGACAGCGGATGCC 1410
|||||

Qy 1407 GCCAAGCTGGAGGAGCGGGCCAATGCGCAGGCTCAGGCAGCAGCGGATGCGCGCTGCCGCC 1466
|||||
Db 1411 GCTCGGCAGCTCTGCAATCCGAGATGGCAAGAGTCCACAGTACTCTTGTGATTAGTAT 1470
|||||
Qy 1467 GAAGAGGCTGCATGCAATCCGGAATGCCAAGAGTCCGAGGTATCTTGTGATCAGCTAT 1526
|||||
Db 1471 GAACGTGTTTGGCGGAGAGGCAACGATGACAAACAACAAAGAGAAGATGTCCATA 1530
|||||
Qy 1527 GAGCTATTTGTTGGCGCGAGAGGGCAACGATGACAACAACAAGAGAAGATGTCCATT 1586
|||||
Db 1531 CGCAGCTCGAAGTGAATCGGAGTCGGTGAAGCTTTATACAAAGACACACGACCTACC 1590
|||||
Qy 1587 CGGAGCTCGAGGTGGAGTCGGTGAAGCTTTATACAAAGACACACGACCTACC 1646
|||||
Db 1591 ACAGCAC--CC--GCTACTAAAGTCCGTCAAGTTAGCAGGACTTCTTATCCTTACCTGGT 1647
|||||
Qy 1647 ACAGCACACCAAGCTACCAAGTTTCGTAAGTGAGCAGGACATCCTTATCCTTACCTGGT 1706
|||||
Db 1648 TCACCAATTTAACCTACGCGGGGATCAGTATGTTTCACACAAGTACACAATACGAATGGG 1707
|||||
Qy 1707 TCACCGTTTAACATACGCGGGGATCAGTATGTTCTCACAAAGTACAGGATACGGAACGGA 1766
|||||
Db 1708 CGTGGACGTTTGGTATACAGGTAGCGATCGCAAGCCATTTGGTACTGCAAAACATATCAG 1767
|||||
Qy 1767 CGTGGCCGCTTGGTATACCGGTAGCGATCGTAAGCCATTGGTATTGTCAACATATCAG 1826
|||||
Db 1768 GATCCCGCAGCAGCTTTGCCCTATGCCGATGACTCGCAATGCCGTAACACCAATGTCCGAA 1827
|||||
Qy 1827 GATCCCGCAGCAGCTTTGCCCTATGCCGACGACTCGCAATGCCGTCACCCCGATGTCCGAA 1886
|||||
Db 1828 GAGAATGGTGCCATTATAGTACCAGCCTACTATTGTAATTTAGTTCTTAGACATCTTCTCA 1887
|||||
Qy 1887 GAGAATGGGCCATCATAGTGCCTGTACTATGCAATCTTAGCTCCCGACACTCATCG 1946
|||||
Db 1888 TATACCTCGCATCAATCAAGNAATCTCGTATACATCAGATGTTGATTTATTTGGGTGGCATG 1947
|||||
Qy 1947 TATACCTCGCATCAATCCGAAATATCGTATACCTCAGATGCGCATCTACTCGGCGGATG 2006
|||||
Db 1948 GCGGCCATGGTGCGCAGCACAAATGACAAAGAGAGCAAAATGCGCAGTTCGCAACACACAGC 2007
|||||
Qy 2007 GCGCTCATGGCGCTCAGCACAATGCCAAGAGAGCAAAATGCGCAACCGCCGCAACACAGC 2066
|||||
Db 2008 AATCAATCAATCGTGTGTGCAACCAATGGTGGGAGTAGTACGGCTGGTGGTATATCCC 2067
|||||
Qy 2067 AATCAATCAGT--GG--GC--GCCACCAATGGCGGCACCA--C--CTG--TC--TGGACA--CC 2114
|||||
Db 2068 GATCCCAATCACAGGAAACAAAGGATTTGAAATGGTTCAGGATTTATACAGACGAAGCT 2127
|||||
Qy 2115 AATCACAAAGCTC---GATCATCGCGACTACGAAATTTGGCTTGGAGTGCACGAGGAAGCT 2171
|||||
Db 2128 GGCAAAATAAACACACGACAATCCCTTTATCAGCCCGTCCCAAACTCAACAGTGGTA 2187
|||||
Qy 2172 GGAAGATTTAAACATCATGACAATCCCTTTATCAGCCCGTCCAGACAAACCGTGGTT 2231
|||||
Db 2188 GACATGAAGAGTGTATGGTCTTAAATGATATCATTTGAACAAGCCGCTGGTTCGCATAGT 2247
|||||
Qy 2232 GATATGAAGAGTGTATGGTCTGATGACATCATCGAAGAGCCGCTGGTTCGGCAGAGT 2291
|||||
Db 2248 CGTCTGTAGTGAACGAGGTG-----AGGACGATGACGAAGAT 2283
|||||
Qy 2292 CGGCAAGCGATCGCGGTGCTCCGTTTACTATTTCACAACAGAGGAGATGACGAGGAT 2351
|||||
Db 2284 GGTCCCACTTCAAGGACATCGCCCTCGATACATCCTTAAGAGCATCGAAATCTTTGT 2343
|||||
Qy 2352 GGGCCGAGTTTCAAGCAAGGCACTCGAAGTGAATCTCAAAAGCATCGATGTGTTTGT 2411
|||||
Db 2344 GTATGGGACTGTTGTTGGTGTGTTAAATTTTCAAGATGGGTGCTCTTATTTGTTGTC 2403
|||||
Qy 2412 GTGTGGGACTGTTGTTGGTGTGTTGAAATTTTCAAGATGGGTGATCGCTCATCGTCTTC 2471
|||||
Db 2404 GATCCATCTGGGAGCTCTTCAATACCTTGATTTGTGGTCAATACATGTTTATGGCC 2463
|||||

QY 2472 GATCCCTTCGTGAGCTCTTCATCACGCTGTGCATTTGGTCAACACGAGTGTCAATGGCA 2531
Db 2464 ATGGATCATCACACATGAATCCCGAATTAGAAGAGTGTGAAAGTGGTAACATATTTTC 2523
QY 2532 ATGGATCACCATGATGAACAGAGATGGAACGGTGTCTCAAGAGTGGCAACTATTTTC 2591
Db 2524 TTCACGGCCACTTTTCGGATTTAGGCGCAGCATGAACACTGATGGCCATGAGCCCGAAGTAC 2583
QY 2592 TTCACGGCCACTTTTCGGATTTAGGCGCAGCATGAACACTGATGGCCATGAGCCCGAAGTAC 2651
Db 2584 TACTTCCAGGAAGGCTGGAACATTTTCGGATTTCAATTTTGTGGCTGTCTCTGCTGGA 2643
QY 2652 TATTTCCAGGAGGCTTGAACATCTTCGACTTCATTTATCGTGGCCCTATCGCTATTGGAA 2711
Db 2644 TTGGGCTTCAGAGGCTCCAGGSCCTCTCGGTGTTGAGAAAGTTTTCGTTTGTCTGCTGTA 2703
QY 2712 CTGGGACTCGAGGCTGTCAGGCTCTGCGTATTCGTTTCCTTTTCGATTGCTGCTGTA 2771
Db 2704 TTCAAAATGGCAAAATCATGGCCACACCTGAATTTACTCATTTTCGATTTAGGCGCGACA 2763
QY 2772 TTCAAAATGGCCAAAGTCTTGGCCACACTTAATTTACTCATTTTCGATTTAGGAGCGACC 2831
Db 2764 ATGGGTGCATTTGGTAAATCTGACATTTGTACTTTTGATTTATCATCTTTCATCCCTGCCGTG 2823
QY 2832 ATGGGCGCTTTGGTAAATCTGACATTTGTACTTTTGATTTATCATCTTTCATCTTTTCGCTG 2891
Db 2824 ATGGGAATCAAACTTTTCGGAAGACCAATATTGACCAAGGATCGCTTACAAAGGACCAT 2883
QY 2892 ATGGGAATCAAACTTTTCGGAAGAAATTTATCATGATCACAAAGGACCGCTTTCCGGATGCC 2951
Db 2884 GAATTCGCCGCTGGAATTTACCGACTTCATGCGACAGCTTCATGATTTGTTCCGAGTG 2943
QY 2952 GACCTGCCGCGTGGAACTTTCACCGACTTTATGCGACAGCTTCATGATCTGTTCCGGGTG 3011
Db 2944 CTGTGCGGAGATGGATCGAGTCCATGCGGACTGCGATGATGTTGGCGCATCTCAGCTGT 3003
QY 3012 CTCTGCGGAGATGATGATCGAGTCCATGTTGGGACTGATGATGTTGGCGCATCTCCTGTCG 3071
Db 3004 ATACCCCTCTCTTGGCCACGCTGCTGATCGGCAATCTTTGTTGTTCTTAATCTTTCTTA 3063
QY 3072 ATTCCTCTCTCTTGGCCACCGCTTGTATCGGCAATCTTTGTTGTTCTTAATCTTTCTTA 3131
Db 3064 GCTTTGCTTTCTTCCAACTTCGGTTCATCTAGTTTATCAGCCCCGACGCGCCGACATGAT 3123
QY 3132 GCTTGTCTTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCGCCGACTGCCGATCAACGAT 3191
Db 3124 ACCAATAAATAGCAGAGCCCTTCAATCGTATTTGCTGCTTTTAAAGAACTGGGTGAAAGCT 3183
QY 3192 ACGAATAAATAGCCGAGGCCCTTCAATCGAATGGCCGATTTTAAAGTTGGGTTAAGCGT 3251
Db 3184 AATATTCGCGATTTTAAAGTTAATTCGAATAAATGACAAATCAATAAGTACCAA 3243
QY 3252 AATATTCGCTGATTTTCAAGTTAATACGTAACAAATGACAAATCAATAAGTACCAA 3311
Db 3244 CCATCAG-----A-A-CA-----TG- -CGAT -A -ATG----- 3265
QY 3312 CCATCAGGTGAGAGACCAACAGATCAGTTGGATTGGAGCGAAGATGGTGACAAAC 3371
Db 3266 -AACTGGAGTTGGGTCATGACGAAATCATGGCGGATGGCTTGATCAAAAAGGATATGAAG 3324
QY 3372 GAACTGGAGCTGGCCACGACGATCTCTCGCCGACGGCCCTCATCAAGAGGGGATCAAG 3431
Db 3325 GCGGAGACCCACTGGAGTGGCCATTTGGCGATGGCATGGAGTTCCACGATACATGGCGAT 3384
QY 3432 GAGCAGACGCAACTGGAGTGGCCATCGGGGATCGGATGGAATTCACGATACACGCGAC 3491
Db 3385 ATGAAAAACAACAGCCAAAGAAATCAAAATTCATAAACAACACACACATGATTCGGAAC 3444
QY 3492 ATGAAGAACAACAGCCGAAGAAATCCAAATATCTAAATAAGCAACACGATGATTCGCAAC 3551
Db 3445 TCAATAAACCCCAAGACAATAGACTGGAACATGAGCTAAACCATAGAGGTTTGTCCATA 3504
QY 3552 TCAATTAACCCCAAGACAATAGACTGGAACACGAGCTAAACCATAGAGGTTTGTCCATA 3611

Db 3505 CAGGACGATGACACTGCCAGCATTAACATCATATGTTAGCCATAAAGATCGACCATTCAAG 3564
QY 3612 CAGGACGACGACTGCCAGCATTAACATCATATGTTAGCCATAAAGATCGACCATTCAAG 3671
Db 3565 GACGAGACCCACAAGGCGAGCCGAGACCATCGAGGCGGAGGAGAAACGCGACGCTCAGC 3624
QY 3672 GACGAGACCCACAAGGCGAGCCGAGACGATGGAGGCGGAGGAGAAACGCGACGCGCAGC 3731
Db 3625 AAAGAGGACCTCGGCTCGAGAGAACTGGACGAGAGGCGGAGGCGGATGAGGCGCCAG 3684
QY 3732 AAGGAGGATTTAGGTCTCGACGAGAACTGGACGAGGAGGCGAATGCGAGGAGGCGCCG 3791
Db 3685 CTGATGTGCATCATCATTCATGCCCAAAACGACGACGAGATAATCGACGACTATCCG 3744
QY 3792 CTCGACGCTGATATCATTTATTCATGACACA---CGACGAGGATATCTCGATGAATATCCA 3848
Db 3745 GCGGACTGTTCCCGACTCGTACTACAAAGTTTCCGATCTTTGGCGGCGGAGGAGGAC 3804
QY 3849 GCTGATGCTGCCCGATTCGTACTATTAAGAAATTTCCGATCTTAGCCGCTGACGATGAC 3908
Db 3805 TCGCCGTTCTGGCAAGGATGGGCAATTTACGACTGAAACCTTTTCATTAATTAATGAAAT 3864
QY 3909 TCGCCGTTCTGGCAAGGATGGGCAATTTACGACTGAAACCTTTTCATTAATTAATGAAAT 3968
Db 3865 AAATATTTTGAACCGCAGTTTATCATTATGATTTTAAATGAGTACTAGCTTTGGCCCTTA 3924
QY 3969 AAATATTTTGAACAGCTGTTATCATTATGATTTTAAATGAGTACTAGCTTTGGCAATTA 4028
Db 3925 GAAGATGTTCAATTTACCCGATCGACTGTATCGAGGATATATTTGATCATCATGACGAG 3984
QY 4029 GAAGATGTTCAATTTACCCGATCGACTGTATCGAGGATATATTTGATCATCATGACGAG 4088
Db 3985 ATATTTACGTTGATATCTTTTTCGAGATGTTGATCAATGGTTGGCCCTGGGCTTTAAG 4044
QY 4089 ATATTTACGTTGATATCTTTTTCGAGATGTTGATCAATGGTTGGCCCTGGGCTTTAAG 4148
Db 4045 GTTACTTTCACCAATGCTGCTGTTGGTGGATTTGCTGATTTGCTGATCTATGCTTATA 4104
QY 4149 GTGTTACTTTCACCAATGCTGCTGTTGGTGGATTTGCTGATTTGCTGATCTATGCTTATC 4208
Db 4105 AATTTGTTGCTGTTGCTGCGGCTTTAAATGATATAGCCGTTTGTAGATCAATCGCAC 4164
QY 4209 AACTTCGTTGCTTTCACCTTTGTTGAGCTGGTGTATTCAGAGCTTTCAGAGCTATCGCAACG 4268
Db 4165 CTGCGCGCTTAAGCCCATTCGCTGCTCTAGATGGGAGGATGAAAGTTGTCGTG 4224
QY 4269 TTAAGACACTGAGACCACTACGTGCCATGTCCTGATGAGGCGATGAGGGTCTGCTGCT 4328
Db 4225 AATCGCTGTTTCAAGCTATACCTCCATCTTCAATGCTTATTTGGTGTCTGCTATTTT 4284
QY 4329 AATCGCTGTTTCAAGCTATACCTCCATCTTCAATGCTTATTTGGTGTCTGCTATTTT 4388
Db 4285 TGGCTTATTTTTCGCTATGAGGAGTACAGCTTTTTCGTTGGAATAATTTTAAAGTGA 4344
QY 4389 TGGCTTATTTTTCGCTATGAGGAGTACAGCTTTTTCGTTGGAATAATTTTAAAGTGA 4448
Db 4345 GATGTTAATGACACTGCTGAGCCATGAATCATACCGAATCGTATGCTGCTGCAAAAGT 4404
QY 4449 GATGTTAATGACACTGCTGAGCCATGAATCATACCGAATCGTATGCTGCTGCAAAAGT 4508
Db 4405 GAAACTACACCTCGGCAAAATTCGGCAATGAACCTTCGATCATGTAGGTATGCTGCTATCTC 4464
QY 4509 GAGAATACACCTCGGCAAAATTCGGCAATGAACCTTCGATCATGTAGGTATGCTGCTATCTC 4568
Db 4465 TGTCTATTTTCAAGTGGCCACCTTTTAAAGGCTGATTCAGATTTTAAAGTGA 4524
QY 4569 TGTCTATTTTCAAGTGGCCACCTTTTAAAGGCTGATTCAGATTTTAAAGTGA 4628
Db 4525 TCACGAGAGTGGCAACAGCAGCCGATCCGAGAAACCAATATCTACATGATTTTATATTTTC 4584
QY 4629 TCACGAGAGTGGCAACAGCAGCCGATCCGAGAAACCAATATCTACATGATTTTATATTTTC 4688

Db 4585 GTATTCCTCATATATTTGGATCATATTTTTCACACTCAATCTGTTCATTTGGTGTATCATTT 4644
Qy 4689 GTATTCCTCATATATTTGGATCATATTTTTCACACTCAATCTGTTCATTTGGTGTATCATTT 4748
Db 4645 GATAATTTTAAAGCAAAAGAAAGAGAGAGGAGGATGATCATTAGAAAATGTTTCATGACAGAA 4704
Qy 4749 GATAATTTTAAAGCAAAAGAAAGAGAGAGGAGGATGATCATTAGAAAATGTTTCATGACAGAA 4808
Db 4705 GATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCACTTAAAAAGCC 4764
Qy 4809 GATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCACTTAAAAAGCC 4868
Db 4765 ATTCCAGAGCCGAGGTGGCGACCAACAGCAATAGTATTGCAATATAGTTACAGATAAAAAA 4824
Qy 4869 ATTCCAGAGCCGAGGTGGCGACCAACAGCAATAGTATTGCAATATAGTTACAGATAAAAAA 4928
Db 4825 TTCGATATATCATATATGTTTTCATTGGCTTAAACATGTTTACCATGACCCCTCGATCGG 4884
Qy 4929 TTCGATATATCATATATGTTTTCATTGGCTTAAACATGTTTACCATGACCCCTCGATCGT 4988
Db 4885 TAGACGCCCTCCGAGCGGTACAACAATGTCCTCGACAAACTCAATGGGATATTCGTAGTT 4944
Qy 4989 TAGCATGCGTCGGACACGTATAACGCGTCTAGACTATCTCAATGCGATATTCGTAGTT 5048
Db 4945 ATTTCAGTGGCGAATCTCTATTAATAATATTCGCTTTACGATATCACTATTTCAAGAG 5004
Qy 5049 ATTTCAGTGGCGAATCTCTATTAATAATATTCGCTTTACGATATCACTATTTTATTAG 5108
Db 5005 CCATGGAATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5064
Qy 5109 CCATGGAATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5168
Db 5065 GACATCATGAGAAATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5124
Qy 5169 GATATTCGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5228
Db 5125 GTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5184
Qy 5229 GTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5288
Db 5185 TTAGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5244
Qy 5289 TTGGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5348
Db 5245 ATCTTTGCTATCTTTTGGCATGCTGCTTCTTCATGATGCTCAAGAGAGAGAGCGGATTAAT 5304
Qy 5349 ATCTTTGCTATCTTTTGGCATGCTGCTTCTTCATGATGCTCAAGAGAGAGAGCGGATTAAT 5408
Db 5305 GCTGTGTATTAATTTAAGACATTTGGCCAAAGTATGATATGCTGTTTCAGATGCTTACC 5364
Qy 5409 GACGCTACAACTTTCAAGACCTTTGGCCAGAGCATGATCCTGCTCTTTCAGATGCTGACG 5468
Db 5365 TCAGCCGGTTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5424
Qy 5469 TCAGCCGGTTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5528
Db 5425 GACACGACAAAGGCTATCCGGGCAATTTGGTTTCAGCGACTGTTTGAATTTACGTTTCTC 5484
Qy 5529 GACACGACAAAGGCTATCCGGGCAATTTGGTTTCAGCGACTGTTTGAATTTACGTTTCTC 5588
Db 5485 CTTCATATCTAGTTTAAAGCTTTTGAATGATGATGATGATGATGATGATGATGATGATGATG 5544
Qy 5589 CTTCATATCTAGTTTAAAGCTTTTGAATGATGATGATGATGATGATGATGATGATGATGATG 5648
Db 5545 GAGAACTATACCCAGGCTACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 5604
Qy 5649 GAGAACTATACCCAGGCTACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 5708
Db 5605 ATGTACTACGAGATTTGGCAACAATTCGATCCGAGGCGACCCAGTACATACGTCAGGAC 5664
Qy 5709 ATGTACTATGAGATCTGGCAGCAATTCGATCCGAGGCGACCCAGTACATACGTCATGAT 5768
Db 5665 CAGCTGTCCGAGTTTCTGGAGCTGCTGGAGCCCGCTGCAGATGCCAAGACCCGAGCAAG 5724

Qy 5769 CACCTGTCCGAATTCCTGGACGCTACTGGAGCCCCCTGCAGATCCACAACCGAACAAG 5828
Db 5725 TACAAAATCATATCGATGACATGCGCATATGTCGGGGCGACATGATGATGATGATGATGATGATG 5784
Qy 5829 TACAAATCATATCGATGACATGCGCATATGTCGGGGTACCTCATGATGATGATGATGATGATG 5888
Db 5785 ATATTGGATGCCCTGACCAAGGACTTCTTTGCGCGCAAGGGTAAATCCGATCGAGGAGACG 5844
Qy 5889 ATCCTCGACGCCCTTACGAAAGACTTCTTTGCGCGCAAGGGCAATCCGATAGAGGAGACG 5948
Db 5845 GGTGAATTTGGTGAATGAGTAGCGGCGCGACCGGACACCGGAGGATATGATCCGGTGTGCTCG 5904
Qy 5949 GGTGAGATTTGGTGAATGAGTAGCGGCGCGCGGATACGAGGGCTACGAGCCCGTCTCATCA 6008
Db 5905 ACACCTGTGGCGCAGCGTGAAGGAGTACTGGCCCAAGCTGATACAGAAATGCGTGGCG 5960
Qy 6009 ACCTGTGGCGTCAAGCTGAGGAGTACTGGCCCGGCTAATCCAGCAGCGCTGGCG 6064

RESULT 12
ID US-08-608-618-2 STANDARD; DNA; UNC; 6318 BP.
AC xxxxxx
DT Sequence 2, Application US/08608618
CC Sequence 2, Application US/08608618
CC GENERAL INFORMATION:
CC APPLICANT: Soderlund, David M.
CC APPLICANT: Knipple, Douglas C.
CC APPLICANT: Ingles, Patricia J.
CC TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
CC TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT
CC TITLE OF INVENTION: HOUSE FLIES
CC NUMBER OF SEQUENCES: 19
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
CC STREET: P.O. Box 1051, Clinton Square
CC CITY: Rochester
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 14603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/608,618
CC FILING DATE:
CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Timian, Susan J.
CC REGISTRATION NUMBER: 34,103
CC REFERENCE/DOCKET NUMBER: 19603/600 (CRF D-1657)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 716-263-1636
CC TELEFAX: 716-263-1600
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6318 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
SQ SEQUENCE 6318 BP; 1713 A; 1349 C; 1592 G; 1664 T; 0 OTHER.

Query Match 56.2%; Score 3660; DB 19; Length 6318;
Best Local Similarity 84.7%; Pred. No. 0.00e+00;
Matches 4978; Conservative 0; Mismatches 814; Indels 84; Gaps 21;
Db 151 ATACGATATGATGACGAGGACGAGGATGAAGGTCACAGCCGATCCACACTTGAACAG 210
Qy 207 ATCCGATATGATGACGAGGACGAGGATGAAGTCCACACCGGATCTACACTTGAACAG 266

2412 GTCTGGGACTGTTGCTGGGTTTGGTTGAAATTTTCAGGAGTGGGTATCGCTCATCGTCTTC 2471
2404 GATCCATTGCTGGAGCTCTTCATTACCTGCTGTATTGTTGGTCAATACATGTTTCATGGCC 2463
2472 GATCCCTTGGTCGAGCTCTTCATCAGCTGTGCTGCTGCTCAACACGATGTTTCATGGCA 2531
2464 ATGGATCATCACACATGAATCCGAAATTAGAGAAGTGTCTGAAAAGTGGTAACTATTTC 2523
2532 ATGGATCACACATGATGACAGGAGATGGAACGGTGTCTCAAGAGTGGCAACTATTTC 2591
2524 TTCACGGCCACTTTTGCATTTAGAGCCAGCATGAAACTGATGCCATGAGCCCGAAGTAC 2583
2592 TTCACGGCCACTTTGCCATCGAGGCCACCATGAAGCTAATGSCCATGAGCCCAAGTAC 2651
2584 TACTTCCAGGAAGCTGGAACTATTTTCGATTTTCATATTGTTGGCCCTGCTCTGCTGGAA 2643
2652 TATTTCCAGGAGGGCTTGGAACTTTTCGACTTTCATATGCTGGCCCTATCGCTATTGGAA 2711
2644 TTGGGCTTGGAGGCTGCCAGGCGCTGCGGTCTTCGAGAAGTTTCGTTTGGTTCGTGTA 2703
2712 CTGGGACTCGAGGGTGTCCAGGGCTGTCCGATTTGCGTTTCGATTTGCTGCGTGA 2771
2704 TTCAAATTTGGCAAAATCATGGCCACACACTCAATTTACTCATTTTCGATTTATGGSCCGGACA 2763
2772 TTCAAACTGGCCAACTTTGGCCACACACTTAATTTACTCATTTTCGATTTATGGACCCACC 2831
2764 ATGGGTGCAATTTGGGTAACTGTGACATTTGATTTGCAATTTATCATCTTCATCTTTGCCGCTG 2823
2832 ATGGGGCTTTGGGTAATCTGACATTTGTACTTTGCAATTTATCATCTTCATCTTTGCCGCTG 2891
2824 ATGGGAATGCAACTTTTCGGAAGAATATATATGACCAAGGATCGCTTCAAGGACCAT 2883
2892 ATGGGAATGCAACTTTTCGGAAGAATATATCATGATCAACAAGGACCGCTTTCCGGATGGC 2951
2884 GAATTAACCGGCTTGGAACTTTACCGGACTTCATGCACAGCTTTCATGATTTGTTCCGAGTG 2943
2952 GACCTGCCGCTTGGAACTTTACCGGACTTTATGCACAGCTTCATGATCGTTCCGGGCTG 3011
2944 CTGTGGGAGAGTGGATCGAGTCCATGTGGGACTGCATGTATGTGGGCGATGTCAGCTGT 3003
3012 CTGTGGGAGAAATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGCGATGTCGTGTC 3071
3004 ATACCTCTTCTTTGCCCGGCTGATCGAGTCCATGTGGGACTGCATGTATGTGGGCGATGTCAGCTGT 3063
3072 ATTCCTCTTCTTTGCCCGGCTGATCGAGTCCATGTGGGACTGCATGTATGTGGGCGATGTCAGCTGT 3131
3064 GCTTTGCTTTTGTCCAACTTCGCTTCATCTAGTTTATCAGCCCGGACTGCCGACATGAT 3123
3132 GCCTTGTCTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCCCGGACTGCCGATACGAT 3191
3124 ACCAATAAATAGCAGAGGCTTTCAATCGTATTGCTCGTTTAAAGAACTGGGTGAAACGT 3183
3192 ACGAATAAATAGCAGAGGCTTTCAATCGAATTTGGCCGATTTAAAGTTGGGTAAAGCT 3251
3184 AATATTGCCGATTTGTTTAAAGTTTAAATTCGAAATAAATGACAAATCAATAAAGTGACCAA 3243
3252 AATATTGCTGATTTTCAAGTTTAAATACGTAAACAAATGACAAATCAATAAAGTGATCAA 3311
3244 CCATCAG-----A-A-CA-----TGG--CGAT-A--ATG----- 3265
3312 CCATCAGTTGAGAGGACCAACAGATCAGTTGGATTTGGAGCGAGAGCATGGTGCACAAC 3371
3266 -AACTGGAGTTGGGTTCATGACGAAATCATGGGCGATGGGTTGATCAAAAAGGGTATGAAG 3324
3372 GAACTGGAGCTGGGCCACGACGAGATCTTCGCGAGGCGCTCATCAAGAAAGGGGATCAAG 3431
3325 GGGGAGACCCAGCTGGAGGTGGCCATTTGGCGATGGCATGGAGTTACGATACATGCGCAT 3384
3432 GAGCAGACGCAACTGGAGGTGGCCATCGGGGATCGGATCGGAATTCACGATACACGCGAC 3491
3385 ATCAAAAACAAACGAGCCAGAAATCAAAATTCATCAACACACACGATGATTGGAAC 3444

3492 ATCAAGAACAAACAGCCGGAAGAAATCCAATATCTAAATAACGCAACGATGATTGCAAC 3551
3445 TCAATAAACCAACCAAGACAATAGACTGGAACATAGACTAAACCATAGAGTTTGTCCATA 3504
3552 TCAATTAACCAACCAAGACAATAGACTGGAACACGAGCTAAACCATAGAGTTTGTCCATA 3611
3505 CAGGAGGATGACACTGCCAGCATTAACCTATGTTAGCCATAAGAAATCGACCATTTCAAG 3564
3612 CAGGAGGACGACTGCCAGCATTAACCTATGTTAGCCATAAGAAATCGACCATTTCAAG 3671
3565 GACGAGAGCCCAAGAGGCGAGCCGAGACCATCGAGGCGAGGAGAAACGCGACGTCAGC 3624
3672 GACGAGAGCCCAAGAGGCGAGCCGAGACCATCGAGGCGAGGAGAAACGCGACGTCAGC 3731
3625 AAAGAGGACCTCGGCTCGACGAGGAACCTGGACGAGGAGCCGAGGCGATGAGGGCCAG 3684
3732 AAGGAGGATTTAGTCTCGACGAGGAACCTGGACGAGGAGGCGAATTCGAGGAGGCCCG 3791
3685 CTGGATGGTGACATTAATCATTTATGCCCCAAAAGGACGACGAGATATATCGACGATTCGG 3744
3792 CTCGAGCGGTGATCATTAATTCATGCACA---CGACGAGGATATATCGATGAATATCCA 3848
3745 GCCGACTGTTCCCGGACTCTACTACAAAGAGTTTCCGATCTTGCCCGCGACGAGGAC 3804
3849 GCTGATGCTGCCCGATTCGTAATAAGAAATTTCCGATCTTTAGCCGGTGACGATGAC 3908
3805 TCGCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAAACCTTTCAATTAATTTGAAAT 3864
3909 TCGCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAAACCTTTCAATTAATTTGAAAT 3968
3865 AATATTTTGAACCGCAGTTATCATATGATTTAATGAGTAGCTTACGTTTGGCCTTA 3924
3969 AATATTTTGAACCGCAGTTATCATATGATTTAATGAGTAGCTTACGTTTGGCCTTA 4028
3925 GAAGATGTTTCAATTTACCGGACTGACCTGTCAGGAGATATCTGCTACATGTCAGGAC 3984
4029 GAAGATGATACATCTGCCACAAGAGCCCTACTGAGGATATTTATATATATATGACAGA 4088
3985 ATATTTACGGTGATATCTTTTGGAGATGTTGATCAAAATGTTGGCCCTTGGCCTTTAAG 4044
4089 ATATTTACGGTGATATCTTTTGGAGATGTTGATCAAAATGTTGGCCTTGGCCTTTAAG 4148
4045 GTCTACTTCACCAATGCTGTTGGCTGGATTTGCGTATGTCATGTCATGTCGCTTATC 4104
4149 GTGTACTTCACCAACGCTGTTGGCTGCTGATTTGCTGATGTCATGTCGCTTATC 4208
4105 AATTTGGTTGCGCTTGGTGGGCTTAAATGATATAGCCGCTTTTATAGATCAATGCCACA 4164
4209 AACTTGGTTGCTTCACTTGTGGAGCTGGTATTTCAAGCCTTCAAGACTATGCGAAGC 4268
4165 CTGCGCGCCTTAAGGCAATTCGCTGCTCTAGATGGGAGGATGAAAGTTGCTG 4224
4269 TTAAGAGCACTGAGACCACTAGTCCGATGTCGCTATCGAGGCGATGAGGTCGCTG 4328
4225 AATGCGCTGGTTCAAGCTATACCGTCCATCTTCAATGTCCTATTTGGTGTGCTGATATTT 4284
4329 AATGCGCTGGTCAAGCTATACCGTCCATCTTCAATGTCCTATTTGGTGTGCTGATATTT 4388
4285 TGGCTTATTTTGGCCATTAATGAGGATGACAGCTTTTGGTGGAAAATATTTTAAAGTGATAA 4344
4389 TGGCTAATTTTGGCCATTAATGAGGATGACAGCTTTTGGTGGAAAATATTTTAAAGTGATAA 4448
4345 GATGTTAATGACATGCTGCTGAGCCATGAAATCAACCAAGCTGATGCTGCTGCAAGCT 4404
4449 GACATGAATGGCAGNAGCTCAGCCACGAGATCATCAAAATCGCAATGCTGCGAGAGC 4508
4405 GAAACTACACCTTGGGAAAATTCGCAATGAACTTCGATCATCTAGGTAAATGCTATCTC 4464
4509 GAGAACTACACCTGGTGAATTCAGCAATGAATTCGATCATGTAGGTAAACGGTATCTG 4568
4465 TGTCTATTTCAAGTGGCCACCTTTAAGGCTCGATTCAGGATTAAGCATGCCATTTGAT 4524
4569 TGCCTTTTCCAAAGTGGCCACCTTCAAGGCTGGATACAAATCATGAACGATGCTCGAT 4628

Db	4525	TCACGAGAGGTGCACAAAGCAGCGCATCCGAGAAACCAATATCTACATGTATTTATATTTTC	4584
Qy	4629	TCACGAGAGGTGCACAAAGCAGCAACCAATTCGTGAACGAAACATCTACATGTATTTATATTTTC	4688
Db	4585	GTATTTCTTCATTAATATTGGATCATTTTTTCACACTCAATCTGTTTCATGGTGGTTATCATTT	4644
Qy	4689	GTATTTCTTCATCAATATTGGATCCCTTTTTCACACTCAATCTGTTTCATGGTGGTTATCATTT	4748
Db	4645	GATAATTTTAAATGAACAAAGAAAGACAGGTGGATCATTTAGAAATGTTTCATGACAGAA	4704
Qy	4749	GATAATTTTAAATGAGCAAAAGAAAAGCAGGTGGATCATTTAGAAATGTTTCATGACAGAA	4808
Db	4705	GATCAGAAAAAGTACTATATGCTATGTAAGAAAGATGGGCTCTAAAAACCAATTTAAAAGCC	4764
Qy	4809	GATCAGAAAAAGTACTATATGCTATGTAAGAAAGATGGGCTCTAAAAACCAATTTAAAAGCC	4868
Db	4765	ATTCCAAGACCGAGGTGGCGACCAACAGCAATAGTATTTCGAAATAGTTTACAGATAAAAAAA	4824
Qy	4869	ATTCCAAGACCAAGTGGCGACCAACAGCAATAGTCTTTGAAATAGTAACCGATAAAGAA	4928
Db	4825	TTCGATATAATCAATATATGTATGTTCATTGGCTTAAACATGTTTTACCATGACCCTCGATCGG	4884
Qy	4929	TTCGATATAATCAATATATGTATTTCAATTTGCTCTGAAACATGTTTCACCATGACCCTCGATCGT	4988
Db	4885	TACGACGCCCTCCGAGCGGTACAACAATGTCCTCGACAACACTCAATGGGATATTCGTAGTT	4944
Qy	4989	TACGATCGTTCGGACACGTATACCGCGGTCTCTAGACTATCTCAATTCGCAATATTCGTAGTT	5048
Db	4945	ATTTTCAGTGGCGAATGTCTATTAAAAATATTTCGGCTTTACGATATCACTATTTCAAAGAG	5004
Qy	5049	ATTTTCAGTTCCGAATGTCTATTAAAAATATTTCGGCTTTACGATATCACTATTTTATTGAG	5108
Db	5005	CCATGGAAATTTATTGATGTAGTAGTTGTCACTTTTATCCACTCTTAGGTCCTGACTCAGC	5064
Qy	5109	CCATGGAAATTTATTGATGTAGTAGTTGTCACTTTTATCCACTCTTAGGTCCTGACTTAGC	5168
Db	5065	GACATCAATTCAGAAAGTATTTCGTATCGCGGACACTGCTCCCGTGTGGTCAGAGTGCCTAAA	5124
Qy	5169	GATATTATCGAAGGTACTTCGTGTTCGCGGACCCCTGCTCCGAGTGGTGTGCTGTGGCGAAA	5228
Db	5125	GTGGGTGCTGCTCTCGGCTTTAGTCAAGGTGCCAAGGATATCCGGACCTTGCTCTTCGCG	5184
Qy	5229	GTGGGCGGTGCTCTTCGACTGTGTGAAGGGAGCAAGGGCAITTCGGACACTGCTCTTCGCG	5288
Db	5185	TTAGCCATGTCTGTGCTTCCTGCTTTATCAACATTTGCTGTGTTGCTGTCTTGGTGATGTTTC	5244
Qy	5289	TTGGCCATGTCTGCTCGCGCCCTGTTCACACTCTCCCTGCTGCTGTCTTCCCTGGTCATGTTTC	5348
Db	5245	ATCTTTGCTATCTTTTGGGATGTCCTTCTTCATGTCATGTCAAAGAGAGAGGCGGATAAAT	5304
Qy	5349	ATCTTTGCCATTTTCGGCATGTCTTCTTCATGCACTGTGAAGGAGAGAGCGGCATTTAAC	5408
Db	5305	GCCTGTGTATAATTTTAAAGACATTTGGCCAAAGTATGATATTGCTGTGTTTCAGATGCTTACC	5364
Qy	5409	GAGCTGTACAACCTTCAAGACCTTTTGGCCAGAGCATGATCTGCTCTTCAGATGCTGACG	5468
Db	5365	TCAGCCGGTGGGATCGGTGTGTTAGATGCCATTATCAATAGGAAAGATTCGGATCCACCC	5424
Qy	5469	TCAGCCGGTGGGATCGGTGTACTGGACGCCATTATCAATAGGAAAGCATGCGATCCACCC	5528
Db	5425	GACAACGACAAGGGCTATCCGGGCAATTTGTGTTTCAGCGCACTGTTGGAATTAACGTTTCTC	5484
Qy	5529	GACAGCGACAAAGGCTATCCGGGCAATTTGTGTTTCAGCGCCGTTTGGAAATAACGTTTCTC	5588
Db	5485	CTTTCATATCTAGTTATAAGCTTTTTTGATAGTTATTAATATGATCATTTGCTGCTCATTTCTC	5544
Qy	5589	CTCTCATACCTAGTTATAAGCTTTTTTGATAGTTATTAATATGATCATTTGCTGCTCATTTCTC	5648
Db	5545	GAGAACTATAGCCAGGCTACGAGAGATGTACAGGAGGTCTCACCGAGGAGGATTTATGAT	5604
Qy	5649	GAGAACTATAGTACGCCACCGAGACGCTGCAAGAGGCTCTAACCGACGAGCTACGAC	5708

Db	5605	ATGTACTACGAGATTGGCAACAATTCGATCCGGAGGGTACCCAGTACATACGATACGAC	5664
Qy	5709	ATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGGCACCAGTACATACGCTATGAT	5768
Db	5665	CAGCTGTCGGAGTTCCTGGACGTCGTGGAGCGCGCTGCAGATCCACAGCCGAAACAAG	5724
Qy	5769	CAGCTGTCGGAATTCCTGGACGTCGTGGAGCCCGCTGCAGATCCACAACCGAACAAG	5828
Db	5725	TACAAAATCATATCGATGGACATGCCGATATATCTCGGGCGGACATGATGTACTGTGTGGAT	5784
Qy	5829	TACAAGATCATATCGATGGACATACCCATCTGTGCGGTGACCTCTGTACTGCGTGCAC	5888
Db	5785	ATATTGGATCCCTGACCAAGGACTCTTTTGGCGCAAGGTAATCCGATCGAGGAGACG	5844
Qy	5889	ATCTCTGACGCCCTTACGAAAGACTCTTTGCGCGGAAGGCAATCCGATAGAGGAGACG	5948
Db	5845	GGTGAATTGGTCAGATAGCGCGGACCGGACACCGGAGGCGCTATGATCCGGTGTCTCG	5904
Qy	5949	GGTGAGATTGGTCAGATAGCGCGGCCCGCGGATACGGAGGGCTACGAGCCGCTCTCATCA	6008
Db	5905	ACACTGTGGCGCCAGCGTGGAGGACTCTGCGCCCAAGCTGATACAGATGCGCTGGCG	5960
Qy	6009	ACGCTGTGGCGTCAGCGTGGAGGACTCTGCGCGCCGCTAATCCAGCAGCGCTGGCG	6064
RESULT 13			
ID	US-08-808-793-26 STANDARD; DNA; UNC; 1237 BP.		
AC	xxxxxx		
DT			
DE	Sequence 26, Application US/08808793		
CC	Sequence 26, Application US/08808793		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Soderlund, David M.		
CC	APPLICANT: Ingles, Patricia J.		
CC	TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS		
CC	TITLE OF INVENTION: AND USE THEREOF		
CC	NUMBER OF SEQUENCES: 32		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP		
CC	STREET: Clinton Square, P.O. Box 1051		
CC	CITY: Rochester		
CC	STATE: New York		
CC	COUNTRY: USA		
CC	ZIP: 14603		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: Floppy disk		
CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: PatentIn Release #1.0, Version #1.30		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/808,793		
CC	FILING DATE:		
CC	CLASSIFICATION: 435		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: US 60/034,361		
CC	FILING DATE: 24-DEC-1996		
CC	CLASSIFICATION: 435		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: US 60/012,649		
CC	FILING DATE: 01-MAR-1996		
CC	CLASSIFICATION: 435		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Braman, Susan J.		
CC	REGISTRATION NUMBER: 34,103		
CC	REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)		
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE: 716-263-1636		
CC	TELEFAX: 716-263-1600		
CC	INFORMATION FOR SEQ ID NO: 26:		
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH: 1237 base pairs		
CC	TYPE: nucleic acid		
CC	STRANDEDNESS: single		

[illegible]

RESULT 7A

RESOL 14
ID US-09-024-030A-1 STANDARD. DNA: UNC. 5977 BP

ID US-09-

AC XXXXXX

DT

Db	4552	GGGATGCTCTTTGATTTGCTCACTCAACAAGCCTTTGACATTTGATCATGATCGTCTCATC	4611
Qy	4896	GCAATAGTCTTTTGAATAGTAAACCGATAAGAAATTCGATATAATCATTTATGTTATTCATT	4955
Db	4612	TGCCTTAACATGTTGACANTGATGGTGGAGACAGACACTCAGAGCAACGACATGGAGAAC	4671
Qy	4956	GGTCTGAACATGTTTCACATGAGCCCTCGATCGTTACGATGGGTGGACACAGCTATAACGGC	5015
Db	4672	ATTCTTTTACGGATTAATCTGGTCTTTGTCATCTTCTTCACTGCGAGTGTGCTCTCAAA	4731
Qy	5016	GTCTAGACTATCTCAATCGGATATTCTGTAGTATTTTTCAGTTCGGAATGTCATTAAAA	5075
Db	4732	ATGTTTCCCTTGAGACACTACTATTTTCCACCATGGCTGGAACATCTTTGACTTTTGGTGG	4791
Qy	5076	ATATTCGCTTTTACGATATCACTATTTTATTAGCCCATGGAATTTATTTGATGTAGTAGTT	5135
Db	4792	GTACATCTCTCCATTTGTTGGGAATGTTCTCGCTGATATCAATGAGAAGTACTTCGTCTCC	4851
Qy	5136	GTCAATTTATCCATCTTAGCTTTGTACTTTACGGATATTTCGAGAAGTACTTCGTGTGG	5195
Db	4852	CCAAACCCTATTTCGAGTTATCCGATTGGCCCGTATTGGCGCATCTTTCGCTCTGATCAAG	4911
Qy	5196	CCGACCCTGCTCCGAGTGGTGGGTGGCGAAGTGGCCGCTGCTTCGACTGGTGAAG	5255
Db	4912	GGCGCCAAAGGGATCCGACCCCTGCTTTTGCTTTAATGATGTCGCTGCCGCCCTGTTTC	4971
Qy	5256	GGAGCCAAAGGGCATTCGGACATGCTTCTTCGGGTTTGGCCATGTCGCTGCCGCCCTGTTTC	5315
Db	4972	AACATCGCCCTCCTGCTCTTCTCTGCTCATGTTTCATCTTCTCCATTTTGGCATGTCCAAC	5031
Qy	5316	AACATCTGCCTGCTGCTGTTCTCTGGTCAATGTTCACTTTTGCCATTTTCGGCATGTCGTT	5375
Db	5032	TTCCGATCATGTAAGCACAGAGCCGGCATTTGACGACATGTTTCAACTTCGAGACATTTGGC	5091
Qy	5376	TTCATGCACGTGAAGAGAAGACGGGCATTTACGACGCTCTACAACCTTCAAGACCTTTGGC	5435
Db	5092	AACAGCATGATCTGTTTGTTCAGATCAACAGCTCTGCTGGCTCGGATGCCCTGCTGCTG	5151
Qy	5436	CAGAGCATGATCTGCTCTTTTTCAGATGTCGAGCTCAGCCGGTTGGGATGTTGACTGGAC	5495
Db	5152	CCATCTCTGAACGCCGCCCTGACTGCAGCTTGGACAAGAGCACCCAGGGAGTGGCTTC	5211
Qy	5496	GCCATTATCAATGAGGAAGC--A-TGC-GATCC-ACCC-GA-CAGCGACAAAG--GCTAT	5546
Db	5212	AAAGGGACTGTGGGAACCCCTCGTGGGCATCTTCTTTTGAGCTACATCATCATC	5271
Qy	5547	CCGGGCMAATGGTTTACGGACCGTTGGAATAAGCTTTCTCTCTCATACCTAGTATATA	5606
Db	5272	TCCTTCTCTGTTGGTGAACATGTACATCGCCATCATCTCTGGAGAACTTTCACGCTGGCC	5331
Qy	5607	AGCTTTTGTAGTTATTAAATGATACATTCGTCTCATCTCTCGAGAATATAGTCAGGCC	5666
Db	5332	ACCGAGGAGCGCCGACCCCTCTGAGTGAGGATGACTTCGAGACTTTCTTAAGAGATCTGG	5391
Qy	5667	ACCGAGGAGCTGCAAGAGGGTCTAACCGACGACGACTACGACATGTACTATGAGATCTGG	5726
Db	5392	GAGAACTTTGACCCAGACGCCACCCAGTTTCATCGAGTACTGTAGCTGGCGAGACTTTGCC	5451
Qy	5727	CAGCAATTCGATCCGGAGGGCACCCAGTACATACGCTATGATCAGCTGTCCGAAATTCCTG	5786
Db	5452	GAGCCCTTGAGACACCCGCTCCGAGTACCCAAAGCCCAACACCATCGAGCTCATCGCCATG	5511
Qy	5787	GAGGTACTGGAGCCCGCTGAGATCCACAAACGGAACAAAGTACAAGATCATATCGATG	5846
Db	5512	GACCTGCCATGTTGAGCGGAGATCGCATCCACTGCTTGGACATCCCTTTTCGCCCTTCACC	5571
Qy	5847	GACATACCCATCTGTGCGGGTGAACCTCATGTACTGCGTGCAGATCTTCGACGCCCTTACG	5906
Db	5572	AA 5573	
Qy	5907	AA 5908	

RESULT	15
ID	US-09-024-020A-2 STANDARD; DNA; UNC; 6007 BP.
AC	xxxxxx
DT	
DE	Sequence 2, Application US/09024020A
CC	Sequence 2, Application US/09024020A
CC	GENERAL INFORMATION:
CC	APPLICANT: DELGADO, STEPHEN G.
CC	APPLICANT: DIETRICH, PAUL S.
CC	APPLICANT: FISH, LINDA M.
CC	APPLICANT: HERMAN, RONALD C.
CC	APPLICANT: SANGAMESWARAN, LAKSHMI
CC	TITLE OF INVENTION: NOVEL CLONED TETRODOXIN-SENSITIVE
CC	TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
CC	NUMBER OF SEQUENCES: 42
CC	CORRESPONDENCE ADDRESS:
CC	ADDRESSEE: JANET PAULINE CLARK
CC	STREET: 3401 HILLVIEW AVENUE, MS A2-250
CC	CITY: PALO ALTO
CC	STATE: CA
CC	COUNTRY: U.S.A.
CC	ZIP: 94304-1397
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: Floppy disk
CC	COMPUTER: IBM PC compatible
CC	OPERATING SYSTEM: PC-DOS/MS-DOS
CC	SOFTWARE: PatentIn Release #1.0, Version #1.30
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: US/09/024,020A
CC	FILING DATE: 16-FEB-1998
CC	CLASSIFICATION: 536
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: US 60/039,447
CC	FILING DATE: 26-FEB-1997
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME: CLARK, JANET P.
CC	REGISTRATION NUMBER: 34,799
CC	REFERENCE/DOCKET NUMBER: R0020B-REG
CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE: (650) 852-3097
CC	TELEFAX: (650) 855-5322
CC	INFORMATION FOR SEQ ID NO: 2:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 6007 base pairs
CC	TYPE: nucleic acid
CC	STRANDEDNESS: single
CC	TOPOLOGY: linear
CC	MOLECULE TYPE: DNA (genomic)
CC	SEQUENCE 6007 BP; 1490 A; 1559 C; 1609 G; 1349 T; 0 OTHER.
Query Match	5.5%; Score 356; DB 23; Length 6007;
Best Local Similarity	65.1%; Pred. No. 0.00e+00;
Matches	899; Conservative 0; Mismatches 471; Indels 12; Gaps 9;
Db	4225 ATCAACTTTGCAGATCGCAGCAGGGTACTGCCCTTCITTCGAAGTGCGAACCTTCAA 4284
QY	
QY	4536 ATGAATTCGATCATGTAGTAGACGGTATCTGTGCTTTTCCAAGTGCGCACCTTCAA 4595
Db	4285 GGCTGGATGACATCATGTATGGGCTGTAGATCCCGAAAGCCAGACGACGCTGAC 4344
QY	
QY	4596 GGCTGGATACAATCATGAACGATGCTATCGATTACGAGAGGTGGACAGCAACAAAT 4655
Db	4345 TAGAGGGCAACATCATCATGTACATCTACTTCGTTCATCTTCATCATCTTCGGCTCCTTC 4404
QY	
QY	4656 CGTGAACAGCAATCATCATGTATTATATTTTCGTATCTTCATCATATAATTTGGATCCTTT 4715
Db	4405 TTCACCCTCAACCTGTTTCATCGGTGCATCATCGACAACCTTCAACAGCAGAGAAGAAAAG 4464
QY	
QY	4716 TTCACACTCAATCTGTTTCATTTGGTGTATCATTTGATTAATTTTATGAGCAAGAAAAA 4775
Db	4465 TTGGAGG--TCAG--GACATCTTTACAGAGGAAACAGAAAGTACTACATGCGCATG 4521

QY 4776 GCAGGTGGATCATTTAGAAATGTTTCATCAGAGAAGATCAGAAAAAGTACTATAATGCTATG 4835
Db 4522 AAAAGCTGGCTCCAGAGAGCCACAGAGCCCATCCCGACCCCTTGAACAAAATCCAA 4581
QY 4836 AAAAGATGGGCTCTAAAAAACCAATTAAGAGCCATTCCAAGACCAAGGTGGCGACCAAA 4895
Db 4582 GGGATTCCTTTGATTTGCTCACTCAACAGCCCTTTCACATTTGTGATCATGATGCTATC 4641
QY 4896 GCATAGCTTTTGAATAGTAAACCGATGAAGAAATTCGATATAATCATATTGTTATTCATT 4955
Db 4642 TGCCTTAACATGTGTGACAATGATGGTGGAGACAGACTCAGAGCAAGCAGATGGAGAAC 4701
QY 4956 GGCTGAACATGTTCAACATGACCCCTCGATCGTTACGATCGTGGACACGATAAACGG 5015
Db 4702 ATTCTTTACTGGATTAATCTGGTCTTTGTCATCTTCTACCTGCGAGTGTGCTCAAA 4761
QY 5016 GTCTAGACTATCTCAATCGGATATCGTAGTTATTTAGTCCGAATGCTATTAAAA 5075
Db 4762 ATGTTTGCCTTGAGACACTACTATTTCACCATGGCTGGGAACATCTTTGACTTTTGGTG 4821
QY 5076 ATATTGCTTTAGCATATCATATTATTAGCCATGGAATTTATTGTAGTAGTAGTT 5135
Db 4822 GTCATCTCTCCATTTGGGAATGTTCTCGCTGATATCATTTGAGAAGTACTTCTGCTCC 4881
QY 5136 GTCATTTTATCCATCTTAGGTCTGTACTTAGCGATATATTCGAGAAGTACTTCTGCTCG 5195
Db 4882 CCAACCCATTTCGAGTTATCCGATTTGGCCGTTATTTGGGCGCATCTTTCGCTCTGATCAAG 4941
QY 5196 CCGACCCCTGCTCCGAGTGTGGGTGGCGAAAGTGGGCGGTGTCCTTCGACTGGTGAAG 5255
Db 4942 GGGCCAAAGGATCCGACCTGCTCTTTGCTTAAATGATGCTGCTGCGCCCTGCTTC 5001
QY 5256 GGAGCCAAAGGCATTCGGACACTGCTCTGCGGTGGCCATGCTGCTGCGGCGCTGCTTC 5315
Db 5002 AACATCGCT 5061
QY 5316 AACATCTGCTCTGCT 5375
Db 5062 TTCGATACGTTGAAGCAGCGCGGCTTACGACATGTTCAACTTCGAGACATTTGGC 5121
QY 5376 TTCATGCAGTGAAGGAGAGAGCGGCTTAAACGCTGACACTTCAAGACCTTTGGC 5435
Db 5122 AACAGATGATCTTTGTTCCAGATCACAACGCTCTCTGCTGGTGGGATGGCTGCTGCTG 5181
QY 5436 CAGAGCATGATCT 5495
Db 5182 CCAATCTGACCCGCCCTCTGCTGAGCTTGGACAAAGACCCAGGAGTGGCTTC 5241
QY 5496 GCCATTATCAATGAGGAGC--A-TGC-GATCC-ACCC-GA-CAGCGACAAAG--GCTAT 5546
Db 5242 AAAGGGACTGTGGGAACCCCTCGGTGGGATCTTCTCTTTGTGAGCTACATCATCATC 5301
QY 5547 CCGGCAATTTGTTTTCAGCGACCGTTTGAATAACGTTTCTCCTCTCATACCTAGTTATA 5606
Db 5302 TCCTTCTGATTTGTTGAACATGATACATCCCATCATCTCTGGAGAACTTCAGCGTGGCC 5361
QY 5607 AGCTTTTGTAGTTATTAAATATGATATGCTGCTCATCTCTCGAGAACTATAGTCAGGCC 5666
Db 5362 ACCGAGGAGCGCGCCCTCTGAGTGAGGATGACTTCGAGACTTTCTATGAGATCTGG 5421
QY 5667 ACCGAGACGTTGAAGAGGGTCTAACCGACGACGACTACGACATGTACTATGAGATCTGG 5726
Db 5422 GAGAAGTTTGACCCAGCGCCAGCTTTCATCGAGTACTGTAAGCTGGCAGACTTTTGGC 5481
QY 5727 CAGCAATTCGATCCGAGGGGACCCAGTACATACGCTATGATCAGCTGTCCGAATTCCTG 5786
Db 5482 GACGCCCTGGAGCACCCTCCGATCCCAAGCCCAACACCATCGAGCTCATCGCCATG 5541
QY 5787 GACGTACTGGAGCCCCGCTCGAGATCCACAAACCGAAGTACAAGATCATATCGATG 5846
Db 5542 GACCTGCCATGGTGGGGAGATCGGATCCACTGCTTGGACATCTCTTTGCGCCTTCACC 5601
QY 5847 GACATACCCATCTCTCGCGGTGACCTCATGTACTGCTGACATCTCTCGACGCGCTTACG 5906

Db 5602 AA 5603

QY 5907 AA 5908

Search completed: Sun Sep 13 08:58:55 1998
Job time : 5574 secs.

THIS PAGE BLANK (USPTO)

MPERLEH (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sun Sep 13 00:05:48 1998; MasPar time 10087.83 Seconds
Tabular output not generated. 1185.989 Million cell updates/sec

Title: >US-08-554-424-7
Description: (1-6513) from US08554424.seq
Perfect Score: 6513 1 TCTAGACGTTGGCCGATAG.....ACCGAGTATTAGCTCTAGA 6513
N.A. Sequence: 6513 AGATCTGCAACCGCGTATC.....TGCCTCATATCGAGATCT
Comp: 1

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 532259 seqs, 918475165 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb155

1:em_ba 2:em_htg 3:em_hum1 4:em_hum2 5:em_in 6:em_om
7:em_or 8:em_ov 9:em_pat 10:em_pl 11:em_ro

genbank107
12:gb_ba 13:gb_htg 14:gb_in 15:gb_om 16:gb_ov 17:gb_pat
18:gb_ph 19:gb_pl 20:gb_pr1 21:gb_pr2 22:gb_ro 23:gb_st
24:gb_sts 25:gb_sy 26:gb_un 27:gb_v1

Statistics: Mean 12.748; Variance 6.375; scale 2.000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	6513	100.0	6513	17	174672	Sequence 7 from patent 0.00e+00
2	6513	100.0	6513	17	125433	Sequence 7 from patent 0.00e+00
3	6513	100.0	6513	17	133685	Sequence 7 from patent 0.00e+00
4	5992	92.0	6883	14	DROSODCHA	Drosophila melanogaste 0.00e+00
5	3676	56.4	6318	14	MDU38813	Musca domestica insect 0.00e+00
6	3676	56.4	6899	14	MDPARA	M. domestica mRNA for v 0.00e+00
7	3664	56.3	6315	14	MDU38814	Musca domestica insect 0.00e+00
8	1912	29.4	6096	14	EGU73584	Blattella germanica pa 0.00e+00
9	1910	29.3	6096	14	EGU73583	Blattella germanica pa 0.00e+00
10	1592	24.4	2144	14	DVU26343	Drosophila virilis sod 0.00e+00
11	1441	22.1	5068	14	EGU71083	Blattella germanica pa 0.00e+00
12	696	10.7	985	14	U83872	Haematobia irritans pa 0.00e+00
13	694	10.7	985	14	U83874	Haematobia irritans pa 0.00e+00
14	485	7.4	1840	14	DMU26715	Drosophila melanogaste 0.00e+00
15	448	6.9	947	14	U83871	Haematobia irritans pa 0.00e+00

15	446	6.8	947	14	U83873	Haematobia irritans pa 0.00e+00
17	391	6.0	5616	14	SQDNACH	Squid sodium channel m 7.23e-288
18	372	5.7	5352	22	MMU26707	Mus musculus voltage-g 6.77e-272
19	363	5.6	6822	22	RNSCIII	Rat mRNA for brain sod 2.43e-264
20	354	5.4	6826	22	RATSCP6A	Rattus norvegicus sodi 8.62e-257
21	352	5.4	7545	22	RATSCAL	Rat cardiac specific s 4.10e-255
22	342	5.3	6328	20	HUMHBAX	Human voltage-gated so 9.79e-247
23	341	5.2	5203	16	FRSCAS2	Fugu rubripes mRNA for 6.73e-246
24	341	5.2	7823	20	HUMSKMIA	Homo sapiens skeletal 6.73e-246
25	336	5.2	8552	22	RATNACHI	Rattus norvegicus sodi 1.03e-241
26	336	5.2	8553	22	RNSCPIIR	Rattus norvegicus sodi 1.03e-241
27	334	5.1	5523	22	RN17153	Rat brain mRNA for sod 4.86e-240
28	334	5.1	6957	22	RATNCHVS	Rat skeletal muscle vo 4.86e-240
29	316	4.9	5952	22	ACU79568	Rattus norvegicus volt 5.38e-225
30	316	4.9	6396	14	ACU66915	Aplysia californica so 5.38e-225
31	320	4.9	8398	22	RNSCPIR	Rat brain mRNA for sod 2.46e-228
32	320	4.9	8399	22	RATNACHI	Rattus norvegicus sodi 2.46e-228
33	320	4.9	8491	20	HUMH11A	Human cardiac tetradot 2.46e-228
34	316	4.9	9316	22	AFU00358	Rattus norvegicus volt 5.38e-225
35	313	4.8	3312	14	DMU26714	Drosophila melanogaste 1.72e-222
36	312	4.8	5955	15	OCU35238	Oryctolagus cuniculus 1.17e-221
37	306	4.7	5505	15	ECU25930	Equus caballus skeleta 1.19e-216
38	308	4.7	6371	20	HSVASCAS	H. sapiens mRNA for vol 2.55e-218
39	302	4.6	542	14	HIU32390	Haematobia irritans ex 2.56e-213
40	298	4.6	6344	22	RNSU3833	Rattus norvegicus sodi 5.50e-210
41	296	4.5	6524	9	RNSNS	R. norvegicus mRNA for 2.54e-208
42	296	4.5	6524	9	A58853	Sequence 1 from Patent 2.54e-208
43	296	4.5	6527	9	A58859	Sequence 7 from Patent 2.54e-208
44	296	4.5	7052	9	A58857	Sequence 5 from Patent 2.54e-208
45	284	4.4	6373	22	MMSNS	M. musculus mRNA for SN 2.44e-198

ALIGNMENTS

RESULT 1
LOCUS I74672 6513 bp DNA PAT 23-DEC-1997
DEFINITION Sequence 7 from patent US 5688917.
ACCESSION I74672
NID g3010813
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6513)
AUTHORS Arena, J.P., Feng, G., Hall, L.M., Liu, K., Van Der Ploeg, L.H.T., Wang, P. and Warmke, J.W.
TITLE Process for functional expression of the para cation channel
JOURNAL Patent: US 5688917-A 7 18-NOV-1997;
FEATURES
source Location/Qualifiers
1..6513
/organism="unknown"
BASE COUNT 1681 a 1548 c 1702 g 1582 t
ORIGIN

Query Match 100.0%; Score 6513; DB 17; Length 6513;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	TCTAGACGTTGGCCGATAGACAAATGACAGAGATTCCTCCACTCGATATCTGAGGAGAAGAC	60
QY	1	TCTAGACGTTGGCCGATAGACAAATGACAGAGATTCCTCCACTCGATATCTGAGGAGAAGAC	60
Db	61	GCAGTTTGTTCGTCCTTTTACCCTCCGGAATCATTTGGTGCAAAATCGAACACGCGATTGCCG	120
QY	61	GCAGTTTGTTCGTCCTTTTACCCTCCGGAATCATTTGGTGCAAAATCGAACACGCGATTGCCG	120
Db	121	CTGAACATGAAAGCAGAGAGGAGCTGGAAAGAAAGAGAGCCGAGGAGAGGTGCCCGCAT	180
QY	121	CTGAACATGAAAGCAGAGAGGAGCTGGAAAGAAAGAGAGCCGAGGAGAGGTGCCCGCAT	180
Db	181	ATGCTCGCAAGAAAAACAAAAAATATCGATATGATGACGAGGACGAGGATGAAGGTC	240
QY	181	ATGCTCGCAAGAAAAACAAAAAATATCGATATGATGACGAGGACGAGGATGAAGGTC	240

Db 241 CACAACCGGATCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTGCAGGCGAGCT 300
|
|
|
QY 241 CACAACCGGATCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTGCAGGCGAGCT 300
|
|
|
Db 301 TCCCGCGGAATTTGGCTCCACATCCCTCTCGAGGATATCGATCCCTACTACAGCAATGTATC 360
|
|
|
QY 301 TCCCGCGGAATTTGGCTCCACATCCCTCTCGAGGATATCGATCCCTACTACAGCAATGTATC 360
|
|
|
Db 361 TGACATTCTGATGTGAAGCAAGAAAGATATTTTTCGCTTTTCGCTATCAAAAGCAA 420
|
|
|
QY 361 TGACATTCTGATGTGAAGCAAGAAAGATATTTTTCGCTTTTCGCTATCAAAAGCAA 420
|
|
|
Db 421 TGTGGATGCTCGATCCATTCATCCGATAGCTGTGTGGCCATTTACATCTAGTGCATC 480
|
|
|
QY 421 TGTGGATGCTCGATCCATTCATCCGATAGCTGTGTGGCCATTTACATCTAGTGCATC 480
|
|
|
Db 481 CATTAATTTCCCTATTTCATCATCACCAAAATTCCTCGTCAACTCCATCCCTGATGATAATGC 540
|
|
|
QY 481 CATTAATTTCCCTATTTCATCATCACCAAAATTCCTCGTCAACTCCATCCCTGATGATAATGC 540
|
|
|
Db 541 CGACAACGCCACCGTTGAGTCCACTGAGTGATATTTCACCGGAATCTACACATTTGAAT 600
|
|
|
QY 541 CGACAACGCCACCGTTGAGTCCACTGAGTGATATTTCACCGGAATCTACACATTTGAAT 600
|
|
|
Db 601 CAGCTGTTAAAGTGTATGCGACAGGTTTCATTTTATGCCGTTTACGTATCTTAGAGATG 660
|
|
|
QY 601 CAGCTGTTAAAGTGTATGCGACAGGTTTCATTTTATGCCGTTTACGTATCTTAGAGATG 660
|
|
|
Db 661 CATGSAATTTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGACCATGGGTATAGATT 720
|
|
|
QY 661 CATGSAATTTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGACCATGGGTATAGATT 720
|
|
|
Db 721 TAGGTAACTAGCAGCCCTCGAAGCTTTAGGTGCTGCGAGCGCTTAAACCGTAGCCA 780
|
|
|
QY 721 TAGGTAACTAGCAGCCCTCGAAGCTTTAGGTGCTGCGAGCGCTTAAACCGTAGCCA 780
|
|
|
Db 781 TTGTGCCAGGCTTGAAGACCATCGTTCGCGCGCTCATCGAATCGGTGAAGAATCTCGCG 840
|
|
|
QY 781 TTGTGCCAGGCTTGAAGACCATCGTTCGCGCGCTCATCGAATCGGTGAAGAATCTCGCG 840
|
|
|
Db 841 ATGTGATTATCCGTACCATGTTCTCCCTGTCGGGTGTCGGCTTATGAGCCCTACAGATCT 900
|
|
|
QY 841 ATGTGATTATCCGTACCATGTTCTCCCTGTCGGGTGTCGGCTTATGAGCCCTACAGATCT 900
|
|
|
Db 901 ATATGGCGTGTCCACGAGAGTGCATCAAGAAGTTCCTCGCTGACCGGTTCTCTGGGSCA 960
|
|
|
QY 901 ATATGGCGTGTCCACGAGAGTGCATCAAGAAGTTCCTCGCTGACCGGTTCTCTGGGSCA 960
|
|
|
Db 961 ATCTGACCGAGACGAACTGGGACTATCAAAATCGCAATAGCTTCCAAATTTGGTATTCGGAGG 1020
|
|
|
QY 961 ATCTGACCGAGACGAACTGGGACTATCAAAATCGCAATAGCTTCCAAATTTGGTATTCGGAGG 1020
|
|
|
Db 1021 ACAGGGCATCTCATTTCCGTTATGGGCAATATATCCGTTGCGGGCAATGCGAGCAGC 1080
|
|
|
QY 1021 ACAGGGCATCTCATTTCCGTTATGGGCAATATATCCGTTGCGGGCAATGCGAGCAGC 1080
|
|
|
Db 1081 ATTTACGTGTGCTGACAGGGTTTGGTCCGAATTCGAATTTATGGCTACACAGCTTCGATT 1140
|
|
|
QY 1081 ATTTACGTGTGCTGACAGGGTTTGGTCCGAATTCGAATTTATGGCTACACAGCTTCGATT 1140
|
|
|
Db 1141 CGTTCCGATGGGTTTTCCTGTCGGCTTCCGCTGATGACAGAGACTTCTGGGAGGATC 1200
|
|
|
QY 1141 CGTTCCGATGGGTTTTCCTGTCGGCTTCCGCTGATGACAGAGACTTCTGGGAGGATC 1200
|
|
|
Db 1201 TGTACCACTGGTGTTCGCGCGCGCGGACCATGGGCATGCTGTTCTTTATAGTCATCA 1260
|
|
|
QY 1201 TGTACCACTGGTGTTCGCGCGCGCGGACCATGGGCATGCTGTTCTTTATAGTCATCA 1260
|
|
|
Db 1261 TCTTCTTAGGTTTCTATCTTGTGAATTTGATTTGGCCATTTGTCCTATGCTATG 1320
|
|
|
QY 1261 TCTTCTTAGGTTTCTATCTTGTGAATTTGATTTGGCCATTTGTCCTATGCTATG 1320
|
|
|

Db 1321 ACGAATTTGCAAGAGAGCGCCGAAGAGAGAGGCTGCCGAGAGAGGAGCGGATACGTGAAG 1380
|
|
|
QY 1321 ACGAATTTGCAAGAGAGCGCCGAAGAGAGAGGCTGCCGAGAGAGGAGCGGATACGTGAAG 1380
|
|
|
Db 1381 CGGAAGAGCTGCCGCGCCCAAGAGCGCCAAAGCTGGAGGAGCGGCAATTCGCAGCGCTC 1440
|
|
|
QY 1381 CGGAAGAGCTGCCGCGCCCAAGAGCGCCAAAGCTGGAGGAGCGGCGCAATTCGCAGCGCTC 1440
|
|
|
Db 1441 AGGAGAGCGGATGCGGCTGCCGCCGAAGAGGCTGCACATTCGCGGAATTCGCCAAGA 1500
|
|
|
QY 1441 AGGAGAGCGGATGCGGCTGCCGCCGAAGAGGCTGCACATTCGCGGAATTCGCCAAGA 1500
|
|
|
Db 1501 GTCCGACGATCTTCTGTGATCAGCTATGAGCTATTTGTTGCGGCGGAGGCAACCGATG 1560
|
|
|
QY 1501 GTCCGACGATCTTCTGTGATCAGCTATGAGCTATTTGTTGCGGCGGAGGCAACCGATG 1560
|
|
|
Db 1561 ACAACAACAAGAGAGATGTCATTCCGAGCGTCGAGGTGGAGTGGAGTTCGCTGAGCG 1620
|
|
|
QY 1561 ACAACAACAAGAGAGATGTCATTCCGAGCGTCGAGGTGGAGTGGAGTTCGCTGAGCG 1620
|
|
|
Db 1621 TTATACAAGACAACCGACCTACCAAGACACACCAAGCTTACCAAGTTTCGTTAAAGTGA 1680
|
|
|
QY 1621 TTATACAAGACAACCGACCTACCAAGACACACCAAGCTTACCAAGTTTCGTTAAAGTGA 1680
|
|
|
Db 1681 GCACGACATCTTATCTTACCTTACCTGGTTTACCGTTTAAACATACGAGGAGTACGTAGTT 1740
|
|
|
QY 1681 GCACGACATCTTATCTTACCTTACCTGGTTTACCGTTTAAACATACGAGGAGTACGTAGTT 1740
|
|
|
Db 1741 CTCACAAGTACACGATACGGAACCGGCTGGCGCTTTGGTATATCCCGGTAGCGATCGTA 1800
|
|
|
QY 1741 CTCACAAGTACACGATACGGAACCGGCTGGCGCTTTGGTATATCCCGGTAGCGATCGTA 1800
|
|
|
Db 1801 AGCCATTTGTTATGATCAATATCAGGATGCCAGCAGCACTTGCCTATGCCGAGCT 1860
|
|
|
QY 1801 AGCCATTTGTTATGATCAATATCAGGATGCCAGCAGCACTTGCCTATGCCGAGCT 1860
|
|
|
Db 1861 CGAATGCCCTCACCGGATGTCGGAAGAGATGGGGCCATCATAGTGCCTGTACTATG 1920
|
|
|
QY 1861 CGAATGCCCTCACCGGATGTCGGAAGAGATGGGGCCATCATAGTGCCTGTACTATG 1920
|
|
|
Db 1921 GCAATCTAGGCTCCCGACACTCATCTGATPACCTGCATCAGTCCCGAATATCGTATACCT 1980
|
|
|
QY 1921 GCAATCTAGGCTCCCGACACTCATCTGATPACCTGCATCAGTCCCGAATATCGTATACCT 1980
|
|
|
Db 1981 CACATGGCATCTACTCGCGGCGCATGGCGTATGGGGTACAGCACATGACCAAGGAGA 2040
|
|
|
QY 1981 CACATGGCATCTACTCGCGGCGCATGGCGTATGGGGTACAGCACATGACCAAGGAGA 2040
|
|
|
Db 2041 GCAAAATGGCAACCGCAACACACGCAATCAATCAGTGGCGGCCACCAATGGCGCACCA 2100
|
|
|
QY 2041 GCAAAATGGCAACCGCAACACACGCAATCAATCAGTGGCGGCCACCAATGGCGCACCA 2100
|
|
|
Db 2101 CTTGTCTGGACACCAATCAAGCTCGATCATCGCGACTACGAAATTTGGCTTGGAGTGA 2160
|
|
|
QY 2101 CTTGTCTGGACACCAATCAAGCTCGATCATCGCGACTACGAAATTTGGCTTGGAGTGA 2160
|
|
|
Db 2161 CGGACGAGCTGCGAGATTAACATCATGACAATCTTTTATCGAGCGCGTCCAGACAC 2220
|
|
|
QY 2161 CGGACGAGCTGCGAGATTAACATCATGACAATCTTTTATCGAGCGCGTCCAGACAC 2220
|
|
|
Db 2221 AAACGGTGGTGTATGAAAGATGTGATGCTCTGAATGACATCATCGAACAGCGCGCTG 2280
|
|
|
QY 2221 AAACGGTGGTGTATGAAAGATGTGATGCTCTGAATGACATCATCGAACAGCGCGCTG 2280
|
|
|
Db 2281 GTCCGACAGTCCGGCAAGCGATCGGGTGTCTCCGTTTACTATTTCGCAACAGAGGACG 2340
|
|
|
QY 2281 GTCCGACAGTCCGGCAAGCGATCGGGTGTCTCCGTTTACTATTTCGCAACAGAGGACG 2340
|
|
|
Db 2341 ATGACGAGGATGGGCCACGCTTCAAAGACAGGCACTTCGAAATGATCTCTCAAAGGATCG 2400
|
|
|
QY 2341 ATGACGAGGATGGGCCACGCTTCAAAGACAGGCACTTCGAAATGATCTCTCAAAGGATCG 2400
|
|
|
Db 2401 ATGTGTTTGTGTGGGACTGTGTGGTGTGGTGTGAAATTCAGGAGTGGGTATCGC 2460

|||||
QY 2401 ATGTTTGTGTGGGACTGTGCTGGTTGGTTGAAATTTACAGGATGGGTATCCG 2460
Db 2461 TCATCGTCTTCGATCCCTTGTGCGAGCTCTTTCATCAGCTGTGCAATTTGGTCAACACGA 2520
QY 2461 TCATCGTCTTCGATCCCTTGTGCGAGCTCTTTCATCAGCTGTGCAATTTGGTCAACACGA 2520
Db 2521 TGTTCATGCAATGGATCACCAGATATGAACAAGAGATGGACCGGTGCTCAAGAGTG 2580
QY 2521 TGTTCATGCAATGGATCACCAGATATGAACAAGAGATGGACCGGTGCTCAAGAGTG 2580
Db 2581 GCAACTATTCTTCACGGCACCTTTGCCATCGAGGCCACCTGAAGCTAAATGGCCATGA 2640
QY 2581 GCAACTATTCTTCACGGCACCTTTGCCATCGAGGCCACCTGAAGCTAAATGGCCATGA 2640
Db 2641 GCCCAAGTACTATTTCCAGGAGGGCTGGAACATCTTCGACTTCATATCGTGGCCCTAT 2700
QY 2641 GCCCAAGTACTATTTCCAGGAGGGCTGGAACATCTTCGACTTCATATCGTGGCCCTAT 2700
Db 2701 CGCTATTGGAACGTGGAGCTCGAGGGTGTCCAGGGTCTGCGGTATTCGCTTTTCGAT 2760
QY 2701 CGCTATTGGAACGTGGAGCTCGAGGGTGTCCAGGGTCTGCGGTATTCGCTTTTCGAT 2760
Db 2761 TCGTGTGTGTAATCAACTGGCCCAAGCTTGGCCACACTTAATTTACTCATTTTCGATTA 2820
QY 2761 TCGTGTGTGTAATCAACTGGCCCAAGCTTGGCCACACTTAATTTACTCATTTTCGATTA 2820
Db 2821 TGGGAGCCACCATGGCGCTTTGGGTAATCTGACATTTGTACTTTGCATATATCATCTTCA 2880
QY 2821 TGGGAGCCACCATGGCGCTTTGGGTAATCTGACATTTGTACTTTGCATATATCATCTTCA 2880
Db 2881 TCCTTCGGGTGATGGGAATGCAACTGTCGGAAGAATATATCATGATCAAGGACCGCT 2940
QY 2881 TCCTTCGGGTGATGGGAATGCAACTGTCGGAAGAATATATCATGATCAAGGACCGCT 2940
Db 2941 TTCGGATGCGACCTTGGCGCGTGGAACTTCACCGACTTATGACAGCTTCATGATCG 3000
QY 2941 TTCGGATGCGACCTTGGCGCGTGGAACTTCACCGACTTATGACAGCTTCATGATCG 3000
Db 3001 TGTTCCGGGTGCTCTCGGAGAAATGGATCGAGTCCATGTGGGACTGCATGTAGTGGGG 3060
QY 3001 TGTTCCGGGTGCTCTCGGAGAAATGGATCGAGTCCATGTGGGACTGCATGTAGTGGGG 3060
Db 3061 ATGCTCGTGCAATCCCTTCTTGGCCACCGTGTGTCATCGGCAATTTGTGGTACTTA 3120
QY 3061 ATGCTCGTGCAATCCCTTCTTGGCCACCGTGTGTCATCGGCAATTTGTGGTACTTA 3120
Db 3121 ACCTTTCTTAGCTTGTCTTTGTCCTCAATTTGGCTCATCTAGCTTATCAGCCCGACTG 3180
QY 3121 ACCTTTCTTAGCTTGTCTTTGTCCTCAATTTGGCTCATCTAGCTTATCAGCCCGACTG 3180
Db 3181 CCATTAACGATACGAATAAATAGCCGAGGCGCTTCAATCGAATGGCGGATTTAAAAGTT 3240
QY 3181 CCATTAACGATACGAATAAATAGCCGAGGCGCTTCAATCGAATGGCGGATTTAAAAGTT 3240
Db 3241 GGGTTAAGCGTAATATGCTGATTTGTTCAAGTTAATACGTAACAAATGACAAATCAAA 3300
QY 3241 GGGTTAAGCGTAATATGCTGATTTGTTCAAGTTAATACGTAACAAATGACAAATCAAA 3300
Db 3301 TAAGTATCAACCATCAGGTGAGAGACCAACCCAGATCAGTTGGATTTGGAGCGGAAGCG 3360
QY 3301 TAAGTATCAACCATCAGGTGAGAGACCAACCCAGATCAGTTGGATTTGGAGCGGAAGCG 3360
Db 3361 ATGGTGACAAAGCAACTGGAGCTGGGCCACGACGAGATCTCTCGCGGACGCGCTCATCAAG 3420
QY 3361 ATGGTGACAAAGCAACTGGAGCTGGGCCACGACGAGATCTCTCGCGGACGCGCTCATCAAG 3420
Db 3421 AGGGGATCAAGGAGCAGACCAACTGGAGGTGGCCATCGGGGATCGGATGGAATTCACGA 3480
QY 3421 AGGGGATCAAGGAGCAGACCAACTGGAGGTGGCCATCGGGGATCGGATGGAATTCACGA 3480
Db 3481 TACAGCGCATGTGAAGAACAAACAGCCGAAGAAATTCCAAATATCTAAATATACGCAACGA 3540
|||||

QY 3481 TACAGCGCATGTGAAGAACAAACAGCCGAAGAAATTCCAAATATCTAAATATACGCAACGA 3540
Db 3541 TGATTGGCAACTCAATTAACCAACCAAGCAATAGACTTGGAAACAGGCTAAACCATAGAG 3600
QY 3541 TGATTGGCAACTCAATTAACCAACCAAGCAATAGACTTGGAAACAGGCTAAACCATAGAG 3600
Db 3601 GTTTGTCTTTACAGACGACGACACTGCCAGCATTAACCTCATATGTTAGCCATAGAATC 3660
QY 3601 GTTTGTCTTTACAGACGACGACACTGCCAGCATTAACCTCATATGTTAGCCATAGAATC 3660
Db 3661 GACCATTAAGCAGCAGAGCCCAAGGGCAGCGCCGAGACGATGGAGGCGGAGGAAGC 3720
QY 3661 GACCATTAAGCAGCAGAGCCCAAGGGCAGCGCCGAGACGATGGAGGCGGAGGAAGC 3720
Db 3721 GCGAGCCACGACGAGGAGGATTTAGTCTCGACGAGGAACCTGGACGAGGAGCGCAATGG 3780
QY 3721 GCGAGCCACGACGAGGAGGATTTAGTCTCGACGAGGAACCTGGACGAGGAGCGCAATGG 3780
Db 3781 AGGAGGCCCGCTCGACGGTGATATCATTTATTCACACGACGAGGATATCTCGATG 3840
QY 3781 AGGAGGCCCGCTCGACGGTGATATCATTTATTCACACGACGAGGATATCTCGATG 3840
Db 3841 AATATCCAGCTGATTCCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTG 3900
QY 3841 AATATCCAGCTGATTCCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTG 3900
Db 3901 AGCATGACTCGCGGCTTCGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTA 3960
QY 3901 AGCATGACTCGCGGCTTCGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTA 3960
Db 3961 TTGAAATTAATATTTTGAACAGCTGTTTATCAGTATGATTTTAAATGAGTCTTAGCTT 4020
QY 3961 TTGAAATTAATATTTTGAACAGCTGTTTATCAGTATGATTTTAAATGAGTCTTAGCTT 4020
Db 4021 TGGCATTAAGACATGATACATCTGCCACAAGACCCATCTGCAGGATATTTTACTATA 4080
QY 4021 TGGCATTAAGACATGATACATCTGCCACAAGACCCATCTGCAGGATATTTTACTATA 4080
Db 4081 TGGACAGAATATTTACGGTTATATTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG 4140
QY 4081 TGGACAGAATATTTACGGTTATATTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG 4140
Db 4141 GCTTCAAAAGTACTTCAACACGCGTGTGTTGGCTCGATTTTCGTTGATGCTATG 4200
QY 4141 GCTTCAAAAGTACTTCAACACGCGTGTGTTGGCTCGATTTTCGTTGATGCTATG 4200
Db 4201 CGCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTGGTATTCAGGCTTCAAGACTA 4260
QY 4201 CGCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTGGTATTCAGGCTTCAAGACTA 4260
Db 4261 TCGCAACGTTAAGAGCAGCTGAGACCACTACGTGCCATGTCCCGTATGCGAGGCGATGAGG 4320
QY 4261 TCGCAACGTTAAGAGCAGCTGAGACCACTACGTGCCATGTCCCGTATGCGAGGCGATGAGG 4320
Db 4321 TCGTCTTAAATCGCTGTGTACAGCTATACCGTCCATCTTCAATGTCTATTTGGTGTGTC 4380
QY 4321 TCGTCTTAAATCGCTGTGTGTACAGCTATACCGTCCATCTTCAATGTCTATTTGGTGTGTC 4380
Db 4381 TAATATTTGGCTTAATTTTGGCATAAATGGGTGTACAGCTTTTGTGCGAAATATTTTA 4440
QY 4381 TAATATTTGGCTTAATTTTGGCATAAATGGGTGTACAGCTTTTGTGCGAAATATTTTA 4440
Db 4441 AGTGCAGGACATGAATGCGACGAGCTCAGCCACGAGATCATACCAATTCGAATGCCT 4500
QY 4441 AGTGCAGGACATGAATGCGACGAGCTCAGCCACGAGATCATACCAATTCGAATGCCT 4500
Db 4501 GCGAGAGCAGAACTACAGCTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAAAGC 4560
QY 4501 GCGAGAGCAGAACTACAGCTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAAAGC 4560
Db 4561 CGTATCTGTGCTTTTCCAAAGTGGCCACCTTCAAAGGCTGGATACAAATCATCAAGCATG 4620
QY 4561 CGTATCTGTGCTTTTCCAAAGTGGCCACCTTCAAAGGCTGGATACAAATCATCAAGCATG 4620
|||||

Db 4621 CTATCGATTCCAGAGAGTGGCAACCAACCAATTGCTGAAACGACATCTACATGTATT 4680
QY |||||
Db 4621 CTATGATTCCAGAGAGTGGCAACCAACCAATTGCTGAAACGACATCTACATGTATT 4680
QY |||||
Db 4681 TATATTTCTGTTATCTTCATCATATTTGGATCTCTTTTTCACACTCAATCTGTTCAATGGTG 4740
QY |||||
Db 4681 TATATTTCTGTTATCTTCATCATATTTGGATCTCTTTTTCACACTCAATCTGTTCAATGGTG 4740
QY |||||
Db 4741 TTATCATTTGATAATTTTAAATGAGCAAAAGAAAACGACAGGTGGATCATTTAGAAATGTTCA 4800
QY |||||
Db 4741 TTATCATTTGATAATTTTAAATGAGCAAAAGAAAACGACAGGTGGATCATTTAGAAATGTTCA 4800
QY |||||
Db 4801 TGACAGAGATCAGAAAAGTACTATAATGCTATGAAAAGATGGCTCTAAAAAACCAT 4860
QY |||||
Db 4801 TGACAGAGATCAGAAAAGTACTATAATGCTATGAAAAGATGGCTCTAAAAAACCAT 4860
QY |||||
Db 4861 TAAAGCCATTCCAAAGACCAAGGTGGCGACCAACGAATAGTCTTTGAAATAGTAACCG 4920
QY |||||
Db 4921 ATAGAAATTCGATATATATCATTTATGTTATTGTTCTGTAACATGTTCAACATGACCC 4980
QY |||||
Db 4921 ATAGAAATTCGATATATATCATTTATGTTATTGTTCTGTAACATGTTCAACATGACCC 4980
QY |||||
Db 4981 TCGATCGTTACGATGCTCGACACGATATAACCGGCTCTAGACTATCTCAATGCGATAT 5040
QY |||||
Db 4981 TCGATCGTTACGATGCTCGACACGATATAACCGGCTCTAGACTATCTCAATGCGATAT 5040
QY |||||
Db 5041 TCGTAGTATTTTCAGTTCGGAATGCTATTAATAATATTCGGTTTACGATATCACTATT 5100
QY |||||
Db 5101 TTATTGACCATGGAATTTATTGATGATAGTATGTTGTCATTTTATCCATCTTAGTCTTG 5160
QY |||||
Db 5101 TTATTGACCATGGAATTTATTGATGATAGTATGTTGTCATTTTATCCATCTTAGTCTTG 5160
QY |||||
Db 5161 TACTTAGCGATATATCGAAGTACTTCGTGTCGCGACCCCTGCTCCGAGTGGTGGTG 5220
QY |||||
Db 5161 TACTTAGCGATATATCGAAGTACTTCGTGTCGCGACCCCTGCTCCGAGTGGTGGTG 5220
QY |||||
Db 5221 TGGCGAAGTGGGCGGTGCTTCGACTGTTGTAAGGAGCCAAAGGGCATTCGGACACTGC 5280
QY |||||
Db 5221 TGGCGAAGTGGGCGGTGCTTCGACTGTTGTAAGGAGCCAAAGGGCATTCGGACACTGC 5280
QY |||||
Db 5281 TCTTCGGGTTGGCCATGTCGTCGCGCCCTGTTCAACATCTGCTGCTGTTCTG 5340
QY |||||
Db 5281 TCTTCGGGTTGGCCATGTCGTCGCGCCCTGTTCAACATCTGCTGCTGTTCTG 5340
QY |||||
Db 5341 TCATGTTCACTTTGCCATTTTCGGCATGTCGTTCTTCATGTCAGCTGAAGGAGAGCG 5400
QY |||||
Db 5341 TCATGTTCACTTTGCCATTTTCGGCATGTCGTTCTTCATGTCAGCTGAAGGAGAGCG 5400
QY |||||
Db 5401 GCATTAACGAGCTCTACAACTTCAAGACCTTTGGCCAGAGCATCTCTGCTTTTCAGA 5460
QY |||||
Db 5401 GCATTAACGAGCTCTACAACTTCAAGACCTTTGGCCAGAGCATCTCTGCTTTTCAGA 5460
QY |||||
Db 5461 TGTGACGTCAGCGGTTGGGATGTTGATGAGTATTAATATGTTACATTTGCTG 5520
QY |||||
Db 5461 TGTGACGTCAGCGGTTGGGATGTTGATGAGTATTAATATGTTACATTTGCTG 5520
QY |||||
Db 5521 ATCCACCCGACGAGCAAAAGGCTATCCGGGCAATTTGTTGTTTCAGCGACCCGTTGGAATAA 5580
QY |||||
Db 5521 ATCCACCCGACGAGCAAAAGGCTATCCGGGCAATTTGTTGTTTCAGCGACCCGTTGGAATAA 5580
QY |||||
Db 5581 CGTTTCTCTCATACCTAGTTAAAGCTTTTGAATGTTTAAATATGTTACATTTGCTG 5640
QY |||||
Db 5581 CGTTTCTCTCATACCTAGTTAAAGCTTTTGAATGTTTAAATATGTTACATTTGCTG 5640
QY |||||
Db 5641 TCATTTCTGAGAACTATAGTCAGGCCACCGAGGAGCTGCAAGAGGGTCTAACCCGACG 5700
QY |||||
Db 5641 TCATTTCTGAGAACTATAGTCAGGCCACCGAGGAGCTGCAAGAGGGTCTAACCCGACG 5700
QY |||||

Db 5701 ACTACGACATGTACTACTAGATCTGGCAGCAATTCGATCCGGAGGGACCCAGTACATAC 5760
QY |||||
Db 5701 ACTACGACATGTACTACTAGATCTGGCAGCAATTCGATCCGGAGGGACCCAGTACATAC 5760
QY |||||
Db 5761 GCTATGATCAGCTGTCGGAATTTCTGACAGTACTGGAGCCCCCGCTGCAGATCCACAAC 5820
QY |||||
Db 5761 GCTATGATCAGCTGTCGGAATTTCTGACAGTACTGGAGCCCCCGCTGCAGATCCACAAC 5820
QY |||||
Db 5821 CGAACAAGTACAAGATCATATCGATGGACATACCCATCTGTCGCGGTGACCTCATGTACT 5880
QY |||||
Db 5821 CGAACAAGTACAAGATCATATCGATGGACATACCCATCTGTCGCGGTGACCTCATGTACT 5880
QY |||||
Db 5881 GCGTCGACATCTCGACGCCCTTACGAAAAGACTTCTTTGGCGGAAGGGCAATCCGATAG 5940
QY |||||
Db 5881 GCGTCGACATCTCGACGCCCTTACGAAAAGACTTCTTTGGCGGAAGGGCAATCCGATAG 5940
QY |||||
Db 5941 AGGAGACGGGTGAGATTTGGTGAGATAGCGGCCCGCGGATACGAGGGGTACGAGCCCG 6000
QY |||||
Db 5941 AGGAGACGGGTGAGATTTGGTGAGATAGCGGCCCGCGGATACGAGGGGTACGAGCCCG 6000
QY |||||
Db 6001 TCTCATCAACGCTGTGGCGTTCAGGCTGAGGAGTACTGCGCCCGCTTAATCCAGCACGCT 6060
QY |||||
Db 6001 TCTCATCAACGCTGTGGCGTTCAGGCTGAGGAGTACTGCGCCCGCTTAATCCAGCACGCT 6060
QY |||||
Db 6061 GCGGAAACACAAAGCGCGCGGAGGAGTGGGTCCTTTGAGCCGGATACGGATCATG 6120
QY |||||
Db 6061 GCGGAAACACAAAGCGCGCGGAGGAGTGGGTCCTTTGAGCCGGATACGGATCATG 6120
QY |||||
Db 6121 GCGATGCGGCTGATCCGGATCCCGGGACCCGCGCGATGAAGCAACGACGCGCGATG 6180
QY |||||
Db 6121 GCGATGCGGCTGATCCGGATCCCGGGACCCGCGCGATGAAGCAACGACGCGCGATG 6180
QY |||||
Db 6181 CCGCCGCTGTTGGAGATGTTAAACGGTACTGCAAGAGGAGTCCCGATCCCGATG 6240
QY |||||
Db 6181 CCGCCGCTGTTGGAGATGTTAAACGGTACTGCAAGAGGAGTCCCGATCCCGATG 6240
QY |||||
Db 6241 AGAGTAATGTAATTAAGTCCGGGTGAGGATGAGGAGTCCCGGCGCGGAGCAGCAGCAG 6300
QY |||||
Db 6241 AGAGTAATGTAATTAAGTCCGGGTGAGGATGAGGAGTCCCGGCGCGGAGCAGCAGCAG 6300
QY |||||
Db 6301 CCGCGGCGCGGCGACGACGCGGGAAGTCCCGGAGCGGTAGCGCGGCGGACAGA 6360
QY |||||
Db 6301 CCGCGGCGCGGCGACGACGCGGGAAGTCCCGGAGCGGTAGCGCGGCGGACAGA 6360
QY |||||
Db 6361 CCGCGGCTTCTGTTGAGAGCGAGGTTCTGTCAGAAAGAACGGCCACAAGTGTCTATCC 6420
QY |||||
Db 6361 CCGCGGCTTCTGTTGAGAGCGAGGTTCTGTCAGAAAGAACGGCCACAAGTGTCTATCC 6420
QY |||||
Db 6421 ACTCGGATCCGCGAGCATCAGTCGCGACGCGGATGTCGTGACCCAGGCTCCGCCCC 6480
QY |||||
Db 6421 ACTCGGATCCGCGAGCATCAGTCGCGACGCGGATGTCGTGACCCAGGCTCCGCCCC 6480
QY |||||
Db 6481 CCTCTCAAGATGCACGCGAGTATTAGCTCTAGA 6513
QY CCTCTCAAGATGCACGCGAGTATTAGCTCTAGA 6513

2
RESULT 2
LOCUS I25433 6513 bp DNA PAT 03-SEP-1996
DEFINITION Sequence 7 from patent US 5550049.
ACCESSION I25433
NID g1605303
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6513)
AUTHORS Van Der Ploeg L.H.T. and Warmke, J.W.
TITLE Process for identifying para cation channel modulators
JOURNAL Patent: US 5550049-A 7 27-AUG-1996;
FEATURES Location/Qualifiers
1. .6513
source /organism="unknown"

BASE COUNT 1681 a 1548 c 1702 g 1582 t
ORIGIN

Query Match 100.0%; Score 6513; DB 17; Length 6513;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TCTAGAGCTGGCGGATGACAAATGACAGAGATTCGAGTCTGATATCTGAGAGAAC 60
QY 1 TCTAGAGCTGGCGGATGACAAATGACAGAGATTCGAGTCTGATATCTGAGAGAAC 60

Db 61 GCAGTTGTTCCGTCCTTACCGCGAATCAATGTTGCAAAATCGACACGATTCGCG 120
QY 61 GCAGTTGTTCCGTCCTTACCGCGAATCAATGTTGCAAAATCGACACGATTCGCG 120

Db 121 CTGAACATGAAGAGAGAGAGTGGAAAGAAAGAGAGCGGAGGAGAGTCCCGAT 180
QY 121 CTGAACATGAAGAGAGAGTGGAAAGAAAGAGAGCGGAGGAGAGTCCCGAT 180

Db 181 ATGTCGCAAGAAAACAAAAGAAATCCGATATGATGACGAGGACGAGATGAAGTC 240
QY 181 ATGTCGCAAGAAAACAAAAGAAATCCGATATGATGACGAGGACGAGATGAAGTC 240

Db 241 CACAACCGGATCTACACTTGAACAGGGTGTGCCAATACCTGTCTGATTCGAGGGAGCT 300
QY 241 CACAACCGGATCTACACTTGAACAGGGTGTGCCAATACCTGTCTGATTCGAGGGAGCT 300

Db 301 TCCCGCGGAATGGCCCTCCACTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360
QY 301 TCCCGCGGAATGGCCCTCCACTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360

Db 361 TGACATTCGTAGTTGTAAGCAAGAAAGATATTTTCGCTTTTCGTCATCAAAAGCAA 420
QY 361 TGACATTCGTAGTTGTAAGCAAGAAAGATATTTTCGCTTTTCGTCATCAAAAGCAA 420

Db 421 TGTGGATGCTCGATCCATCAATCCGATAGCTGTGTGGCCATTTACATTCATAGTGATC 480
QY 421 TGTGGATGCTCGATCCATCAATCCGATAGCTGTGTGGCCATTTACATTCATAGTGATC 480

Db 481 CATTATTTCCCTATTCATCATCACCAATTCCTCGCAACTGCATCTGATGATATGC 540
QY 481 CATTATTTCCCTATTCATCATCACCAATTCCTCGCAACTGCATCTGATGATATGC 540

Db 541 CGACAACGCCACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600
QY 541 CGACAACGCCACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600

Db 601 CAGCTGTTAAGTATGGCAGAGGTTTCATTTATGCCGTTTACGTATCTTAGAGATG 660
QY 601 CAGCTGTTAAGTATGGCAGAGGTTTCATTTATGCCGTTTACGTATCTTAGAGATG 660

Db 661 CATGGAATGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTACCATGGTATAGATT 720
QY 661 CATGGAATGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTACCATGGTATAGATT 720

Db 721 TAGGTAACTAGCAGCCCTCGCAACGTTTGGGTGCTGCGAGCGCTTAAACCGTAGCCA 780
QY 721 TAGGTAACTAGCAGCCCTCGCAACGTTTGGGTGCTGCGAGCGCTTAAACCGTAGCCA 780

Db 781 TTGTGCCAGGCTTGAAGACCATGTCGGCGCGTTCATCGAATCGGTGAAGAAATCTGCGCG 840
QY 781 TTGTGCCAGGCTTGAAGACCATGTCGGCGCGTTCATCGAATCGGTGAAGAAATCTGCGCG 840

Db 841 ATGTGATTATCTGACCATGTTCTCCCTGTCGGTGTTCGGTGTGATGGGCTACAGATCT 900
QY 841 ATGTGATTATCTGACCATGTTCTCCCTGTCGGTGTTCGGTGTGATGGGCTACAGATCT 900

Db 901 ATATGGCGTGTCTCACCGAAGTGCATCAAGAAAGTTCCCGCTGGAGCGTTCTCTGGGCA 960
QY 901 ATATGGCGTGTCTCACCGAAGTGCATCAAGAAAGTTCCCGCTGGAGCGTTCTCTGGGCA 960

Db 961 ATCTGACCGAGAGACTGGGACTATCACAAATCGCAATAGCTCCAAATTTGGTATTCGAGG 1020
QY 961 ATCTGACCGAGAGACTGGGACTATCACAAATCGCAATAGCTCCAAATTTGGTATTCGAGG 1020

QY 961 ATCTGACCGAGAGAACTGGGACTATCAAAATCGCAATAGCTCCAAATTTGGTATTCGAGG 1020
Db 1021 ACAGAGGCATCTCATTTCCGTTATGCGGCAATATATCCGTCGGGGCAATGCGAGACG 1080
QY 1021 ACAGAGGCATCTCATTTCCGTTATGCGGCAATATATCCGTCGGGGCAATGCGAGACG 1080

Db 1081 ATTACGTGCTGCGAGAGGTTTGGTCCGAATCCGAATATGCTTACACAGCTTCGATT 1140
QY 1081 ATTACGTGCTGCGAGAGGTTTGGTCCGAATCCGAATATGCTTACACAGCTTCGATT 1140

Db 1141 CGTTCGATGGGCTTCTCTGCGCTTCCGCTGATGACACAGGACTTCTGGAGATC 1200
QY 1141 CGTTCGATGGGCTTCTCTGCGCTTCCGCTGATGACACAGGACTTCTGGAGATC 1200

Db 1201 TGTACAGCTGTGTTGCGCGCGCGGACCATGGCACATGCTGTCTTTATAGTCATCA 1260
QY 1201 TGTACAGCTGTGTTGCGCGCGCGGACCATGGCACATGCTGTCTTTATAGTCATCA 1260

Db 1261 TCTTCCTAGTTCTATCTTGTGAAATTTGATTTTGGCCATTTGTCATGCTGATG 1320
QY 1261 TCTTCCTAGTTCTATCTTGTGAAATTTGATTTTGGCCATTTGTCATGCTGATG 1320

Db 1321 ACCAATTGCAAGAGAGCGCGGAGAGAGGCTCCGGAAGAGGAGGCGATACGTGAAG 1380
QY 1321 ACCAATTGCAAGAGAGCGCGGAGAGAGGCTCCGGAAGAGGAGGCGATACGTGAAG 1380

Db 1381 CGGAAGAAGCTGCGCGCGCGGCAAGCTGGAGGAGCGGCAATGCGCAGGCTC 1440
QY 1381 CGGAAGAAGCTGCGCGCGCGGCAAGCTGGAGGAGCGGCAATGCGCAGGCTC 1440

Db 1441 AGCAGCAGCGGATGCGGTCGCGCGGAGAGGCTGCACATCGGAAATCGGCAAGA 1500
QY 1441 AGCAGCAGCGGATGCGGTCGCGCGGAGAGGCTGCACATCGGAAATCGGCAAGA 1500

Db 1501 GTCCGAGCTATCTTCGATCAGCTATGAGCTATTTGTTGGCGCGGAGAGGCAAGATG 1560
QY 1501 GTCCGAGCTATCTTCGATCAGCTATGAGCTATTTGTTGGCGCGGAGAGGCAAGATG 1560

Db 1561 ACAACAAGAGAGAGATGTCATTTCGAGGCTCGAGGTGGAGTTCGGTTCGAGCG 1620
QY 1561 ACAACAAGAGAGAGATGTCATTTCGAGGCTCGAGGTGGAGTTCGGTTCGAGCG 1620

Db 1621 TTATACAAAGACACACGACCTTACCACAGCACACCAAGCTACCAAGTTTCGTAAGTGA 1680
QY 1621 TTATACAAAGACACACGACCTTACCACAGCACACCAAGCTACCAAGTTTCGTAAGTGA 1680

Db 1681 GCAGGATCTTATCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTT 1740
QY 1681 GCAGGATCTTATCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTT 1740

Db 1741 CTCAAGTACAGATACGGAACGAGCTGCGCGCTTTGGTATACCCGTTAGCGATCGTA 1800
QY 1741 CTCAAGTACAGATACGGAACGAGCTGCGCGCTTTGGTATACCCGTTAGCGATCGTA 1800

Db 1801 AGCCATTGTTATGTCACAAATATCAGATGCCAGCAGCACTTGCCTATGCCAGCACT 1860
QY 1801 AGCCATTGTTATGTCACAAATATCAGATGCCAGCAGCACTTGCCTATGCCAGCACT 1860

Db 1861 CGAATGCCCTCACCCGATGTCGGAAGAGAAATGGGCGCATATAGTCCCGTGTACTATG 1920
QY 1861 CGAATGCCCTCACCCGATGTCGGAAGAGAAATGGGCGCATATAGTCCCGTGTACTATG 1920

Db 1921 GCAATCTAGGCTCCGACACTCATCTATACCTCGCATAGTCCGCAATATCTATACCT 1980
QY 1921 GCAATCTAGGCTCCGACACTCATCTATACCTCGCATAGTCCGCAATATCTATACCT 1980

Db 1981 CACATGGCATCTTACGCGGATGCGGCTCATGGCGCTCAGCACAATGACCAAGGAGA 2040
QY 1981 CACATGGCATCTTACGCGGATGCGGCTCATGGCGCTCAGCACAATGACCAAGGAGA 2040

Db 2041 GCAATTTGCGCAACCGCAACACAGCAATCAATAGTGGGCGCCACCAATGGCGGACCA 2100
QY 2041 GCAATTTGCGCAACCGCAACACAGCAATCAATAGTGGGCGCCACCAATGGCGGACCA 2100

Db 2101 CCTGTCTGGACACCAATCACAAAGCTCGATCATCGACTAGCAATTTGGCTTGAGTGCA 2160
Qy 2101 CCTGTCTGGACACCAATCACAAAGCTCGATCATCGACTAGCAATTTGGCTTGAGTGCA 2160
Db 2161 CGGAGAGCTGGGAAGATTAAACATCATGACATTCCTTTTATCGAGCCGCTCAGACAC 2220
Qy 2161 CGGAGAGCTGGGAAGATTAAACATCATGACATTCCTTTTATCGAGCCGCTCAGACAC 2220
Db 2221 AAACGGTGGTGGATGAAGATGTGATGGTCCCTGAATGACATCATGAAACAGGCCGCTG 2280
Qy 2221 AAACGGTGGTGGATGAAGATGTGATGGTCCCTGAATGACATCATGAAACAGGCCGCTG 2280
Db 2281 GTGCGCACAGTCGGGCAAGCCGATCGCGTGTCTCGTTTACTATTTCCTCCACAGAGGACG 2340
Qy 2281 GTGCGCACAGTCGGGCAAGCCGATCGCGTGTCTCGTTTACTATTTCCTCCACAGAGGACG 2340
Db 2341 ATGACAGGATGGGCGGACGTTCAAAGACAAGGCACCTGAAAGTATCTCCTCAAGGCGATCG 2400
Qy 2341 ATGACAGGATGGGCGGACGTTCAAAGACAAGGCACCTGAAAGTATCTCCTCAAGGCGATCG 2400
Db 2401 ATGCTGTTTGTGTGGGACGTGTTCTGGGTTTGGTTGAAATTTTCAGGAGTGGGTATCGC 2460
Qy 2401 ATGCTGTTTGTGTGGGACGTGTTCTGGGTTTGGTTGAAATTTTCAGGAGTGGGTATCGC 2460
Db 2461 TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATCACGCTGTGCTATTTGGTCAACACGA 2520
Qy 2461 TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATCACGCTGTGCTATTTGGTCAACACGA 2520
Db 2521 TGTTCATGGCAATGATCACACGATATGAACAGGAGATGAACGCGTGTCAAGAGTG 2580
Qy 2521 TGTTCATGGCAATGATCACACGATATGAACAGGAGATGAACGCGTGTCAAGAGTG 2580
Db 2581 GCAACTATTTCTCACCGCCACTTTGCCATCGAGGCCACATGAAGCTAATGGCCATGA 2640
Qy 2581 GCAACTATTTCTCACCGCCACTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA 2640
Db 2641 GCCCAAGTACTATTTCACAGAGGCTGGAACATCTTCGACTTCATATCGTGGCCCTAT 2700
Qy 2641 GCCCAAGTACTATTTCACAGAGGCTGGAACATCTTCGACTTCATATCGTGGCCCTAT 2700
Db 2701 CGCTATTGGAATCGGACTCGAGGCTGTCAGGGTCTGTCGCTATTTGGTTCCTTCGAT 2760
Qy 2701 CGCTATTGGAATCGGACTCGAGGCTGTCAGGGTCTGTCGCTATTTGGTTCCTTCGAT 2760
Db 2761 TGTCTGCTGATTCAAACCTGGCCAAAGTCTTGGCCACACACTTAATTTACTCATTTTCGATTA 2820
Qy 2761 TGTCTGCTGATTCAAACCTGGCCAAAGTCTTGGCCACACACTTAATTTACTCATTTTCGATTA 2820
Db 2821 TGGGACGCACCATGGGCGCTTTGGGTAATCTGACATTTTGTACTTTGTCATTTATCATCTTCA 2880
Qy 2821 TGGGACGCACCATGGGCGCTTTGGGTAATCTGACATTTTGTACTTTGTCATTTATCATCTTCA 2880
Db 2881 TCTTTTCGGTGTGGAATGCAACTGTTCCGAAAGATTTATCATGATCAACAGGACCGCT 2940
Qy 2881 TCTTTTCGGTGTGGAATGCAACTGTTCCGAAAGATTTATCATGATCAACAGGACCGCT 2940
Db 2941 TTCGGATGGGACCTGCGCGCTGGAATTCACCGACTTTATGACAGCTTCATGATCG 3000
Qy 2941 TTCGGATGGGACCTGCGCGCTGGAATTCACCGACTTTATGACAGCTTCATGATCG 3000
Db 3001 TGTTCGGTGTCTCGGAGAAATGGATCGATGCCATGTGGGACTGCGATGTACGTGGGG 3060
Qy 3001 TGTTCGGTGTCTCGGAGAAATGGATCGATGCCATGTGGGACTGCGATGTACGTGGGG 3060
Db 3061 ATGCTCTGTCATTCCTTCTTCTGGCCACCGTTCATCGCATCGCAATCTTGGTACTTA 3120
Qy 3061 ATGCTCTGTCATTCCTTCTTCTGGCCACCGTTCATCGCATCGCAATCTTGGTACTTA 3120
Db 3121 ACCTTTTCTAGCCTTGTCTTTTGTCAATTTTGGCTTCATCTAGCTTATCAGGCCGACTG 3180
Qy 3121 ACCTTTTCTAGCCTTGTCTTTTGTCAATTTTGGCTTCATCTAGCTTATCAGGCCGACTG 3180

Db 3181 CCGATTAACGATACGAATAAAATAGCGAGGCGCTTCAATCGAATTTGCCGATTTAAAGTT 3240
Qy 3181 CCGATTAACGATACGAATAAAATAGCGAGGCGCTTCAATCGAATTTGCCGATTTAAAGTT 3240
Db 3241 GGGTTAAGCGTATATTTGCTGATTGTTTCAAGTTAATACGTAACAAATTGACAAATCAAA 3300
Qy 3241 GGGTTAAGCGTATATTTGCTGATTGTTTCAAGTTAATACGTAACAAATTGACAAATCAAA 3300
Db 3301 TAAAGTATCAACCATCAGGTGAGAGGACCAACCCAGATCAGTTGGATTGAGCGAAGAGC 3360
Qy 3301 TAAAGTATCAACCATCAGGTGAGAGGACCAACCCAGATCAGTTGGATTGAGCGAAGAGC 3360
Db 3361 ATGGTGACAAAGCTGAGAGTGGGCCACGACGAGATCCTCGCCGACGGCTCATCAAGA 3420
Qy 3361 ATGGTGACAAAGCTGAGAGTGGGCCACGACGAGATCCTCGCCGACGGCTCATCAAGA 3420
Db 3421 AGGGGATCAAGGAGCAGACGCAACTGGAGTGGCCATCGGGGATCGGATGGAATTCACGA 3480
Qy 3421 AGGGGATCAAGGAGCAGACGCAACTGGAGTGGCCATCGGGGATCGGATGGAATTCACGA 3480
Db 3481 TACACGCGACATGAAGACAACCAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA 3540
Qy 3481 TACACGCGACATGAAGACAACCAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA 3540
Db 3541 TGATTTGGCAACTCAATTAACCAACCAAGACATAGACTGGAAACGAGCTTAAACCATAGAG 3600
Qy 3541 TGATTTGGCAACTCAATTAACCAACCAAGACATAGACTGGAAACGAGCTTAAACCATAGAG 3600
Db 3601 GTTTGTCTTTACAGGACGACGACATGCCAGCATTAACCTCATATGTTAGCATTAAAGATC 3660
Qy 3601 GTTTGTCTTTACAGGACGACGACATGCCAGCATTAACCTCATATGTTAGCATTAAAGATC 3660
Db 3661 GACCATTAAGGACGAGAGCCCAAGGGCAGCCGACGAGATGGAGGCGGAGGAGAAGC 3720
Qy 3661 GACCATTAAGGACGAGAGCCCAAGGGCAGCCGACGAGATGGAGGCGGAGGAGAAGC 3720
Db 3721 GCGAGCCGACAGGAGGATTTAGGCTCGACGAGGAACTGGAGGAGGCGGAAATGCG 3780
Qy 3721 GCGAGCCGACAGGAGGATTTAGGCTCGACGAGGAACTGGAGGAGGCGGAAATGCG 3780
Db 3781 AGGAGGCGCGCTCGAGCGTGTATCATATTATCATGCACACGAGGATATCTCGATG 3840
Qy 3781 AGGAGGCGCGCTCGAGCGTGTATCATATTATCATGCACACGAGGATATCTCGATG 3840
Db 3841 AATATCCAGCTGATGTCGCCCGGATTCGATTAAGAAATTCGATCTTAGCCGGTG 3900
Qy 3841 AATATCCAGCTGATGTCGCCCGGATTCGATTAAGAAATTCGATCTTAGCCGGTG 3900
Db 3901 ACGATGACTCGCCGCTTCGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTA 3960
Qy 3901 ACGATGACTCGCCGCTTCGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTA 3960
Db 3961 TTGAAATTAATATTTTGAACAGCTGTTTACATGATTTTAAAGTATGATGATGATGAT 4020
Qy 3961 TTGAAATTAATATTTTGAACAGCTGTTTACATGATTTTAAAGTATGATGATGATGAT 4020
Db 4021 TGGCATTAGAAGATGTACATCTGCCAAGACCCACTGACGAGGATTTTATACATATA 4080
Qy 4021 TGGCATTAGAAGATGTACATCTGCCAAGACCCACTGACGAGGATTTTATACATATA 4080
Db 4081 TGGACAGATATTTACGGTATATTTCTTGGAAATGTTAATCAAGTGGTGGCGCTCG 4140
Qy 4081 TGGACAGATATTTACGGTATATTTCTTGGAAATGTTAATCAAGTGGTGGCGCTCG 4140
Db 4141 GCTTCAAAAGTACTTCAACCAACGCTGGTGGCTCGAATTTCTGATTTGCTATGAT 4200
Qy 4141 GCTTCAAAAGTACTTCAACCAACGCTGGTGGCTCGAATTTCTGATTTGCTATGAT 4200
Db 4201 GCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTGGTATTCAGGCTTCAAGACTA 4260
Qy 4201 GCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTGGTATTCAGGCTTCAAGACTA 4260
Db 4261 TGGCAAGCTTAAAGACACTGAGACCACTACGTGCCATGTCTCCGTATGAGGCGCATGAGG 4320

||||| 4261 TGGACGCTTAAGAGCACTGAGACCACTAGCTGCCATGTCCTCCATATGCAGGCAATGAGG 4320
Db 4321 TCCTCGTTAATGCGCTGGTACAAAGCTATACCGTCCATCTCTCAATGCTCATTTGGTGTGTC 4380
QY 4321 TCCTCGTTAATGCGCTGGTACAAAGCTATACCGTCCATCTCTCAATGCTCATTTGGTGTGTC 4380
Db 4381 TAATATTTGGCTAAATTTTGGCCATTAATGGGTGTACAGCTTTTGGCTGGAAATATTTTA 4440
QY 4381 TAATATTTGGCTAAATTTTGGCCATTAATGGGTGTACAGCTTTTGGCTGGAAATATTTTA 4440
Db 4441 AGTGCAGGACATGAATGGCACCAGCTCAGCCACGAGATCATACCAATCGCAATGCGCT 4500
QY 4441 AGTGCAGGACATGAATGGCACCAGCTCAGCCACGAGATCATACCAATCGCAATGCGCT 4500
Db 4501 GCAGAGCGAGAACTACACGTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAAGC 4560
QY 4501 GCAGAGCGAGAACTACACGTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAAGC 4560
Db 4561 CGTATCTGTCCTTTTCCAAAGTGGCCACCTTCAAAGCTGGATACAAATCATGAAGCATG 4620
QY 4561 CGTATCTGTCCTTTTCCAAAGTGGCCACCTTCAAAGCTGGATACAAATCATGAAGCATG 4620
Db 4621 CTATCGATTCCAGCAGAGGTGGCAAGCAACCAATTCGTGAACGAACATCTACATGATT 4680
QY 4621 CTATCGATTCCAGCAGAGGTGGCAAGCAACCAATTCGTGAACGAACATCTACATGATT 4680
Db 4681 TATATTCGTATTCTTCATCATATTTGGATCCCTTTTTCACATCAATCTGTCATTGGTG 4740
QY 4681 TATATTCGTATTCTTCATCATATTTGGATCCCTTTTTCACATCAATCTGTCATTGGTG 4740
Db 4741 TTATCATTTGTAATTTTAATGACAAAAGAAAAGAGGTGATCATAGAAATGTTC 4800
QY 4741 TTATCATTTGTAATTTTAATGACAAAAGAAAAGAGGTGATCATAGAAATGTTC 4800
Db 4801 TGACAGAAGATCAGAAAAGTACTAATGCTATGAAAAGATGGGCTCTAAAACCAT 4860
QY 4801 TGACAGAAGATCAGAAAAGTACTAATGCTATGAAAAGATGGGCTCTAAAACCAT 4860
Db 4861 TAAAGCCATTCCAAGACCAAGGTGGCGACCACCAAGCAATAGTCTTTGAAATAGTAACCG 4920
QY 4861 TAAAGCCATTCCAAGACCAAGGTGGCGACCACCAAGCAATAGTCTTTGAAATAGTAACCG 4920
Db 4921 ATAAGAAATTCGATATAATCATTTATGTTATTCATTTGGTCTGAACATGTTCAACCATGACCC 4980
QY 4921 ATAAGAAATTCGATATAATCATTTATGTTATTCATTTGGTCTGAACATGTTCAACCATGACCC 4980
Db 4981 TCCATCGTTACGATGCGTCGGACACGTATAACCGGTCCTAGACTATCTCAATGCGATAT 5040
QY 4981 TCGATCGTTACGATGCGTCGGACACGTATAACCGGTCCTAGACTATCTCAATGCGATAT 5040
Db 5041 TCGTAGTTATTTTCAGTTCGGAATGCTATTAATAATATTCGCTTACGATATCACTATT 5100
QY 5041 TCGTAGTTATTTTCAGTTCGGAATGCTATTAATAATATTCGCTTACGATATCACTATT 5100
Db 5101 TTATTAGCCATGGAATTTATTTGATGTAGTAGTTGTCATTTTATCCATCTTAGGCTTG 5160
QY 5101 TTATTAGCCATGGAATTTATTTGATGTAGTAGTTGTCATTTTATCCATCTTAGGCTTG 5160
Db 5161 TACTTAGCGATATATCGAAGTACTTCTGTGTCGGGACCCCTGCTCCGAGTGGTGGTG 5220
QY 5161 TACTTAGCGATATATCGAAGTACTTCTGTGTCGGGACCCCTGCTCCGAGTGGTGGTG 5220
Db 5221 TGGCGAAAGTGGGCGGTGCTCTTCGACTGGTGAAGGAGCAAGGGCATTCGGACACTGC 5280
QY 5221 TGGCGAAAGTGGGCGGTGCTCTTCGACTGGTGAAGGAGCAAGGGCATTCGGACACTGC 5280
Db 5281 TCTTCGGTTGGCCATGTCGCTCCGSCCCTGTTCACATCTGCCCTGCTGCTTCTG 5340
QY 5281 TCTTCGGTTGGCCATGTCGCTCCGSCCCTGTTCACATCTGCCCTGCTGCTTCTG 5340
Db 5341 TCATGTTTCATCTTTGGCATTTTCGGCATGTCGTTCTTCATGCAAGTGAAGGAGAGCG 5400
|||||

QY 5341 TCATGTTTCATCTTTGCCATTTTTCGCATGTCGTTCTTCTATGCACGTAAGGAGAAGCGG 5400
Db 5401 GCATTAAAGACGCTGTACAACTTCAAGACCTTTGGCCAGAGCATGATCCTGCTCTTTTCA 5460
QY 5401 GCATTAAAGACGCTGTACAACTTCAAGACCTTTGGCCAGAGCATGATCCTGCTCTTTTCA 5460
Db 5461 TGTCCAGCTCAGCCGGTTGGGATGGTGTACTGGACGCCATTATCAATGAGGAAGCATGGC 5520
QY 5461 TGTCCAGCTCAGCCGGTTGGGATGGTGTACTGGACGCCATTATCAATGAGGAAGCATGGC 5520
Db 5521 ATCCACCCGACAGCAGCAAAAGCTATCCGGGCAATTGTTGTTAGCGACCGTTGGAATAA 5580
QY 5521 ATCCACCCGACAGCAGCAAAAGCTATCCGGGCAATTGTTGTTAGCGACCGTTGGAATAA 5580
Db 5581 CGTTTCTCTCTCATACCTAGTTATAAGCTTTTGTATAGTTATTAATATGATATGCTG 5640
QY 5581 CGTTTCTCTCTCATACCTAGTTATAAGCTTTTGTATAGTTATTAATATGATATGCTG 5640
Db 5641 TCATTCTCAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGCTCTAAACGACGAGC 5700
QY 5641 TCATTCTCAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGCTCTAAACGACGAGC 5700
Db 5701 ACTAGCAGATGTATGAGATCTGSCAGCAATTCGATCCGGAGGCGACCCAGTACATAC 5760
QY 5701 ACTAGCAGATGTATGAGATCTGSCAGCAATTCGATCCGGAGGCGACCCAGTACATAC 5760
Db 5761 GCTATGATCAGCTGTCCGAATTCCTGGAGCTACTTGAGCCCCCGCTGCAGATCCACAAC 5820
QY 5761 GCTATGATCAGCTGTCCGAATTCCTGGAGCTACTTGAGCCCCCGCTGCAGATCCACAAC 5820
Db 5821 CGAACAAGTACAAGATCATATCGATGGACATACCCATCTGTCGGGTGACCTCATGCT 5880
QY 5821 CGAACAAGTACAAGATCATATCGATGGACATACCCATCTGTCGGGTGACCTCATGCT 5880
Db 5881 GGTGTCACATCTCGACGCTTACGAAAGCTCTTTCGCGGAGGCAATCCGATAG 5940
QY 5881 GGTGTCACATCTCGACGCTTACGAAAGCTCTTTCGCGGAGGCAATCCGATAG 5940
Db 5941 AGGAGACGGGTGAGATTGTTGATAGTAGCGGCCCGCGGATACGGAGGCTACGAGCCCG 6000
QY 5941 AGGAGACGGGTGAGATTGTTGATAGTAGCGGCCCGCGGATACGGAGGCTACGAGCCCG 6000
Db 6001 TGTATCAACGCTGTGGCTCAGCGTGAAGAGTACTGCGCCCGGCTTAATCCAGCAGCCT 6060
QY 6001 TGTATCAACGCTGTGGCTCAGCGTGAAGAGTACTGCGCCCGGCTTAATCCAGCAGCCT 6060
Db 6061 GCGGAAAGCAGACGCGCGCGGAGGAGTGGGTCTTTGAGCCGGATACGGATCATG 6120
QY 6061 GCGGAAAGCAGACGCGCGCGGAGGAGTGGGTCTTTGAGCCGGATACGGATCATG 6120
Db 6121 GCGATGGCGGTGATCCGGATGCGGGACCCCGCGCGGATGAAGCAACGAGCGGATG 6180
QY 6121 GCGATGGCGGTGATCCGGATGCGGGACCCCGCGCGGATGAAGCAACGAGCGGATG 6180
Db 6181 CGCCCGCTGGTGGAGTGTAGTTAAACGGTACTGACGAAGAGCTGCCGATGCCGATG 6240
QY 6181 CGCCCGCTGGTGGAGTGTAGTTAAACGGTACTGACGAAGAGCTGCCGATGCCGATG 6240
Db 6241 AGAGTAATGTAATAGTCCGGGTGAGGATGTCAGCGCGCGGAGGAGGAGGAGGAGGAG 6300
QY 6241 AGAGTAATGTAATAGTCCGGGTGAGGATGTCAGCGCGCGGAGGAGGAGGAGGAGGAG 6300
Db 6301 CGCGCGCGGCGGACGACGAGCGCGGGAAGTCCCGAGCGGATACGCGCGGCGACAG 6360
QY 6301 CGCGCGCGGCGGACGACGAGCGCGGGAAGTCCCGAGCGGATACGCGCGGCGGACAG 6360
Db 6361 CGCGCGCTTCTCGTGGAGAGCAGCGGTTCTGACGAAGAACGCCACAAAGGTGTCATCC 6420
QY 6361 CGCGCGCTTCTCGTGGAGAGCAGCGGTTCTGACGAAGAACGCCACAAAGGTGTCATCC 6420
Db 6421 ACTCGGATCGCGGAGCATCAGTCCGCGACGGCGGATGTCTGAGCCAGGCTCGCCCCC 6480
QY 6421 ACTCGGATCGCGGAGCATCAGTCCGCGACGGCGGATGTCTGAGCCAGGCTCGCCCCC 6480

Db 6481 CCCTCAAGATGACGCGAGTATTAGCTCTAGA 6513
|||||
Qy 6481 CCCTCAAGATGACGCGAGTATTAGCTCTAGA 6513

RESULT 3
LOCUS 133685 6513 bp DNA PAT 27-JAN-1997
DEFINITION Sequence 7 from patent US 5593864.
ACCESSION 133685
NID 91824476
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 6513)
AUTHORS Arena,J.P., Feng,G., Hall,L.M., Liu,K., Van Der Ploeg,L.H.T.,
Wang,P. and Warmke,J.W.
TITLE Process for functional expression of the para cation channel
JOURNAL Patent: US 5593864-A 7 14-JAN-1997;
FEATURES Location/Qualifiers
1. 6513
source /organism="unknown"
BASE COUNT 1681 a 1548 c 1702 g 1582 t
ORIGIN

Query Match 100.0%; Score 6513; DB 17; Length 6513;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TCTAGAGTTGGCGGATAGACAATGACAGAAGATTCGGACTCGATATCTGAGGAAGAC 60
|||||
Qy 1 TCTAGAGTTGGCGGATAGACAATGACAGAAGATTCGGACTCGATATCTGAGGAAGAC 60

Db 61 GCAGTTTGTCCGTCCTTACCCGCGCAATCATTTGGTGCAAATCGAACACGCAATTCGCCG 120
|||||
Qy 61 GCAGTTTGTCCGTCCTTACCCGCGCAATCATTTGGTGCAAATCGAACACGCAATTCGCCG 120

Db 121 CTGAACATGAAAGCAGAAGGAGCTGGAAAGAAAGAGAGCGGAGGAGAGGTGCCGGAT 180
|||||
Qy 121 CTGAACATGAAAGCAGAAGGAGCTGGAAAGAAAGAGAGCGGAGGAGAGGTGCCGGAT 180

Db 181 ATGTCGCAAGAAAAACAAGAAATCCGATATGATGACGAGGACGAGATGAAGGTC 240
|||||
Qy 181 ATGTCGCAAGAAAAACAAGAAATCCGATATGATGACGAGGACGAGATGAAGGTC 240

Db 241 CACAACGGATCCTACACTTGAACAGGCTGGCCAATACCTGTTCTGATTCGAGGCGAGCT 300
|||||
Qy 241 CACAACGGATCCTACACTTGAACAGGCTGGCCAATACCTGTTCTGATTCGAGGCGAGCT 300

Db 301 TCCGCGCGGAATGGCCCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360
|||||
Qy 301 TCCGCGCGGAATGGCCCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360

Db 361 TGACATTCGTAGTTGTAAGCAAGAAAGAAATATTTTCGCTTTTCTGCATCAAAAGCAA 420
|||||
Qy 361 TGACATTCGTAGTTGTAAGCAAGAAAGAAATATTTTCGCTTTTCTGCATCAAAAGCAA 420

Db 421 TGTGGATGCTCGATCCATTAATCCGATACCTGCTGGCCGATTTACATTTCTAGTGCATC 480
|||||
Qy 421 TGTGGATGCTCGATCCATTAATCCGATACCTGCTGGCCGATTTACATTTCTAGTGCATC 480

Db 481 CATTAATTTCCCTATTCATCATACCAACAATTCGTCGAATGCTCCTGATGATAATGC 540
|||||
Qy 481 CATTAATTTCCCTATTCATCATACCAACAATTCGTCGAATGCTCCTGATGATAATGC 540

Db 541 CGACAGCCCAACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600
|||||
Qy 541 CGACAGCCCAACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600

Db 601 CAGCTGTTAAAGTGATGCGCAGGTTTCATTTTATGCCCGTTTACGTTATCTTAGAGATG 660
|||||
Qy 601 CAGCTGTTAAAGTGATGCGCAGGTTTCATTTTATGCCCGTTTACGTTATCTTAGAGATG 660

Db 661 CATGGAATTTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT 720
|||||
Qy 661 CATGGAATTTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT 720

Db 721 TAGGTAATCTAGCAGCCCTGCGAACGTTTATAGGTGCTGGAGCGCTTAAACCCGTAGCCA 780
|||||
Qy 721 TAGGTAATCTAGCAGCCCTGCGAACGTTTATAGGTGCTGGAGCGCTTAAACCCGTAGCCA 780

Db 781 TTGTGCCAGGCTTGAAGACCATCGTCGGCGCGTTCATCGAATCGGTGAAGATCTGCGCG 840
|||||
Qy 781 TTGTGCCAGGCTTGAAGACCATCGTCGGCGCGTTCATCGAATCGGTGAAGATCTGCGCG 840

Db 841 ATGTGATTATCTCTGACCATGTTCTCCCTGCTCGGTGTTGCGTGTGATGGGCCCTACAGATCT 900
|||||
Qy 841 ATGTGATTATCTCTGACCATGTTCTCCCTGCTCGGTGTTGCGTGTGATGGGCCCTACAGATCT 900

Db 901 ATATGGCGTGTCTACCGAGAAGTGCATCAAGAAAGTTCGCCGTGGACGGTTCCTGGGGCA 960
|||||
Qy 901 ATATGGCGTGTCTACCGAGAAGTGCATCAAGAAAGTTCGCCGTGGACGGTTCCTGGGGCA 960

Db 961 ATCTGACCCAGCAGAACTGGGACTATCACAATCGCAATAGCTCCAATTGGTATTCGGAGG 1020
|||||
Qy 961 ATCTGACCCAGCAGAACTGGGACTATCACAATCGCAATAGCTCCAATTGGTATTCGGAGG 1020

Db 1021 ACGAGGCAATCTCATTTCCGTTATGCGGCAATATATCCGGTGGGGGCAATCGCAGGAGC 1080
|||||
Qy 1021 ACGAGGCAATCTCATTTCCGTTATGCGGCAATATATCCGGTGGGGGCAATCGCAGGAGC 1080

Db 1081 ATTACGTGTGCTGAGGGGTTTGGTCCGAATCCGAAATTTATGGCTACACCACTTCGATT 1140
|||||
Qy 1081 ATTACGTGTGCTGAGGGGTTTGGTCCGAATCCGAAATTTATGGCTACACCACTTCGATT 1140

Db 1141 CGTTCCGATGGGCTTTCCTGTCGCGCTTGATGACACAGGACTTCTGGGAGGATC 1200
|||||
Qy 1141 CGTTCCGATGGGCTTTCCTGTCGCGCTTGATGACACAGGACTTCTGGGAGGATC 1200

Db 1201 TGTACAGCTGTTGTGCGCGCGCGGACCATGCTGTTCCTTTATAGTCATCA 1260
|||||
Qy 1201 TGTACAGCTGTTGTGCGCGCGCGGACCATGCTGTTCCTTTATAGTCATCA 1260

Db 1261 TCTTCTAGGTTCAATCTATCTTGTAATTTGATTTTGCCATTTGTCATGTCGTATG 1320
|||||
Qy 1261 TCTTCTAGGTTCAATCTATCTTGTAATTTGATTTTGCCATTTGTCATGTCGTATG 1320

Db 1321 ACCAATTGCAAGAGGCGCGGAGAGAGGCTCCCAAGAGGAGGCGATACGTGAAG 1380
|||||
Qy 1321 ACCAATTGCAAGAGGCGCGGAGAGAGGCTCCCAAGAGGAGGCGATACGTGAAG 1380

Db 1381 CGGAAGAGCTGCGCGCGCGCAAGCGGCCCAAGCTGGAGGAGCGGCCAATGGCAGGCTC 1440
|||||
Qy 1381 CGGAAGAGCTGCGCGCGCGCAAGCGGCCCAAGCTGGAGGAGCGGCCAATGGCAGGCTC 1440

Db 1441 AGGCACGCGGATGCGCTGCGCGGAGAGGCTGCTGCTGATCCGAAATGGCCCAAGA 1500
|||||
Qy 1441 AGGCACGCGGATGCGCTGCGCGGAGAGGCTGCTGCTGATCCGAAATGGCCCAAGA 1500

Db 1501 GTCCGACGATTCTTCATCAGCTATGAGCTATTTGTCGCGCGGAGAGGCGCAACGATG 1560
|||||
Qy 1501 GTCCGACGATTCTTCATCAGCTATGAGCTATTTGTCGCGCGGAGAGGCGCAACGATG 1560

Db 1561 ACAACAAGAGAGAGATGTCATTCGAGGCGTTCGAGTGGAGTGGGTGAGGCGGAGG 1620
|||||
Qy 1561 ACAACAAGAGAGAGATGTCATTCGAGGCGTTCGAGTGGAGTGGGTGAGGCGGAGG 1620

Db 1621 TTATACAAAGACACCAACGACCTACCAAGCTACCAAGTTCTGTAAGTGA 1680
|||||
Qy 1621 TTATACAAAGACACCAACGACCTACCAAGCTACCAAGTTCTGTAAGTGA 1680

Db 1681 GCACGACATCCTTATCCTTACCTGGTTCCACCGTTTAACTACGAGGGATCAGTAGTT 1740
|||||
Qy 1681 GCACGACATCCTTATCCTTACCTGGTTCCACCGTTTAACTACGAGGGATCAGTAGTT 1740

QY 3901 ACGATGCTCCCGTCTGTGCAAGGATGGGCAATTTACGACTGAAAACCTTTTCAATTA 3960
Db 3961 TTGAAATAAATATTTGAAACAGCTGTATCACTATGATTTTAAATGAGTAGCTTACGCTT 4020
QY 3961 TTGAAATAAATATTTGAAACAGCTGTATCACTATGATTTTAAATGAGTAGCTTACGCTT 4020
Db 4021 TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATCTACGAGATATTTTATACATA 4080
QY 4021 TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATCTACGAGATATTTTATACATA 4080
Db 4081 TGGCAGAAATATTTACGGTTATATCTTCTTGGAAATGTTAATCAAGTGGTGGCGCTCG 4140
QY 4081 TGGCAGAAATATTTACGGTTATATCTTCTTGGAAATGTTAATCAAGTGGTGGCGCTCG 4140
Db 4141 GCTTCAAAAGTGTACTTACCAACGCGTGTGTGGCTCGAATTCGTGATTTGCTATGCTAT 4200
QY 4141 GCTTCAAAAGTGTACTTACCAACGCGTGTGTGGCTCGAATTCGTGATTTGCTATGCTAT 4200
Db 4201 CGCTTATCAACTTCGCTTCACTTGTGGAGCTGGTGGTATTCAAGCCCTTCAAGACTA 4260
QY 4201 CGCTTATCAACTTCGCTTCACTTGTGGAGCTGGTGGTATTCAAGCCCTTCAAGACTA 4260
Db 4261 TCGCAACGTTAAGACACTGAGACACATACGTCGCATGTCCCGTATGCGAGGCGATGAGG 4320
QY 4261 TCGCAACGTTAAGACACTGAGACACATACGTCGCATGTCCCGTATGCGAGGCGATGAGG 4320
Db 4321 TCGTCTTAATCGCTGTGACAAAGCTATACGTCGCATCTTCAATGTGCTATTGGTGTGTC 4380
QY 4321 TCGTCTTAATCGCTGTGACAAAGCTATACGTCGCATCTTCAATGTGCTATTGGTGTGTC 4380
Db 4381 TAATATTTTGGCTAAATTTTGGCAATATGGGTGTACAGCTTTTCTGGAAATATTTTA 4440
QY 4381 TAATATTTTGGCTAAATTTTGGCAATATGGGTGTACAGCTTTTCTGGAAATATTTTA 4440
Db 4441 AGTGGAGACATGAATGGCAGAGCTCAGCCAGAGATCATACCAATGCGAATGCGT 4500
QY 4441 AGTGGAGACATGAATGGCAGAGCTCAGCCAGAGATCATACCAATGCGAATGCGT 4500
Db 4501 GCGAGAGCAGAACTACAGCTGGGTGAATTCAGCAATGAATTCGATCATGTAGTAACG 4560
QY 4501 GCGAGAGCAGAACTACAGCTGGGTGAATTCAGCAATGAATTCGATCATGTAGTAACG 4560
Db 4561 CGTATCTGCTCTTTTCCAAAGTGGCCACCTTCAAAGGTGGATCAAAATCATGAACGATG 4620
QY 4561 CGTATCTGCTCTTTTCCAAAGTGGCCACCTTCAAAGGTGGATCAAAATCATGAACGATG 4620
Db 4621 CTATCGAATTCAGAGAGTGGCAAGCAACCAATTCGTGAAACGAACTCTACATGTAT 4680
QY 4621 CTATCGAATTCAGAGAGTGGCAAGCAACCAATTCGTGAAACGAACTCTACATGTAT 4680
Db 4681 TATATTTCTGATTTCTTCATCATATTTGGATCCTTTTTCACACTCAATCTGTTTCAATGGTG 4740
QY 4681 TATATTTCTGATTTCTTCATCATATTTGGATCCTTTTTCACACTCAATCTGTTTCAATGGTG 4740
Db 4741 TTAATCATGATTAATTTAATAGCAAAAGAAAGAGCAGGTGGATCATTTAGAAATGTTC 4800
QY 4741 TTAATCATGATTAATTTAATAGCAAAAGAAAGAGCAGGTGGATCATTTAGAAATGTTC 4800
Db 4801 TGACAGAAGATCAGAAAAGTACTATAATGCTATGAAAGATGGCTCTTAAAAACCAT 4860
QY 4801 TGACAGAAGATCAGAAAAGTACTATAATGCTATGAAAGATGGCTCTTAAAAACCAT 4860
Db 4861 TAAAGCCATTTCCAGACCAAGTGGCGACCCCAAGCAATAGTCTTTTGAATAGTAACCG 4920
QY 4861 TAAAGCCATTTCCAGACCAAGTGGCGACCCCAAGCAATAGTCTTTTGAATAGTAACCG 4920
Db 4921 ATAAGAAATTCGATTAATCATTTATGTTATTCATTTGGTCTGAACATGTTTACCATGACCC 4980
QY 4921 ATAAGAAATTCGATTAATCATTTATGTTATTCATTTGGTCTGAACATGTTTACCATGACCC 4980
Db 4981 TCGATCTTACGATGGCTCGGACACGCTATTAACCGGCTCTAGACTATCTCAATGCGATAT 5040
QY 4981 TCGATCTTACGATGGCTCGGACACGCTATTAACCGGCTCTAGACTATCTCAATGCGATAT 5040

Db 5041 TCGTAGTATTTTTCAGTTCCGAATGTCTATTAAAAATATTTCGCTTTACGATATCACTATT 5100
QY 5041 TCGTAGTATTTTTCAGTTCCGAATGTCTATTAAAAATATTTCGCTTTACGATATCACTATT 5100
Db 5101 TTATTGAGCCATGGAATTTTATTGATGTAGTAGTTGTCTATTTTATCCATCTTAGGCTTGG 5160
QY 5101 TTATTGAGCCATGGAATTTTATTGATGTAGTAGTTGTCTATTTTATCCATCTTAGGCTTGG 5160
Db 5161 TACTTAGCCATATTATCGAGAAAGTACTTCTGTGCGCGACCTGTCTCCAGTGGTGGCTGG 5220
QY 5161 TACTTAGCCATATTATCGAGAAAGTACTTCTGTGCGCGACCTGTCTCCAGTGGTGGCTGG 5220
Db 5221 TGGCAAAAGTGGGCCCTGTCTTCGACTGGTGAAGGAGGCCAAGGCGATTCGCGACACTGC 5280
QY 5221 TGGCAAAAGTGGGCCCTGTCTTCGACTGGTGAAGGAGGCCAAGGCGATTCGCGACACTGC 5280
Db 5281 TCTTCGCGTGGCCATGTCGTCGCCGGCCCTGTCTCAACATCTGCCCTGTCTTCTCTGG 5340
QY 5281 TCTTCGCGTGGCCATGTCGTCGCCGGCCCTGTCTCAACATCTGCCCTGTCTTCTCTGG 5340
Db 5341 TCATGTTTCATCTTTCGCAATTTTCGGCATGTCTGTTCTTCATGACAGTGAAGGAGAGCG 5400
QY 5341 TCATGTTTCATCTTTCGCAATTTTCGGCATGTCTGTTCTTCATGACAGTGAAGGAGAGCG 5400
Db 5401 GCATTAACGACGCTTACAACCTTCAAGACCTTTGGCCAGAGCATGATCTCTCTTTTCA 5460
QY 5401 GCATTAACGACGCTTACAACCTTCAAGACCTTTGGCCAGAGCATGATCTCTCTTTTCA 5460
Db 5461 TGTGCGAGCTACGCCGTTGGGATGGTGTACTGGACGCCATTAATCAATGAGGAGCATGCG 5520
QY 5461 TGTGCGAGCTACGCCGTTGGGATGGTGTACTGGACGCCATTAATCAATGAGGAGCATGCG 5520
Db 5521 ATCCACCCGACGACGACAAAGGCTATCCGGCAATTTGTGTTCCAGCAGCGCTTGGAAATA 5580
QY 5521 ATCCACCCGACGACGACAAAGGCTATCCGGCAATTTGTGTTCCAGCAGCGCTTGGAAATA 5580
Db 5581 CGTTTCTCTCTCATACCTAGTTATAGCTTTTGTAGTATTAATGATGATGATGCTGCTG 5640
QY 5581 CGTTTCTCTCTCATACCTAGTTATAGCTTTTGTAGTATTAATGATGATGATGCTGCTG 5640
Db 5641 TCATTTCTGAGAACTATAGTCAGGCCACCGAGGAGCTGCAAGAGGGTCTAACCCGAGCG 5700
QY 5641 TCATTTCTGAGAACTATAGTCAGGCCACCGAGGAGCTGCAAGAGGGTCTAACCCGAGCG 5700
Db 5701 ACTACGACATGTACTATGAGATCTGGCAGCAATTCGATCCGAGGCGACCCAGTACATAC 5760
QY 5701 ACTACGACATGTACTATGAGATCTGGCAGCAATTCGATCCGAGGCGACCCAGTACATAC 5760
Db 5761 GCTATGATCAGCTGTCGGAATTCCTGGACGTACTGGAGCCCCCGCTGCGAGATCCACAAAC 5820
QY 5761 GCTATGATCAGCTGTCGGAATTCCTGGACGTACTGGAGCCCCCGCTGCGAGATCCACAAAC 5820
Db 5821 CGAACAAGTCAAGATCATATCGATGGACATACCCATCTCTGCGGGTGAACCTCATGFACT 5880
QY 5821 CGAACAAGTCAAGATCATATCGATGGACATACCCATCTCTGCGGGTGAACCTCATGFACT 5880
Db 5881 CGCTCGACATCTCTCGAGCCCTTACGAAAGACTTCTTTGCGCGAAGGCGCAATCCGATAG 5940
QY 5881 CGCTCGACATCTCTCGAGCCCTTACGAAAGACTTCTTTGCGCGAAGGCGCAATCCGATAG 5940
Db 5941 AGGAGAGGGTGAATTTGGTGAATAGCGGCCCGCCCGGATACGAGGGGTACGAGCCCG 6000
QY 5941 AGGAGAGGGTGAATTTGGTGAATAGCGGCCCGCCCGGATACGAGGGGTACGAGCCCG 6000
Db 6001 TCTCATCAACGCTGTGGCGTCAAGTACTCGCCCGGCTAATCAGCACCCCT 6060
QY 6001 TCTCATCAACGCTGTGGCGTCAAGTACTCGCCCGGCTAATCAGCACCCCT 6060
Db 6061 GCGGAAAGCACAAGCGCGCGGAGGAGGTGGTCTTTGACCGGATACGATCATG 6120
QY 6061 GCGGAAAGCACAAGCGCGCGGAGGAGGTGGTCTTTGACCGGATACGATCATG 6120

Db 6121 GCATGCGGTGATCGGATGCCGGGACCCGCCCGCGATGAAGCAACGACGCGGATG 6180
|||||
QY 6121 GCATGCGGTGATCGGATGCCGGGACCCGCCCGCGATGAAGCAACGACGCGGATG 6180
|||||
Db 6181 CGCCCGCTGCTGAGATGAGTGTAAACGGTACTCAGAGAGAGCTGCCGATGCCGATG 6240
|||||
QY 6181 CGCCCGCTGCTGAGATGAGTGTAAACGGTACTCAGAGAGAGCTGCCGATGCCGATG 6240
|||||
Db 6241 AGAGTAATGTAATAGTCCGGGTGAGATGACGACGCGCGCGGAGAGCAGACGACGAG 6300
|||||
QY 6241 AGAGTAATGTAATAGTCCGGGTGAGATGACGACGCGCGCGGAGAGCAGACGACGAG 6300
|||||
Db 6301 CGCGCGCGCGGACGACGACGCGCGGAGTCCCGGAGCGGTAGCGCGCGGCGACAGA 6360
|||||
QY 6301 CGCGCGCGCGGACGACGACGCGCGGAGTCCCGGAGCGGTAGCGCGCGGCGACAGA 6360
|||||
Db 6361 CCGCCGTCTCGTGGAGAGCGAGCGGTCTCGTACGAGACGCGCCACAGGTGCTCATCC 6420
|||||
QY 6361 CCGCCGTCTCGTGGAGAGCGAGCGGTCTCGTACGAGACGCGCCACAGGTGCTCATCC 6420
|||||
Db 6421 ACTCGGATCGCGGACGATCAGTCCGCGACGCGGATGCTGAGCGAGCGCTCGCCGCC 6480
|||||
QY 6421 ACTCGGATCGCGGACGATCAGTCCGCGACGCGGATGCTGAGCGAGCGCTCGCCGCC 6480
|||||
Db 6481 CCCTCAAGATGCACGCGAGTATTAGCTCTAGA 6513
|||||
QY 6481 CCCTCAAGATGCACGCGAGTATTAGCTCTAGA 6513
|||||

4 DROSODCHA 6883 bp mRNA INV 28-SEP-1993
LOCUS Drosophila melanogaster para locus, sodium channel alpha subunit
DEFINITION mRNA, complete cds.
ACCESSION M32078 M24285 M32079 M32080
NID 9403441
KEYWORDS alternative splicing; opa repetitive sequence; sodium channel alpha subunit.
SOURCE D.melanogaster (strain para-hd2), cDNA to mRNA, clone ZS10.3.
ORGANISM Drosophila melanogaster
Eukaryotae; mitochondrion eukaryotes; Metazoa; Arthropoda;
Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 6883)
AUTHORS Lounibey, K., Kreber, R. and Ganetzky, B.
TITLE Molecular analysis of the para locus, a sodium channel gene in Drosophila
Cell 58, 1143-1154 (1989)
JOURNAL 89376565
MEDLINE 2 (sites)
REFERENCE Ramaswami, M. and Tanouye, M.A.
AUTHORS Two sodium channel genes in Drosophila: Implications for channel diversity
TITLE Proc. Natl. Acad. Sci. U.S.A. 86, 2079-2082 (1989)
JOURNAL 89184571
MEDLINE 3 (sites)
REFERENCE Thackeray, J.R. and Ganetzky, B.
AUTHORS Developmentally regulated alternative splicing generates a complex array of Drosophila para sodium channel isoforms
TITLE Unpublished (1993)
JOURNAL Draft entry and computer-readable sequence for [Proc. Natl. Acad. Sci. U.S.A. 58, 1143-1154 (1989)] kindly submitted by B.Ganetzky, 25-APR-1989.
FEATURES
source 1. .6883
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
repeat_region 1. .93
/rpt_family="opa"
gene 1. .6883
/note="paralytic"
/gene="para"
/allele=""
/db_xref="FlyBase:FBgn0003036"

CDS

join(272..3010,3173..6667)
/gene="para"
/note="alternative exon d. All para mRNAs contain either alternative exon c (see variation) or alternative exon d at this site."
/codon_start=1
/product="sodium channel alpha subunit"
/db_xref="PID:g40344"
/translation="MTEDSDSISEERSLFRPFTRESLVQIEQRIAAEHEKQELERK
RAEGVPYGRKKKQKEIRYDDEDEGPQDPPIEQGVPIPVRLQSGFPPELSTPL
EDIDPYSNLTFVVSXGKDIREFSASKAMMLDPFNPRIIRVAILIIVHPLFSLFI
TTILVNCILIMPTTPTVESTEIVTIGYTFESAVKVMARGFILCPFTYLRDANWLD
FVVALAYVTMGIDLGNLAALTRFVRLAKTVALVPGKTIIVGAVISVRLRDVII
LTMSLSVFMALGQIYMGVLTKEIKKFPIDGSGNLTDENWYHNRNSNWSYSEDE
GISPLCGNISAGOCDDYVCLQGFNPNGYTSFDSFGWAFLSAFLMTQDWEDE
LYQLVRAAGPWHMLFFVIIFLAGSYLVNLIILAVMSYDELOKRAEAEAESEAI
REDEPAAKAAKLEERANAQAADAAAEALHPMAKSPYSCISYELFVGGE
KGNDDNKKMSIRSEVESVSQIROPAPTTAHOATKYKYSTTSLSPGSPFNI
RGRSSSHKYIRNGRFGIPGSRKELVLTSTQDAQOHLPIYADDSNAVTPMSSENG
AIIIVPVYVYNGLSRHSSTSHOSISYTSGLDGLGGMAVGVMTKESKURNTRN
QSVGATNGGTTCLDTHNKLDRHYEIGLECTDEAGIKIHDNPFTPEVQOTVVDMDK
VAVLNDIIEQAAGHRASDRGVSYYEPTEDDDGPTFKDKALEVILKGIDVFCVW
DCVWYLFQEWVSLIVDFPVFELFITLICIVVNTMFAMDHDMKMERVLKSNYF
ETAFATIEATMKLAMSPPKYYEQEGNIFDELIIVALSLELGLGEGVQGLSVLSRDL
HKDRPDGDLFRNFTDFNHSFMIVFVLCGEWIESMMDCTVGVSCIPFLATVVI
GNLVNLFALLISNFGSSLSAPTADNTKTAENRIGRFKSWKRNIAIDCFKL
IRNKLTNQSIPGSGRTNQSITWSEKGVCRGISAEHGDNELELGHLEIADGLIK
KGIEQTOLEVAIGDMETIHDGMMKPKKSKYLNNAATDDDTASINSYGHKNRPF
KDESHKSAETMEGEERKASKEDLGLDEELDEGECEGLDGDIIITHANDEDILDE
YPADCCPDSYKPKPILAGDDSPWQWGNLRLKTFRLIEDKYETAVIYIMLSSSL
ALALDEHLRPILODILYIMDRIFTVIFLEMLIKWLALGKRVLYNACWLDQFVI
VWVSLNFAVLGAGGQIAQFTMTLRALRPLRAMSRQGVNRVNVNVAQIPISFN
VLLVCLIFWLFAINGVQLFAGKYCEDMGTKLSHEIIPNRNACESENTWNSAM
NFDHVGNAYLCFLVATFEGWTOIMNDAIDSGREVDPQPIRETNIYLYFVFFIFGS
FETLNLFGVIIDNENQKKAGSLEMFTEDOKKYYSAMKMGSKKPLKAIPRPQ
RPOAVFIEVTDKKFDIIMLFIFGLMFTWLDVDSDTYNVLDYLNALFVIFSS
ECLKIFALRIHYFIEPNLFDVVVILSIGLVLSDIIEKIFYVSLVVRVAVKVG
RVYLRVKGAGKITLLFALMSLPALNICLLFLVMFIFAIFGSMFHMVKESGIN
DYNFKTFQGMILLFQMSAGMDVLDIAINEACDPDNDKGPNGCSAGTIGIT
FLSYLVISFLVINMYIAVILENSQATEVQEGLTDDDYDMEIYIQWDPQCTQY
IRYDLSSEFLVLEPPLQIHKPNKYIISMDIPICRGLMYCVDILALTIDKDFARK
NPIETGEIGIEAARPDTEGYEYVSTLWROREYCARLIOHAKRKHAKGEGGSFE
PDTDHGGDDPDADPEATDADPAGDGSVNTAGGAADAEVNSNPGDEAAA
AAAAAATAAGTTAGSPGAGSAGRTAVLVESDGFVTKNGHKVYIHSRSPSITSRT
ADV"

CDS

join(272..2558,2583..6667)
/gene="para"
/note="alternative exon b for optional inclusion in mRNA"
/codon_start=1
/product="sodium channel alpha subunit"
/db_xref="PID:g403443"
/translation="MTEDSDSISEERSLFRPFTRESLVQIEQRIAAEHEKQELERK
RAEGVPYGRKKKQKEIRYDDEDEGPQDPPIEQGVPIPVRLQSGFPPELSTPL
EDIDPYSNLTFVVSXGKDIREFSASKAMMLDPFNPRIIRVAILIIVHPLFSLFI
TTILVNCILIMPTTPTVESTEIVTIGYTFESAVKVMARGFILCPFTYLRDANWLD
FVVALAYVTMGIDLGNLAALTRFVRLAKTVALVPGKTIIVGAVISVRLRDVII
LTMSLSVFMALGQIYMGVLTKEIKKFPIDGSGNLTDENWYHNRNSNWSYSEDE
GISPLCGNISAGOCDDYVCLQGFNPNGYTSFDSFGWAFLSAFLMTQDWEDE
LYQLVRAAGPWHMLFFVIIFLAGSYLVNLIILAVMSYDELOKRAEAEAESEAI
REDEPAAKAAKLEERANAQAADAAAEALHPMAKSPYSCISYELFVGGE
KGNDDNKKMSIRSEVESVSQIROPAPTTAHOATKYKYSTTSLSPGSPFNI
RGRSSSHKYIRNGRFGIPGSRKELVLTSTQDAQOHLPIYADDSNAVTPMSSENG
AIIIVPVYVYNGLSRHSSTSHOSISYTSGLDGLGGMAVGVMTKESKURNTRN
QSVGATNGGTTCLDTHNKLDRHYEIGLECTDEAGIKIHDNPFTPEVQOTVVDMDK
VAVLNDIIEQAAGHRASDRGDDDDGPTFKDKALEVILKGIDVFCVWDCGWMLK
FOEWSLIVDFPFVFLFITLICIVVNTMFAMDHDMKMERVLKSGNYFTATATIE
ATMKLAMSPPKYYEQEGNIFDELIIVALSLELGLGEGVQGLSVLSRFLRLKLA
WPTLDMHSFMIVFVLCGEWIESMMDCMYGVDSVCIPEFLATVYIGNLVNLFAL
LLSNFGSSLSAPTADNTKTAENRIGRFKSWKRNIAIDCFKLIRNKLTNQSIDQ
PSGERTNQSITWSEKGVCRGISAEHGDNELELGHLEIADGLIKIGIKOTOLEVA
IGDGMETIHDGMMKPKKSKYLNNAATDDDTASINSYGHKNRPFKDESHKSAETM
EGEKRDASKEDLGLDEELDEGECEGLDGDIIITHANDEDILDEYPADCCPSYK

```
KPPILAGDDSPFWGNGNLRLKTRLETKYFETAVITAMILMSLALALADVDHLPQR
PILODLYYMDRIEFTVIFLEMLIKWLAIGFKVYLTNACWLDLFIYVWVSLINVASL
VAGQLOAFKQWTRTIRALRPLRAMSGMRVYVALVQAIPWISFNVLQSLWFLIF
AINGVLFAGKFKEDMGTKLSHIEIIPNRNACESENTPWSNMANHDHVGAYLCL
FOVATFKWQIMDAIDSDREYDKQPIRETNIYKLYLVFFIIFGFFTLNLFIGVII
DNFEOKKAGGLEMTEDOKKYISAMKMGSKPKAKAIPRPRRPOAIVFEITD
KFEDIIMFLIGLNMFTLDRDASDYNAVLYDLNFAVYIFSECLLIFALRYH
YFIEPLNFEDVVVILSLGLVLSIDIEKYFVSPDLLRVVRVAKVGRVLRLVKAAGKI
RTLLFALMSLPALNICLLLVLMFIFAIKCFKMFHVKESGINDVYKPTGQSM
ILLFQMSAGMDGVLDALINEEACDPDNDKGYFGNCGSATVGTIFLLSLYISFLI
VINMYTAVILENYSQATEDVQELTDDDDYMEIWWQDPDEGTQYIRYDLSSEFLDV
LEPPLQIHKPNKYIISMDPIICRGDLMTCDVIDLALTKDFPARKGNPIETEGEIGEI
AARPDTEGTPVSTLRQREYCARLQIOWARKHKHARGEGGSEPTDHDGDDGDPD
AGDPADEATDGDAPAGDGSVNGTAGAADADESNVSPGEDAAAAAANAANAANA
TTAGSPGAGSAGRTAVLVESDGFYTKNGHKVVIHSRSPSITSRTADV"
272..6667
/gene="para"
/codon_start=1
/product="sodium channel alpha subunit"
/db_xref="PID:g403442"
/translation="MTEDSDSISEERSLFRPFTRESLVIQIQRVIAAEHKEKELERK
RAGEVPRGRKKKQKEIRYDDEDEGPOPTLEQGVIPVRLOGSPPELSTPL
EDIDPYSNVLTIVVSKGDIIFRSASRAMWMLDFNPIRRVAIYLIVHPLFLSFI
TTLVNCILMIMPPTTVESTIEFTGTYTFESAVKVMARGETILCPFTYLRDANWLD
FVVALAYVTMGIDLGNLAALRTFRVLRALKTVAIYPGLKTIIVGAVIESVKNLRDVI
LTFSLVSFALMGLOIYMGVLTKECIKFPDLGSGNLTLDENWDYHNRNMSWYSEDE
GISFPLGNTSGAGQDDYVCLQGFPGPNPYGTSFDSFGWAFLSAFRLMTQDFWED
LYOLVLAAPGPHMLPEFVIFLGSFYLNLILAIIVAMSYDELQRAKEEAEAEAEAI
REAEAAAAAKLEBRANAQAQAAAAEAALHPMAKSPYSCISYELFVGGE
KGNDDNNKMSIRSVESVSVIQRQAPTAHQKTVKRYKVTISLSLGSFPNI
RGRSSHKYTIIRNGRFGIPGSDRKLPLVLTQDQOHLFPADDSNAVTPMSENRG
AIIVPVYVGLSGRHSYSTSHOSRISYTHGDLGGWAMGVSTMTKESKLNRNTRN
QVWATNGTCLDTHKLDHYEIGLECTDEAGKIKHNDNPFIEPVQTVVDMKD
SMGLNLEOAGRHSPASDRGVSVYFPTEDDDEGPTFKDKALEVILQIDVFCWV
DCCHWLKQEWVSLIVDFPVELEITLCIVVNTFMANDHDMKEMERVLKSGNYF
FTVFALEAKMLMAMSPKYIFQEGWNIFDIIVALSLELLEGLGVQGLSVLRSPLF
RVFLAKSWPLNLISINGRTGALGNLTFVLCIIFIVMGMOLFGKNHDKDR
FPDGLPRLNFTDMHSMFIVFVLCGEWIESMDCMRYGDSVCPFFLATVYILNGLV
VLNGLLWLLSNFGSSLSATADNDNTKIAEAFNRKFSWKVKNRIADCCVLIKNR
LTNOISDQPSGERTNOISWISGEGKVCRCISAEHGDNELELGHDELADGLKKGKIG
EQTOLEVAIGDGHEFTIGDMKNKPKSKYLANATDDDTASINSXSGHKNRPFKDES
HKGSAETMEGEEKKADKDLGLDELDDEGECEBPLDGDIIIIHAHDEDLDEYEPAD
CCPSYKPKPILAGDDSPFWGNGNLRLKTRLETKYFETAVITAMILMSLALAL
EDVHLPOIPLQDLYLYMDRIEFTVIFLEMLIKWLAIGFKVYLTNACWLDLFIYVWV
LINESVLAIGAGGQIQAFTWTRLRALRPLRAMSGMRVYVALVQAIPWISFNVLV
CLIFWLIFAIMGVOLFAGKYFKCEDMNGTKLSHIEIPNRNACESENTPWNSAMNFDH
VGNAYLCIFQVATFKGQIOMDAIDSDREYDKQPIRETNIYKLYLVFFIIFGFFTL
NLFTGVLIIDNEOKKAGGLEMTEDOKKYISAMKMGSKPKAKAIPRPRRPOA
IVFEIVDKFEDIIMFLIGLNMFTLDRDASDYNAVLYDLNFAVYIFSECLL
KIFALRYHIFEPNLDVIVVILSLGLVLSIDIEKYFVSPDLLRVVRVAKVGRVLR
LVKGAIGRTLLFALMSLPALNICLLLVLMFIFAIKCFKMFHVKESGINDVYN
FKTFCQSMILLFAMTSTAGMDGVLDALINEEACDPDNDKGYFGNCGSATVGTIFLLS
YLVISFLIVIMYIATLENYSQATEDVQELTDDDDYMEIWWQDPDEGTQYIRYD
OLSEFLDLEPLOIHKPNKYIISMDPIICRGDLMTCDVIDLALTKDFPARKGNPIE
ETGEIGELAAPRDEGTPVSTLRQREYCARLQIOWARKHKHARGEGGSEPTD
HDGDDPDAGDPADEATDGDAPAGDGSVNGTAGAADADESNVSPGEDAAAAAANA
AAAAAAGTTTAGSPGAGSAGRTAVLVESDGFYTKNGHKVVIHSRSPSITSRTADV"
join(272..1933,1997..6667)
/gene="para"
/note="alternative exon for optional inclusion in mRNA"
/codon_start=1
/label-exon_a
/product="sodium channel alpha subunit"
/db_xref="PID:g403442"
/translation="MTEDSDSISEERSLFRPFTRESLVIQIQRVIAAEHKEKELERK
RAGEVPRGRKKKQKEIRYDDEDEGPOPTLEQGVIPVRLOGSPPELSTPL
EDIDPYSNVLTIVVSKGDIIFRSASRAMWMLDFNPIRRVAIYLIVHPLFLSFI
TTLVNCILMIMPPTTVESTIEFTGTYTFESAVKVMARGETILCPFTYLRDANWLD
FVVALAYVTMGIDLGNLAALRTFRVLRALKTVAIYPGLKTIIVGAVIESVKNLRDVI
LTFSLVSFALMGLOIYMGVLTKECIKFPDLGSGNLTLDENWDYHNRNMSWYSEDE
GISFPLGNTSGAGQDDYVCLQGFPGPNPYGTSFDSFGWAFLSAFRLMTQDFWED
LYOLVLAAPGPHMLPEFVIFLGSFYLNLILAIIVAMSYDELQRAKEEAEAEAEAI
REAEAAAAAKLEBRANAQAQAAAAEAALHPMAKSPYSCISYELFVGGE
```

CDS

... Note: remainder of annotations omitted.

Query Match 92.0%; Score 5992; DB 14; Length 6883;
Best Local Similarity 97.8%; Pred. No. 0.00e+00;
Matches 6359; Conservative 0; Mismatches 97; Indels 45; Gaps 28;

Db	255	CGTTGGCGCATAGACAATGACAGAAGATCCGACTCGATATCTTGAGGAAGAACGCAGTT	314
Qy	7	CGTTGGCGCGCATAGACAATGACAGAAGATCCGACTCGATATCTTGAGGAAGAACGCAGTT	66
Db	315	TGTTCCGTCCTTTTACCCCGCAATCATTGGTGCAAAATCGAAACGCAATTCGCCGCTGAAC	374
Qy	67	TGTTCCGTCCTTTTACCCCGCAATCATTGGTGCAAAATCGAAACGCAATTCGCCGCTGAAC	126
Db	375	ATGAAAGCAGAGAGCTGGAAGAAAGAGAGCGGAGAGAGTGCCTGGGATATGTC	434
Qy	127	ATGAAAGCAGAGAGCTGGAAGAAAGAGAGCGGAGAGAGTGCCTGGGATATGTC	186
Db	435	GCAAGAAAAACAAAAAGAAATCCGATATGATGACGAGAGAGGATCAAGTCCACAAAC	494
Qy	187	GCAAGAAAAACAAAAAGAAATCCGATATGATGACGAGAGAGGATCAAGTCCACAAAC	246
Db	495	CGGATCCTACACTTGAAACAGGGTGTGCCAATACCTTGTTCGATTGCGAGGCGAGTTC	554
Qy	247	CGGATCCTACACTTGACAGGGTGTGCCAATACCTTGTTCGATTGCGAGGCGAGTTC	306
Db	555	CGGAATTGCCCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTACTGACAT	614
Qy	307	CGGAATTGCCCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTACTGACAT	366
Db	615	TCGTAGTTGTAAGCAAGAAAGATATTTTCGCTTTTCTGCATCAAAAGCAATGTGGA	674
Qy	367	TCGTAGTTGTAAGCAAGAAAGATATTTTCGCTTTTCTGCATCAAAAGCAATGTGGA	426
Db	675	TGCTCGATCCATTCATCCGATACGTCGCTGGCCATTTACATCTTAGTGCAATCATAT	734
Qy	427	TGCTCGATCCATTCATCCGATACGTCGCTGGCCATTTACATCTTAGTGCAATCATAT	486
Db	735	TTTCCCTATTATCATCACCACAAATTCCTGCAACTGCATCCTGATGATAATGCCGACAA	794
Qy	487	TTTCCCTATTATCATCACCACAAATTCCTGCAACTGCATCCTGATGATAATGCCGACAA	546
Db	795	CGCCACAGGTTGAGTCCACTGAGGTGATATTACCCGGAATCTACACATTTGAATCAGCTG	854
Qy	547	CGCCACAGGTTGAGTCCACTGAGGTGATATTACCCGGAATCTACACATTTGAATCAGCTG	606
Db	855	TTAAAGTGATGGCAGGAGTTTCATTTTATGCCCGTTTACGTATCTTAGAGATGCATGA	914
Qy	607	TTAAAGTGATGGCAGGAGTTTCATTTTATGCCCGTTTACGTATCTTAGAGATGCATGA	666
Db	915	ATTGGCTGGACTTCGTAGTAATAGCTTTTAGCTTATGTGACCATGGGTATAGATTAGGTA	974
Qy	667	ATTGGCTGGACTTCGTAGTAATAGCTTTTAGCTTATGTGACCATGGGTATAGATTAGGTA	726
Db	975	ATCTAGCAGCCCTCGCAACGTTTGGGTGCTGCGAGCGCTTAAAAACCGTAGCATTGTGC	1034
Qy	727	ATCTAGCAGCCCTCGCAACGTTTGGGTGCTGCGAGCGCTTAAAAACCGTAGCATTGTGC	786
Db	1035	CAGCCTTGAAGACCATCGTCGGCGCGCTCATCGAATCGGTGAAGAATCTCGCGGATGTA	1094
Qy	787	CAGCCTTGAAGACCATCGTCGGCGCGCTCATCGAATCGGTGAAGAATCTCGCGGATGTA	846

CDS

Db 1095 TTATCCTGACCATGTTCTCCCTGTCCGTTGTTCCGCTTACAGATCTATATGG 1154
Qy |||||
Db 847 TTATCCTGACCATGTTCTCCCTGTCCGTTGTTCCGCTTACAGATCTATATGG 906
Qy |||||
Db 1155 GGGTCTCACCAGAAAGTGCAACAAGAGTTCCCGCTGGACGGTTCTGGGCAATCTGA 1214
Qy |||||
Db 907 GGGTCTCACCAGAAAGTGCAACAAGAGTTCCCGCTGGACGGTTCTGGGCAATCTGA 966
Qy |||||
Db 1215 CCGACGAGAACTGGGACTATCAACATCGCAATAGCTCCAATTGGTATTCCGAGGACGAGG 1274
Qy |||||
Db 967 CCGACGAGAACTGGGACTATCAACATCGCAATAGCTCCAATTGGTATTCCGAGGACGAGG 1026
Qy |||||
Db 1275 GCATCTCATTTCCGTTATGCGGCAATATATCCGGTGGGGGCAATGCGACGAGATTACG 1334
Qy |||||
Db 1027 GCATCTCATTTCCGTTATGCGGCAATATATCCGGTGGGGGCAATGCGACGAGATTACG 1086
Qy |||||
Db 1335 TGTGGCTGCAGGGGTTTGGTCCGAATCCGAATTTAGGCTACACCACTTCGATTGGTTCCG 1394
Qy |||||
Db 1087 TGTGGCTGCAGGGGTTTGGTCCGAATCCGAATTTAGGCTACACCACTTCGATTGGTTCCG 1146
Qy |||||
Db 1395 GATGGGCTTTCTGTCGCGCTTCCGGCTGATGACACAGGACTTCTGGAGGATCTGTACC 1454
Qy |||||
Db 1147 GATGGGCTTTCTGTCGCGCTTCCGGCTGATGACACAGGACTTCTGGAGGATCTGTACC 1206
Qy |||||
Db 1455 AGCTGGTGTGGCGCGCGCGGACCATGGCACATGCTGTCTTTATAGTCATCTCTTCC 1514
Qy |||||
Db 1207 AGCTGGTGTGGCGCGCGCGGACCATGGCACATGCTGTCTTTATAGTCATCTCTTCC 1266
Qy |||||
Db 1515 TAGGTTCACTTCTATCTGTGAATTTGATTTGGCCATTTGTTGCCATGTCGTATGACGAAT 1574
Qy |||||
Db 1267 TAGGTTCACTTCTATCTGTGAATTTGATTTGGCCATTTGTTGCCATGTCGTATGACGAAT 1326
Qy |||||
Db 1575 TCAAGAAGGAGCCGAAGAAGAGGCTGCGCAAGAGAGGAGCGGATACGTGAAGCGGAG 1634
Qy |||||
Db 1327 TCAAGAAGGAGCCGAAGAAGAGGCTGCGCAAGAGAGGAGCGGATACGTGAAGCGGAG 1386
Qy |||||
Db 1635 AAGCTGCGCGCGCGCAAGGCGCAAGCTGGAGGAGCGGGCCAAATCGGAGGCTCAGGCGAG 1694
Qy |||||
Db 1387 AAGCTGCGCGCGCGCAAGGCGCAAGCTGGAGGAGCGGGCCAAATCGGAGGCTCAGGCGAG 1446
Qy |||||
Db 1695 CAGCGGATGCGGCTGCCCGGAGAGGCTGCACTGCATCCCGGAATGSCCAAGATCCGA 1754
Qy |||||
Db 1447 CAGCGGATGCGGCTGCCCGGAGAGGCTGCACTGCATCCCGGAATGSCCAAGATCCGA 1506
Qy |||||
Db 1755 CGTATTCTTGCAATCAGCTATGAGCTATTGTTGGCGGCGAGAAGGCAACGATGACAACA 1814
Qy |||||
Db 1507 CGTATTCTTGCAATCAGCTATGAGCTATTGTTGGCGGCGAGAAGGCAACGATGACAACA 1566
Qy |||||
Db 1815 ACAAGAAGATGTCCATTCGGAGCGTGAGGTTGGAGTGGAGTGGGTCGGTGTATAC 1874
Qy |||||
Db 1567 ACAAGAAGATGTCCATTCGGAGCGTCGAGGTGGAGTGGAGTGGGTCGGTGTATAC 1626
Qy |||||
Db 1875 AAAGACACCCACCTACCAACAGACACACCAAGCTACCAAAAGTTGCTAAAGTGACACGA 1934
Qy |||||
Db 1627 AAAGACACCCACCTACCAACAGACACACCAAGCTACCAAAAGTTGCTAAAGTGACACGA 1686
Qy |||||
Db 1935 CATCTTATCTTACCTAGCTTCCAGCTTTAACAATACGAGGGGATCAGTAGTCTCTACA 1994
Qy |||||
Db 1687 CATCTTATCTTACCTAGCTTCCAGCTTTAACAATACGAGGGGATCAGTAGTCTCTACA 1746
Qy |||||
Db 1995 AGTACACGATACGGAACGAGCTGGCGCTTTGGTATACCCGGTAGCGATCGTAAGCCAT 2054
Qy |||||
Db 1747 AGTACACGATACGGAACGAGCTGGCGCTTTGGTATACCCGGTAGCGATCGTAAGCCAT 1806
Qy |||||
Db 2055 TGGTATTGTCAACATATCAGGATGCCAGCAGACTTGGCCCTATGCCGACGACTCGAATG 2114
Qy |||||
Db 1807 TGGTATTGTCAACATATCAGGATGCCAGCAGACTTGGCCCTATGCCGACGACTCGAATG 1866
Qy |||||
Db 2115 CCGTACCCCGGATGTCGGAAGAGATGGGGCATCATAGTGGCCGTACTATGCGCAATC 2174
Qy |||||
Db 1867 CCGTACCCCGGATGTCGGAAGAGATGGGGCCATCATAGTGGCCGTACTATGCGCAATC 1926
Qy |||||

Db 2175 TAGGCTCCCGACACTCATCTGATACCTCGCATCAGTCCCGAATATCGTATACCTCACATG 2234
Qy |||||
Db 1937 TAGGCTCCCGACACTCATCTGATACCTCGCATCAGTCCCGAATATCGTATACCTCACATG 1986
Qy |||||
Db 2235 CGCATCTACTCGGGGGATGGCGCTCATGGCGTCAGCACAAATGACCAAGGAGAGCAAAAT 2294
Qy |||||
Db 1987 CGCATCTACTCGGGGGATGGCGCTCATGGCGTCAGCACAAATGACCAAGGAGAGCAAAAT 2046
Qy |||||
Db 2295 TGCACAACCGCAACACACGCAATCAATAGTGGCGCCACCAATGGCGGCAACCACTGTCTC 2354
Qy |||||
Db 2047 TGCACAACCGCAACACACGCAATCAATAGTGGCGCCACCAATGGCGGCAACCACTGTCTC 2106
Qy |||||
Db 2355 TGGACACCAATCACAAGCTCGATCATCGCGACTAGGAAATTTGGGCTGGAGTGCAGGAGC 2414
Qy |||||
Db 2107 TGGACACCAATCACAAGCTCGATCATCGCGACTACGAAATTTGGGCTGGAGTGCAGGAGC 2166
Qy |||||
Db 2415 AAGCTGGCAAGATTAAACATCATGACAAATCTTTATCGAGCCCGTCCAGACACAAGCGG 2474
Qy |||||
Db 2167 AAGCTGGCAAGATTAAACATCATGACAAATCTTTATCGAGCCCGTCCAGACACAAGCGG 2226
Qy |||||
Db 2475 TGGTTGATATGAAAGATGTGATGGTCTCTGAATGACATCATCGAACAGGCGCTGTCTCGGC 2534
Qy |||||
Db 2227 TGGTTGATATGAAAGATGTGATGGTCTCTGAATGACATCATCGAACAGGCGCTGTCTCGGC 2286
Qy |||||
Db 2535 ACAGTCGGGCAAGGATCGCGGTGTCTCCGTTTACTATTTCCCAACAGAGACGATGAGC 2594
Qy |||||
Db 2287 ACAGTCGGGCAAGGATCGCGGTGTCTCCGTTTACTATTTCCCAACAGAGACGATGAGC 2346
Qy |||||
Db 2595 AGGATGGGCGCCAGCTTCAAGACAGGCACTCGAAGTGATCTCTCAAGGCAATCGATGTGT 2654
Qy |||||
Db 2347 AGGATGGGCGCCAGCTTCAAGACAGGCACTCGAAGTGATCTCTCAAGGCAATCGATGTGT 2406
Qy |||||
Db 2655 TTTGTGTGTGGGACTGTGCTGGGTTTGGTTGAAATTTCAAGAGTGGGTATCGCTCATCG 2714
Qy |||||
Db 2407 TTTGTGTGTGGGACTGTGCTGGGTTTGGTTGAAATTTCAAGAGTGGGTATCGCTCATCG 2466
Qy |||||
Db 2715 TCTTCGATCCCTTCGTGAGCTTTCATFACGCTGTGCAATTTGGTCAACAGATGTTTCA 2774
Qy |||||
Db 2467 TCTTCGATCCCTTCGTGAGCTTTCATFACGCTGTGCAATTTGGTCAACAGATGTTTCA 2526
Qy |||||
Db 2775 TGGCAATGGAATCACACGATATGACAGGAGATGGAAGCGGTCTCAAGAGTGGCAACT 2834
Qy |||||
Db 2527 TGGCAATGGAATCACACGATATGACAGGAGATGGAAGCGGTCTCAAGAGTGGCAACT 2586
Qy |||||
Db 2835 ATTTCTTCACCGCCACCTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGAGCCCCA 2894
Qy |||||
Db 2587 ATTTCTTCACCGCCACCTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGAGCCCCA 2646
Qy |||||
Db 2895 AGTACTATTTCCAGAGGGCTGGAAACATCTTCGACTTCATTTATCGTGGCCCTATCGCTAT 2954
Qy |||||
Db 2647 AGTACTATTTCCAGAGGGCTGGAAACATCTTCGACTTCATTTATCGTGGCCCTATCGCTAT 2706
Qy |||||
Db 2955 TGGAACTGGGACTCGAGGGTGTCCAGGGTCTGTCGGTATTCGGTTCCTTTTCGATTGCTGC 3014
Qy |||||
Db 2707 TGGAACTGGGACTCGAGGGTGTCCAGGGTCTGTCGGTATTCGGTTCCTTTTCGATTGCTGC 2766
Qy |||||
Db 3015 GTGTATTCAAACTGGCCAAAGTCTTGGCCACACTTAATTTACTCATTTTCGATTATGGGAC 3074
Qy |||||
Db 2767 GTGTATTCAAACTGGCCAAAGTCTTGGCCACACTTAATTTACTCATTTTCGATTATGGGAC 2826
Qy |||||
Db 3075 GCACCATGGGCGCTTTGGGTAATCTGACATTTGTACTTTGCAATTCATTCATCTTTTG 3134
Qy |||||
Db 2827 GCACCATGGGCGCTTTGGGTAATCTGACATTTGTACTTTGCAATTCATCTTCATCTTTG 2886
Qy |||||
Db 3135 CGGTGATGGGAATGCAACTGTTCCGAAAGAAATTAATCATGATCACAAGGACCGCTTTCGG 3194
Qy |||||
Db 2887 CGGTGATGGGAATGCAACTGTTCCGAAAGAAATTAATCATGATCACAAGGACCGCTTTCGG 2946
Qy |||||
Db 3195 ATGGGACCTCCCGGCTGGAACTTCACCGACTTTATCGACAGCTTCATGATCGTGTTC 3254
Qy |||||
Db 2947 ATGGGACCTCCCGGCTGGAACTTCACCGACTTTATCGACAGCTTCATGATCGTGTTC 3006
Qy |||||
Db 3255 GGGTGTCTGCGGAGAAATGAGTCCATGTGGGACTGATGTACGTGGCGGATGTCT 3314
Qy |||||

Db 5430 AAGTGGCCGTGCTTCCGACTGGTGAAGGAGCCAAAGGSCATTCGACACTGCTCTTCG 5489
|||||
QY 5227 AAGTGGCCGTGCTTCCGACTGGTGAAGGAGCCAAAGGSCATTCGACACTGCTCTTCG 5286
Db 5490 CGTTGGCCATGTGCTGCCGCCCTGTTCAACATCTCCCTGCTGCTGCTTCTGCTCATGT 5349
|||||
QY 5287 CGTTGGCCATGTGCTGCCGCCCTGTTCAACATCTCCCTGCTGCTGCTTCTGCTCATGT 5346
Db 5550 TCATCTTTGCCATTTTCGGCATGCTGCTTCTCATGACGTGAAGGAGAAAGAGCGGCATTA 5609
|||||
QY 5347 TCATCTTTGCCATTTTCGGCATGCTGCTTCTCATGACGTGAAGGAGAAAGAGCGGCATTA 5406
Db 5610 ACNACGTCTACAACCTTCAAGACCTTTGGCCAGAGCATGATCCTGCTCTTTCAGATGTCGA 5669
|||||
QY 5407 ACNACGTCTACAACCTTCAAGACCTTTGGCCAGAGCATGATCCTGCTCTTTCAGATGTCGA 5466
Db 5670 CGTCAGCGGTGGGATGGTGTACTGACGCCCATTAATCAATGAGGAAGCATGCGATCCAC 5729
|||||
QY 5467 CGTCAGCGGTGGGATGGTGTACTGACGCCCATTAATCAATGAGGAAGCATGCGATCCAC 5526
Db 5730 CCGAACACGACAAAGGCTATCCGGGCAATTGTGGTTCAGCGACCGTTTGAATAACGTTTC 5789
|||||
QY 5527 CCGAACACGACAAAGGCTATCCGGGCAATTGTGGTTCAGCGACCGTTTGAATAACGTTTC 5586
Db 5790 TCCTCTCATACCTAGTTTATAGCTTTTGTAGTATTATATATGATGCTGTCTATTC 5849
|||||
QY 5587 TCCTCTCATACCTAGTTTATAGCTTTTGTAGTATTATATATGATGCTGTCTATTC 5646
Db 5850 TCGAGAACTATAGTCAGGCCACCGAGCGTGCAGAGGCTTAACCGACGACGACTACG 5909
|||||
QY 5847 TCGAGAACTATAGTCAGGCCACCGAGCGTGCAGAGGCTTAACCGACGACGACTACG 5706
Db 5910 ACATGTACTATGATCTGCGACGAATTCGATCCGAGGCGACCCAGTACATACGCTATG 5969
|||||
QY 5707 ACATGTACTATGATCTGCGACGAATTCGATCCGAGGCGACCCAGTACATACGCTATG 5766
Db 5970 ATCAGCTGTCGGAATTCCTGACGCTACTGAGCCCCCGCTGCGATCCACAACCGGAACA 6029
|||||
QY 5767 ATCAGCTGTCGGAATTCCTGACGCTACTGAGCCCCCGCTGCGATCCACAACCGGAACA 5826
Db 6030 AGTACAAGATCATATCCATGACATACCATCTCTGCGGTGACCTATGCTACTGCGTCG 6089
|||||
QY 5827 AGTACAAGATCATATCCATGACATACCATCTCTGCGGTGACCTATGCTACTGCGTCG 5886
Db 6090 ACATCCTCGACGCCCTTACGAAAGACTTCTTTGCGCGGAAGGCAATCCGATAGAGAGA 6149
|||||
QY 5887 ACATCCTCGACGCCCTTACGAAAGACTTCTTTGCGCGGAAGGCAATCCGATAGAGAGA 5946
Db 6150 CGGTGATGATGGTGAGATACGCGCCCGCCCGGATACGAGGGCTACGAGCCCGCTCTCAT 6209
|||||
QY 5947 CGGTGATGATGGTGAGATACGCGCCCGCCCGGATACGAGGGCTACGAGCCCGCTCTCAT 6006
Db 6210 CAAGCGTGTGCGTACGCGTACGAGAGTACTGCGCCCGGCTAATCCACACGACGCTGGCGAA 6269
|||||
QY 6007 CAAGCGTGTGCGTACGCGTACGAGAGTACTGCGCCCGGCTAATCCACACGACGCTGGCGAA 6066
Db 6270 AGCAAAAGGCGCGCGAGGAGTGGTCTTTGAGCCGATACGATGATGCGCGATG 6329
|||||
QY 6067 AGCAAAAGGCGCGCGAGGAGTGGTCTTTGAGCCGATACGATGATGCGCGATG 6126
Db 6330 GCGGTGATCGGATGTCGCGGAGACCGCGGCCCGGATGAAGCAACGAGCGGCGATGCGCCCG 6389
|||||
QY 6127 GCGGTGATCGGATGTCGCGGAGACCGCGGCCCGGATGAAGCAACGAGCGGCGATGCGCCCG 6186
Db 6390 CTGCTGAGATGGTACTGTTAACGGTACTGACGAAGAGCTGCCGATGCCGATGAGAGTA 6449
|||||
QY 6187 CTGCTGAGATGGTACTGTTAACGGTACTGACGAAGAGCTGCCGATGCCGATGAGAGTA 6246
Db 6450 ATGTAATAAGTCCGGGTGAGGATCAGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAG 6509
|||||
QY 6247 ATGTAATAAGTCCGGGTGAGGATCAGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAG 6306

Db 6510 CGCGGGCAGCAGCAGCGGGGAAGTCCCGGACGGGTAGCGCCGCGGCGACACACCGCCG 6569
|||||
QY 6307 CGCGGGCAGCAGCAGCGGGGAAGTCCCGGACGGGTAGCGCCGCGGCGACACACCGCCG 6366
Db 6570 TTCTCTGTGAGACGACGCGGTTCGTGACGAAGAACGCCACAAGGTGGTCACTACCTCGC 6629
|||||
QY 6367 TTCTCTGTGAGACGACGCGGTTCGTGACGAAGAACGCCACAAGGTGGTCACTACCTCGC 6426
Db 6630 GATCGCGCAGCATCAGCTCGCGCACGCGGATGCTCTGAGCCAGGCTTCGCCGCCCTCC 6689
|||||
QY 6427 GATCGCGCAGCATCAGCTCGCGCACGCGGATGCTCTGAGCCAGGCTTCGCCGCCCTCC 6486
Db 6690 AAGATGACCGGAGTATTAGC 6710
|||||
QY 6487 AAGATGACCGGAGTATTAGC 6507

5
RESULT MDU38813 6318 bp mRNA INV 19-FEB-1997
LOCUS Musca domestica insecticide-susceptible strain voltage-sensitive
DEFINITION sodium channel mRNA, complete cds.
ACCESSION U38813
NID g1783372
KEYWORDS house fly.
SOURCE Musca domestica
ORGANISM
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Muscoidea; Muscidae; Musca.
REFERENCE 1 (bases 1 to 6318)
Knipple,D.C., Doyle,K.E., Marsella-Herrick,P.A. and Soderlund,D.M.
Tight genetic linkage between the kdr insecticide resistance trait
and a voltage-sensitive sodium channel gene in the house fly
Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2483-2487 (1994)
94195766
REFERENCE 2 (bases 1 to 6318)
Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.
Characterization of voltage-sensitive sodium channel gene coding
sequences from insecticide-susceptible and knockdown-resistant
house fly strains
Insect Biochem. Mol. Biol. 26 (4), 319-326 (1996)
96245434
REFERENCE 3 (bases 1 to 6318)
Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.
Direct Submission
Submitted (17-OCT-1995) Dave M. Soderlund, Entomology, New York
State Agricultural Experiment Station, Cornell University, Castle
Street, Geneva, NY 14456, USA
4 (bases 1 to 6318)
Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.
Direct Submission
Submitted (15-JAN-1997) Dave M. Soderlund, Entomology, New York
State Agricultural Experiment Station, Cornell University, Castle
Street, Geneva, NY 14456, USA
REMARK Nucleotide and protein update by submitter
FEATURES Location/Qualifiers
source
1. .6318
/organism="Musca domestica"
/strain="NAIDM"
/note="insecticide-susceptible reference strain"
/db_xref="taxon:7370"
/chromosome="3"
1. .6318
/codon_start=1
/product="voltage-sensitive sodium channel"
/db_xref="PID:g1783373"

1827 GATCCGAGAGCACTTGGCCCTATGCGCAGACATCGAATGCCCGTACCCCGATGTCGAA 1886
1828 GAGAAATGGTGCATATAGTACCAACCTACTATTGTAATTTAGTTCTAGACATTCCTCA 1887
1887 GAGAAATGGGCCATCATATGCGCGTGTACTATGGCAATCTAGGCTCCCGACATCATCG 1946
1888 TATACCTCGCATCAATCAAGAAATCTGTATACATCATCATGGTGTATTTATTTGGGTGGGATG 1947
1947 TATACCTCGCATAGTCCGCAATATCGTATATACCTCATCATGGCGATCTACTCGCGCGATG 2006
1948 GCGGCCATGGTGCACGACAAATCACCAGAGAGCAAAATGGCCAGTCCGCAACACACGC 2007
2007 GCGGTATGGCGGTACGACAAATGACCAGAGAGCAAAATGGCCAGCGCAACACACGC 2066
2008 AATCAATCAATTCGGTGTGCAACCAATGGTGGCAGTAGTAGCGGTGGTGGGTATATCCC 2067
2067 AATCAATCAGT-GG-GC-GCCACCAATGGCGCACCA---C-CTG-TC-TGGACA--CC 2114
2068 GATGCCAATACAAAGGAAGGATATGAATGGGTGAGGATATACAGACGAAGCT 2127
2115 AATCACAAGCTC---GATCATCGCGACTACGAAATTTGGCCTGGAGTGCACGGACGAAGCT 2171
2128 GGCAAAATAAACACCAGGACAATCCTTTTATCGAGCCCGTCCAACTCAACAGAGTGGTA 2187
2172 GGCAGGATTAACACATCATGACAATCCTTTTATCGAGCCCGTCCAGACACAAACGGTGGTT 2231
2188 GACATGAAGATGTATGGTCTTAAATGATATCATTTGAACAGCGCTGGTGGCGCATAGT 2247
2292 CGGGCAAGCGATCGCGGTGTCTCGTTTACTATTTCCCAACAGAGAGCATGACGAGGAT 2351
2284 GGTCCACATTAAGGACATCGCCCTCGAATACATCTCTAAAGGCATCGAATCTTTGT 2343
2352 GGGCGAGGTTCGAAGACAAGGCATCGAAGTGAATCTCTCAAGGCGATCGATGTTTGT 2411
2344 GTATGGGACTGTTGTGGGTGGTAAATTTAGGAATGGGTGTCCTTTATTGTGTTTC 2403
2412 GTGTGGGACTGTTGCTGGGTTGGTGAATTTGAGGATGGGTATCGCTCATGCTCTTC 2471
2404 GATCCATTCGTGGAGCTCTTCATACCTGTGTATTTGGTCAATACGATGTTTATGGCC 2463
2472 GATCCCTTCGTGAGCTCTTCATACGCTGTGCAATTTGGTCAACACGATGTTTCATGGCA 2531
2464 ATGGATCATCAGCATGAATCCGGAATTAGAAGAGTGTGAAAGTGGTAATTTTC 2523
2532 ATGGATCACACGATATGAACAAGGAGATGGAACGCGTGTCTCAAGAGTGGCAACTATTTTC 2591
2524 TTCAGGCGCACTTTTGCAATTTGAAGCAGCATGAACTGATGGCATGAGCCCGGAAGTAC 2583
2592 TTCACCGCCACTTTGGCATCGAGGCCACCATGAAGCTAATGGCCATGAGCCCAAGTAC 2651
2584 TACTTCCAGGAGGCTGGAACATTTTCGATTTTCATTTATTTGGCCTGTCCTCTGCTGAA 2643
2652 TATTTCCAGGAGGCTGGAACATCTTCGACTTCATTTATCGTGGCCCTATCGCTATTGGA 2711
2644 TTGGCCCTGGAGGTGTCCAGGCGCTGTGGGTGTTGAGAAGTTTTGGTTGCTTCGTTGTA 2703
2712 CTGGGACTCGAGGGGTGTCAGGGTGTGCGGTATTGCGTATTGCGTATTCGATTTGCTGCTGTA 2771
2704 TTCAATTTGGCAAAATCATGCCCCACACTCAATTTACTTCATTTGATTTATGGCGGACA 2763
2772 TTCAAACTGGCCAGCTGTGGCCCACTTAATTTACTTCATTTGATTTATGGGAGCCACC 2831
2764 ATGGGTGATTTGGTAACTCTGACATTTTACTTTGATTTATCATCTCTTCATCTTTGCGGTG 2823
2832 ATGGGCGCTTTGGGTAACTGACATTTTACTTTGCAATTTATCATCTCTTCATCTTTGCGGTG 2891
2824 ATGGGAATGCAACTTTTCGGAAAGAACTATATTTGACCACAGGATTCGCTTCAAGGACCAT 2883
1827 GATCCGAGAGCACTTGGCCCTATGCGCAGACATCGAATGCCCGTACCCCGATGTCGAA 1886
1828 GAGAAATGGTGCATATAGTACCAACCTACTATTGTAATTTAGTTCTAGACATTCCTCA 1887
1887 GAGAAATGGGCCATCATATGCGCGTGTACTATGGCAATCTAGGCTCCCGACATCATCG 1946
1888 TATACCTCGCATCAATCAAGAAATCTGTATACATCATCATGGTGTATTTATTTGGGTGGGATG 1947
1947 TATACCTCGCATAGTCCGCAATATCGTATATACCTCATCATGGCGATCTACTCGCGCGATG 2006
1948 GCGGCCATGGTGCACGACAAATCACCAGAGAGCAAAATGGCCAGTCCGCAACACACGC 2007
2007 GCGGTATGGCGGTACGACAAATGACCAGAGAGCAAAATGGCCAGCGCAACACACGC 2066
2008 AATCAATCAATTCGGTGTGCAACCAATGGTGGCAGTAGTAGCGGTGGTGGGTATATCCC 2067
2067 AATCAATCAGT-GG-GC-GCCACCAATGGCGCACCA---C-CTG-TC-TGGACA--CC 2114
2068 GATGCCAATACAAAGGAAGGATATGAATGGGTGAGGATATACAGACGAAGCT 2127
2115 AATCACAAGCTC---GATCATCGCGACTACGAAATTTGGCCTGGAGTGCACGGACGAAGCT 2171
2128 GGCAAAATAAACACCAGGACAATCCTTTTATCGAGCCCGTCCAACTCAACAGAGTGGTA 2187
2172 GGCAGGATTAACACATCATGACAATCCTTTTATCGAGCCCGTCCAGACACAAACGGTGGTT 2231
2188 GACATGAAGATGTATGGTCTTAAATGATATCATTTGAACAGCGCTGGTGGCGCATAGT 2247
2292 CGGGCAAGCGATCGCGGTGTCTCGTTTACTATTTCCCAACAGAGAGCATGACGAGGAT 2351
2284 GGTCCACATTAAGGACATCGCCCTCGAATACATCTCTAAAGGCATCGAATCTTTGT 2343
2352 GGGCGAGGTTCGAAGACAAGGCATCGAAGTGAATCTCTCAAGGCGATCGATGTTTGT 2411
2344 GTATGGGACTGTTGTGGGTGGTAAATTTAGGAATGGGTGTCCTTTATTGTGTTTC 2403
2412 GTGTGGGACTGTTGCTGGGTTGGTGAATTTGAGGATGGGTATCGCTCATGCTCTTC 2471
2404 GATCCATTCGTGGAGCTCTTCATACCTGTGTATTTGGTCAATACGATGTTTATGGCC 2463
2472 GATCCCTTCGTGAGCTCTTCATACGCTGTGCAATTTGGTCAACACGATGTTTCATGGCA 2531
2464 ATGGATCATCAGCATGAATCCGGAATTAGAAGAGTGTGAAAGTGGTAATTTTC 2523
2532 ATGGATCACACGATATGAACAAGGAGATGGAACGCGTGTCTCAAGAGTGGCAACTATTTTC 2591
2524 TTCAGGCGCACTTTTGCAATTTGAAGCAGCATGAACTGATGGCATGAGCCCGGAAGTAC 2583
2592 TTCACCGCCACTTTGGCATCGAGGCCACCATGAAGCTAATGGCCATGAGCCCAAGTAC 2651
2584 TACTTCCAGGAGGCTGGAACATTTTCGATTTTCATTTATTTGGCCTGTCCTCTGCTGAA 2643
2652 TATTTCCAGGAGGCTGGAACATCTTCGACTTCATTTATCGTGGCCCTATCGCTATTGGA 2711
2644 TTGGCCCTGGAGGTGTCCAGGCGCTGTGGGTGTTGAGAAGTTTTGGTTGCTTCGTTGTA 2703
2712 CTGGGACTCGAGGGGTGTCAGGGTGTGCGGTATTGCGTATTGCGTATTCGATTTGCTGCTGTA 2771
2704 TTCAATTTGGCAAAATCATGCCCCACACTCAATTTACTTCATTTGATTTATGGCGGACA 2763
2772 TTCAAACTGGCCAGCTGTGGCCCACTTAATTTACTTCATTTGATTTATGGGAGCCACC 2831
2764 ATGGGTGATTTGGTAACTCTGACATTTTACTTTGATTTATCATCTCTTCATCTTTGCGGTG 2823
2832 ATGGGCGCTTTGGGTAACTGACATTTTACTTTGCAATTTATCATCTCTTCATCTTTGCGGTG 2891
2824 ATGGGAATGCAACTTTTCGGAAAGAACTATATTTGACCACAGGATTCGCTTCAAGGACCAT 2883

2892 ATGGGAATGCAACTGTTTCGGAAAGAATTTATCATGATCACAAAGACCGCTTTCCGGATGCG 2951
2884 GAATTAACCGCGCTGGAACCTTCACCGACTTCATGCACAGCTTTCATGATTTGTTCGGAGTG 2943
2952 GACCTGCGCGCTGGAACCTTCACCGACTTTATGCACAGCTTTCATGATCGTGTTCGGGGTG 3011
2944 CTGTGGGAGAGTGGATCGAGTCCATGTGGGACTGATGTATGTGGCGGATGTCAAGTGT 3003
3012 CTGTGGGAGAATGGATCGAGTCCATGTGGGACTGATGTACGTGGGCGATGTCTCGTGC 3071
3004 ATACCTTCTTCTTGGCCACGGTCTGATAGCAATCTTGTGTCTTAACTTTCTTCTTA 3063
3072 ATTCCCTTCTTCTTGGCCACCGTGTGATCGGCAATCTTGTGTACTTAACCTTTCTTA 3131
3064 GCTTTGCTTTTTCACACTTCGTTTTCATCTAGTTTATATACGCCCGGACTGCGCAATGAT 3123
3132 GCCTTGTCTTTTTCCTAATTTTGTCTATCTAGCTTATATACGCCCGGACTGCGGATAACGAT 3191
3124 ACCAATAAATAGCAGAGGCTTCAATCTGATTGCTGCTTTTAAAGAACTGGGTGAACGCT 3183
3192 ACGAATAAATAGCAGGCGCTTCAATCTGAATTTGGCGGATTTAAAAGTTGGGTAAAGCT 3251
3184 AATATTCGCCGATTTTAAAGTTTAAATTCGAATAAATTTGACAAATCAATTAAGTGACAA 3243
3252 AATATTGCTGATTGTTTCAAGTTAATACGTAAACAAATGACAAATCAATTAAGTGATCAA 3311
3244 CCATCAG-----A-CA-----TGG--CGAT-A--ATG----- 3265
3312 CCATCAGGTGAGAGGACCAACAGATCAGTTGGATTGGAGCGAAGAGCATGTTGACAAAC 3371
3266 -AATCGAGTTGGTCTATGACGAATCATGGCGATGGCTTGTATCAAAAAGGTPATGAAG 3324
3372 GAATCGAGCTGGGCCACGACGAGATCCTCGCGACGCGCTCATCAAGAAGGGGATCAAG 3431
3325 GCGGAGACCCAGCTGGAGTGGCCATTTGGCGATGGCATGGATTCACGATACATGCGCAT 3384
3432 GAGCAGACGCACTGGAGGTGGCCATCGGGATCGGATGAATTCAGATACACGGCGAC 3491
3385 ATGAAAACCAACAGCGCGAAGAATCAAAATTCATGAACCAACACAGCATGATTGGAAC 3444
3492 ATGAAGAACAACAGCGCGAAGAATCCAAATATCTAAATAACGCAACGATGATTGGCAAC 3551
3445 TCAATAAACCAACAGCAATAGACTGGAACATAGAGCTAAACCATAGAGGTTTGTCCATA 3504
3552 TCATTAACCAACCAAGACAATAGACTGGAACAGAGCTAAACCATAGAGGTTTGTCCCTTA 3611
3505 CAGGACCATGACACTGCCAGCATTAATCTATGTTAGCCATAGAAATCGACCATTTCAAG 3564
3612 CAGGACGACGACACTGCCAGCATTAATCTATGTTAGCCATAGAAATCGACCATTTCAAG 3671
3565 GACGAGACCAACAGGCGCAGCGAGACCATCGAGGCGAGGAGAAACGCGAGCTCAGC 3624
3672 GACGAGACCAACAGGCGCAGCGCGAGACCATGAGGCGCGAGGAGAGCGCGAGCGCAGC 3731
3625 AAAGAGGACCTCGGCTCTGACGAGGAATGGAGGAGGCGCGGCGGCGATGAGGCGCAG 3684
3732 AAGGAGGATTTAGTCTCTGACGAGGAATCGACGAGGAGGCGGAATCGCAGGAGGCGCGC 3791
3685 CTGATGGTGACATTAATCATTCATCGCCAAACCGACGACGAGATAATCGACGACTATCCG 3744
3792 CTCACGCTGATATCATTTATTCATGACACA---CGACGAGGATATCTCATGAATATCCA 3848
3745 GCCGACTGTTTCCCGGACTCGTACTACAAGAAGTTTCCGATCTTGGCGGCGAGGAGAC 3804
3849 GCTGATTTGCTGCCCGGATTCGTACTATAGAAATTTCCGATCTTAGCGGTGACGATGAC 3908
3805 TCGCCGTTCTGGCAAGGATGGGCAATTTACGACTGAAAACCTTTTCAATTAATTAATTAAT 3864
3909 TCGCCGTTCTGGCAAGGATGGGCAATTTACGACTGAAAACCTTTTCAATTAATTAATTAAT 3968
3865 AAATATTTTGAAACCGGAGTTATCACTATGATTTTATGAGTAGCTTAGCTTTGGCCTTA 3924
3969 AAATATTTTGAAACAGCTGTTATCACTATGATTTTATGAGTAGCTTAGCTTTGGCATT 4028

Db	3925	GAAGATGTTCAATTTACCCGATGCACCTGTCATGCAGGATATACTGTACTACATGCACAGG	3984
Qy	4029	GAAGATGTACATCTGCCAAGAAGCCCATCTGCAGGATATTTTATATCTATATGCACAGA	4088
Db	3985	ATATTACCGTGATATCTTTTTGGAGATGTTGTATCAAAATGGTTGGCCCTGGGCTTTTAAG	4044
Qy	4089	ATATTACGGTTATATCTTCTGTGGAATGTTAATCAAGTGGTTGGCCTCGGCTTCAAA	4148
Db	4045	GTTTACTTCAACAATGCGTGGTGTGGCTGGAAATTCGTGATGTCAATGCTATCGCTTATA	4104
Qy	4149	GTGTACTTCAACAACGCGTGGTGTGGCTGCGATTTTCGTGATGTCATGGTATCGCTTATC	4208
Db	4105	AAATTGGTTCGCGTTTGGTCGGCCTTAAATGATATAGCCGTGTTTAGATCAATCGGCACA	4164
Qy	4209	AACCTCTGCTTCACTGTTGTGGAGCTGGTGATTTCAAGCCTTCAAGACTATGCGCAAGC	4268
Db	4165	CTGCGGCCCTTAAGGCCATTTGGCTGTCTCTAGATGGAGGGTATGAAGATTTGTCGTG	4224
Qy	4269	TTAAGAGCACTGAGACCACTAGCTGCCATGTCCCGTATGCAGGCGCATGGGTCGTGTT	4328
Db	4225	AATCGCTGTTTCAAGTATACGCTCCATCTTCAATGTGCTATTGGGTGFTGTGATATTT	4284
Qy	4329	AATCGCTGTGTACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTCTAAATATTT	4388
Db	4285	TGGCTATATTTTGCCTAATATGGGAGTACAGCTTTTGGCTGGAAATATTTTAAGTGTAAA	4344
Qy	4389	TGGCTAATTTTGCCTAATATGGGTGTACAGCTTTTGGCTGGAAATATTTTAAGTGGCAG	4448
Db	4345	GATGGTAATGACACTGTGCTGAGCCATGAATCATACCGAATCTGATGCTCGTCAAAAGT	4404
Qy	4449	GACATGAATGGCAGGAAGCTCAGCCACGAGATCATACCAATCGCATGCTCGGAGAGC	4508
Db	4405	GAAAACTACACTGGGAAAATTTGGCGAATGAACCTTCGATCATGTAGTGAATGCGTATCTC	4464
Qy	4509	GAGAACTACAGTGGGTGAATTCAGCAATGAATTTCCGATCATGTAGTGAACGGTATCTG	4568
Db	4465	TGCTATTTCAAGTGGCCACCTTTAAGCGCTGGATCCAGATATTAAGCATGCCATGTGAT	4524
Qy	4569	TGCGTTTTCAGTGGCCACCTTTCAAGCGCTGGATACAAATCATGAACGATGCTATCGAT	4628
Db	4525	TCACGAGAGTGGACAAGCAGCGCATCCGAGAAACCAATATCTACATGTATTTATATTTTC	4584
Qy	4629	TCACGAGAGTGGACAAGCAACCAATTCGTGAACGAACATCTACATGTATTTATTTTC	4688
Db	4585	GTATTTCTCATATATTTTGGATCATTTTTCACACTCAATCTGTTTCATTTGGTGTATCAT	4644
Qy	4689	GTATTTCTCATATATTTTGGATCCTTTTTCACACTCAATCTGTTTCATTTGGTGTATCAT	4748
Db	4645	GATAATTTTAAAGCAAAAGAAAGAGCTGGTGGATCATTTAGAAATGTTTCATGCACAGAA	4704
Qy	4749	GATAATTTTAAAGCAAAAGAAAGAAAGCGAGTGGATCATTTAGAAATGTTTCATGCACAGAA	4808
Db	4705	GATCAGAAAAGTACTATTAATGCTATGAAAAGATGGGCTCTAAAAACCATTTAAAGCC	4764
Qy	4809	GATCAGAAAAGTACTATTAATGCTATGAAAAGATGGGCTCTAAAAACCATTTAAAGCC	4868
Db	4765	ATTTCCAGACCGAGGTGGCGACCAACGAATAGTATTCGAAATAGTTCAGATATAAAAA	4824
Qy	4869	ATTTCCAGACCAAGGTGGCGACCAACGAATAGTCTTTGAAATAGTAAACCGATAGAAA	4928
Db	4825	TTCGATATATCATATATGTTGTTTCATGCTTTAAACATGTTTACCATGACCCCTGCATCG	4884
Qy	4929	TTCGATATATCATATATGTTTTCATTTGGTCTGAACATGTTTCACCATGACCCCTGCATCG	4988
Db	4885	TACGAGCCTTCGAGGCGTACAAACATGTCTCTCGACAACCTCAATGGGATATTTCGTAGTT	4944
Qy	4989	TAGCATCGCTGGACACGATTAACCGGCTCTAGACTATCTCAATGCGATATTTCGTAGTT	5048
Db	4945	ATTTTCAGTGGCGAATGTCTATAAATAATTTCCGTTTACGATATCACTATTTTCAAGAG	5004
Qy	5049	ATTTTCAGTGGCGAATGTCTATAAATAATTTCCGTTTACGATATCACTATTTTATGAG	5108

[illegible]

ORGANISM Musca domestica
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Muscoidea; Muscidae; Musca.
REFERENCE 1 (bases 1 to 6899)
AUTHORS Williamson, M.S., Martinez-Torres, D., Hick, C.A. and Devonshire, A.L.
TITLE Identification of mutations in the housefly para-type sodium channel gene associated with knockdown resistance (kdr) to pyrethroid insecticides
JOURNAL Mol. Gen. Genet. 252 (1-2), 51-60 (1996)
MEDLINE 96397509
2 (bases 1 to 6899)
AUTHORS Williamson, M.S.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-1996) M.S. Williamson, IACR-Rothamsted, Department of Biological & Ecological Chemistry, Harpenden, Hertfordshire, AL5 2JQ, UK
FEATURES
source Location/Qualifiers
1..6899 /organism="Musca domestica"
/strain="Cooper"
/db_xref="taxon:7370"
/chromosome="autosome III, short arm"
14..6340
/gene="para-like"
14..6340
/gene="para-like"
/note="alpha subunit"
/codon_start=1
/product="voltage-sensitive sodium channel"
/db_xref="pid:e229762"
/db_xref="pid:g1550781"
/translation="MTEDSDISEERSLFRPFTRESLQIETORIAEHEKOKELERK
AAEGFOIRVDEDEQGPDPPTLEQGVIPVRMOGSPPELASPLEDIDPEFNSVL
TFVWISKDQIPRESASAKAMLLDPENIRVAIVLHPLESLFIITLITNCLMI
MPTTVESTEVIPTITFESAVKAMGFLPCTTYLRDANWLDVFLVLAAYVAM
GIDGLNLAERFVRLKATVAIVPGLKTIIVGAVIESKLNRLDILITMFSLSVFL
MGLQYMGVLTQCKIKRPFDSGNLNDENFLHNSNSNMFTENDGESYPVQGNV
GAGCGGVYKQCGFGPNPDYTSFDSFGNWLAFRLMTQDFWEDILQHVLAAGP
WHMLFFIIFLGSFYLNLIIAIVMSYDELOKKAEEEAEEAIEAEAEAAAKA
AKLEERANVAQAQADAAALHPEMAKSPYSCISYSELYFVGGEGNDNNKKEM
SLRSEVESVSVLQRPAPATAPATKVRKVSPTSLSLPGSPNLRGSDNNKTYI
RNGRFRGSDRPLVLTQYDQAQLHPYADDSNAVTPMSSENGALIVPAYCNLG
SHRSYTSIQSRISYTHGDLGMAAGASTKRESKLRNTRNQSIGATNGGSS
TAGGYDPANKEORDYEMGODYDEAGKIRKHDNPFIEPVQTOFVDMKDVMLNDI
TEQAGRHSRASEGDEDDGPTFKDIALEYILKGIIEFCVDCWCWVLAFOEVSF
IVDFPVELFITLCIVVNTFMMDHDMNPELEKVLKSGNYEFTATFAIESAKLMA
MSPKYFOEGWNIFDIIVALSLELLEGVGLSVLSRFLRLRVFKLAKSWPTLNLIL
ISIMGRTGALGNLTVLCIIFIFAVGMQLFGKNYIDKDRFXDHELPRWNTDFM
HSFMTVFLCGEWSMDCMYGVGDSVCIFFFLATVYIGNLVNLFLALLSNFGS
SLSAPTADNOTNKIAEAFNRIAREKNVKRNADCFKLIRNKLNTQISDQPSSEHDN
EULEGHDEIMDGLIKGMGETOLEVALGDMEFTIHGDMKNKPKKSKFINNTMI
GNSINHQNRLEHNLHRLSLQDDDTASINSYSGSKNRPKDESHKGSATISGEK
RDVSKDELDEDEEAEGDQDGDIIHAQNDDELIDYPADCFPSYTKKFPPI
LADSDSPFQWGWGNRLTKQLIENKYFETAVITMILMSLALADELHLPDRPVQ
DLYTYMDRIFTYIFFLEMLIKWALFKRYFTNMCWLDVFVIMLSLNLVAVMSGLN
DIAVRSRNTRALRPLRAVSRWEGKVVNALVOAIPSNVLVLCILFLWILPIMG
VOLFAKGYCKCKDNDTVLSHEIIPNRNACKSENYSWNSAMNPDHVNALICLFOVA
TFKGIQIMNDIADSDREVDKQPIREINIIWYLYFVFFIIFGCSFFLNLFIQVIDNFN
EQKRAKGSLEMFMTEDQKYNAMKMSKRLKAIAPRPRWRPOAIVFIDYDKFD
IILMFLIGNMTDLRYDASEAYNNVLDLKFIVFISGECLLKIFALRYHFKY
PNWLPDVFVILSLGLVSLDIERFYSPITLLRVVRVARKVRLVRKLGARGITLL
PALMSLPALFNCLLLFLVMFIFAIFGMSFPMVKESGINAVYNFTFGOSMTLLF
OMSTVAGWDGLDAIINEEDCDPDNDKGYGNCGSATVGTIFLLSLVIFSLVINM
YIAVLENYQSATEDVQBLGTDDDIDMIEYIEWQDPEGTQYIRIDQISELDELPP
LQIHPKNYKIISMDMPICRDMYCVLDILDALTKDFARKGNPLEETGEIGETAARP
DTEGDPVSSITLWRQREYCAKLIQNAWRKYGNPPQEGDEGEAAGGEGGEG
GSGGGGGGGGSGATATAAAGATSPSDPDAGDASVGGPLSPGCVSGGSNGRQ
TAVLVESDGFVTKNGKVIHRSRPSISRTADV"
BASE COUNT 1965 a 1445 c 1660 g 1829 t
ORIGIN
Query Match 56.4%; Score 3676; DB 14; Length 6899;

Best Local Similarity 84.9%; Pred. No. 0.00e+00;
Matches 4986; Conservative 0; Mismatches 806; Indels 84; Gaps 22;
Db 164 ATACCATATGATGACGAGGACGAAGATCAAGTCCACAGCGGATCCACACTTCCAAACAG 223
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 207 ATCCGATATGATGACGAGGACGAAGTCCACAGCGGATCCACACTTCCAAACAG 266
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 224 GGTGTGCTATACCTGTTTCGAATGCAGGCGAGCTTCCCGCCGGAATGGCCTCCACTCCT 283
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 267 GGTGTGCCAATACCTGTTTCGATTCGAGGCGAGCTTCCCGCCGGAATGGCCTCCACTCCT 326
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 284 CTCGAGGATATCGATCCCTTCTACAGTAATGTACTGACATTTGTAGTAATAGTAAAGA 343
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 327 CTCGAGGATATCGATCCCTTCTACAGTAATGTACTGACATTTGTAGTAATAGTAAAGA 386
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 344 AAGGATATTTTCGTTTTCGCTCAAAAGCAATGTGGCTGCTCGATTCATTCATTCG 403
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 387 AAGATATATTTTCGTTTTCGCTCAAAAGCAATGTGGCTGCTCGATTCATTCATTCG 446
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 404 ATACCTGCTGAGCAATTTATTTTAGTGCATCCCTTGTTCGTTTATTCATTATCACC 463
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 447 ATACCTGCTGAGCAATTTATTTTAGTGCATCCCTTGTTCGTTTATTCATTATCACC 506
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 464 ACTATTTCTAATTAATTTTATTTATGATATGCGCAACAGCCACCGTGAATTCACA 523
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 507 ACAATTCCTGCAACTGATCCTGATGATAATGCCGACAACGCCACCGTTGAGTCCACT 566
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 524 GAGGTGATATTACACGGAATCTACACATTTGAATCAGCTGTTTAAAGTATGSCAGAGT 583
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 567 GAGGTGATATTACCGGAATCTACACATTTGAATCAGCTGTTTAAAGTATGSCAGAGT 626
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 584 TTCAATTTATGCGCTTACGTTTACGTTTATGATGATGCAATTTGGCTGACATTCCTAGTA 643
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 627 TTCAATTTATGCGCTTACGTTTATGATGATGCAATTTGGCTGACATTCCTAGTA 686
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 644 ATAGCTTTAGCTTATGTGACCATGCGCATAGATTAATGTAGTAATCTCGAGCTTTGAGA 703
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 687 ATAGCTTTAGCTTATGTGACCATGCGCATAGATTAATGTAGTAATCTCGAGCTTTGAGA 746
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 704 TTTAGGTACTGCGAGCTCTGAAAACCTGAGCAATGTCGCAAGTCTAAAACCACTTTC 763
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 747 TTTAGGTGCTCGAGCGCTTAAAACCTGAGCAATGTCGCAAGTCTAAAACCACTTTC 806
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 764 GGTGTGCTGATGAATCTGTAATAATCTACCGATGATGAATTTTGACAAATGTTTTC 823
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 807 GCGCGCTCATGATCGGTGAAGATCTGCGCATGATGATTAATCTGACCATGTTTCC 866
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 824 CTGTGCGTGTGCGCTGATGGGCTACAAATCTATATGGGTGTTCTAACACAAAGTGC 883
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 867 CTGTGCGTGTGCGCTGATGGGCTACAGATCTATATGGGCTGTCTACCCGAGAAGTGC 926
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 884 ATTAACGATTCCTCCCTCGAGCGAGTGGGCAATCTGACCGATGAAACCTGTTTCTA 943
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 927 ATCAAGAGTTCCTCCCTCGAGCGAGTGGGCAATCTGACCGAGAGAACTGGGACTAT 986
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 944 CACAATAGCAACAGTTCCAATTTGGTTTACGAGAGACGATGGCGAGTCAATATCCGGTGC 1003
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 987 CACAATAGCAATAGCTCCAATTTGGTATTCGAGAGAGAGGATCTCATTTCCGTTATGC 1046
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1004 GGAATATATCCGGTGGGAGCAATTCGCGCAAGATTAAGTCTGCTCGAGGGCTTCGCG 1063
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1047 GGAATATATCCGGTGGGAGCAATTCGCGCAAGATTAAGTCTGCTCGAGGGCTTCGCG 1106
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1064 CCAATCCCACTAGATTAACCACTTTCGATTCATTCGGTTGGGCTTTCCTGTCGGG 1123
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1107 CGGAATCGAATTAATGGCTACACAGCTTCGATTCGTTGGGATGGGCTTTCCTGTCGGC 1166
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1124 TTTCTGCTCATGACCAAGATTTCTGGGAGGATCTGTATCAGCAGCTGCTGCAAGCAGCT 1183
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1167 TTCGGCTGATGACACAGGACTTCTGGGAGGATCTGTATCAGCAGCTGCTGTCGGCCGCC 1226
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1184 GGACCTGSCACATGTTGTTCTTTTATAGTCAATCTTCTAGGTTCAATTCATCTTGTG 1243
Qy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 1227 GGACCATGGCACATCGTGTCTTTATAGTCATCATCTTCTCCTAGGTTCAATCTATCTTTGTG 1286
Db 1244 AATTGTATTTGGCCATTGTGGCATCTCTTATGACGAATTGCAAAAGAAAGCGCGAAGAA 1303
QY 1287 AATTGTATTTGGCCATTGTGGCATCTGCTATGACGAATTGCAAAAGAAAGCGCGAAGAA 1346
Db 1304 GAAGAGCGCTCGGAGGAGGAGCGGATACGAGAGAGCTGAAGAGGGGAGGAGCGCAAGGCG 1363
QY 1347 GAAGAGCGCTCGGAGGAGGAGGAGATACGTAAGCGGAAGAGTGCGCGCGCAAGCG 1406
Db 1364 GCCAAATCGAGAGCGGGCCAAATGTAGCAGCTCAAGCGCTCAGGATGCGAGCGATGCC 1423
QY 1407 GCCAAGCTGGAGAGCGGGCCAAATGCCAGGCTCAGGAGCGGATGCGGTGCGCGC 1466
Db 1424 GCTCGGCAGCTCTGCAATCCCGAGATGGCAAGAGTCCCAAGTCTCTTGCATTTAGCTAT 1483
QY 1467 GAAGAGCGCTGCATGCTCGGAATGCCAAGAGTCCGACGTATCTTGCATCAGCTAT 1526
Db 1484 GAATCTGTTTGTGGCGGAGAGGAGGCAAGATGACAAACAAGAGAGATGTCCATA 1543
QY 1527 GAGCTATTTGTGGCGGAGAGGAGGCAAGATGACAAACAAGAGAGATGTCCATT 1586
Db 1544 CGCAGCGTCGAAGTGAATCGGAGTCCGTGAGCGTTATACAAAGACACACGACCTACC 1603
QY 1587 CGGAGCGTCGAGGTGGAGTCGGAGTCGGTGAGCGTTATACAAAGACACACGACCTACC 1646
Db 1604 ACAGCAC--GCTACTAAAGTCCGTAAGTTAGCAGGACTCTCTTATCCTTACCTGGT 1660
QY 1647 ACAGCACCAAGCTACCAAGTTTCGTAAGTGAGCAGCAGACATCTTATCCTTACCTGGT 1706
Db 1661 TCACCATTTAACCTACCGCGGGGATCAGTAGTTTCACACAAGTACACAATACGAATGGG 1720
QY 1707 TCACCGTTTAAACATACGACGGGATCAGTAGTTCTCACAAGTACAGGATACGGAACGGA 1766
Db 1721 CGTGACGTTTGTGTATACAGGTAGCGATCGCAAGCCATTGGTACTGCAACATATCAG 1780
QY 1767 CGTGCGCGCTTGTGTATACCGGTAGCGATCGTAAGCCATTGGTATTGTCAACATATCAG 1826
Db 1781 GATCCCGCAGCAGCATTTGCCCTATGCCGATGACATCGAATGCCGTAAACACCAATGTCGGAA 1840
QY 1827 GATCCCGCAGCAGCATTTGCCCTATGCCGAGCTCGAATGCCGTACCCCGCATGTCCGAA 1886
Db 1841 GAGAAATGGTGCCATTATAGTACCAGCCTACTATTGTAAATTTAGTTCTAGACATTTTCA 1900
QY 1887 GAGAAATGGGCGCATATAGTGCCTGTACTATGGAATCTAGGCTCCCGACACATCATCG 1946
Db 1901 TATACCTCGCATCAATCAAGAATCTCGTATACATCAGATGGTGAATTTATGGGTGGCATG 1960
QY 1947 TATACCTCGCATCAGTCCCGAATATCGTATACCTCAGATGCCGATCTACTCGGCGGCGATG 2006
Db 1961 GCGGCCATGGTGCCAGCACAATGACCAAGAGAGCAAAATTTGCGCAGTCTGCAACACACGC 2020
QY 2007 GCGCTCATGGGCGTCAGCACAATGACCAAGAGAGCAAAATTTGCGCAACCGCAACACACGC 2066
Db 2021 AATCAATCAATCGGTGTGCAACCAATGGTGGCAGTAGTACGGCCGGTGGTGGCTATCCA 2080
QY 2067 AATCAATCAGT--GG--GCCACCAATGGGCGCACCA--CTGTC--TGGA--C--CCA 2115
Db 2081 GATCCCAATCAAGGAACAAAGGATTTGAAATGGTGAGGATTTACAGATGAGGCT 2140
QY 2116 -ATCACAGCTC---GATCATCGCATACGAAATTTGGCTGGAGTGCACGGAGGAGCT 2171
Db 2141 GGCAAAATAAACACCAACGACAATCCCTTTTATCGAGCCCGTCCAAACTCAACAGTGGTA 2200
QY 2172 GGCAAGATTAACATCATGACAATCCCTTTTATCGAGCCCGTCCAGACACAAACGGTGGTT 2231
Db 2201 GACATGAAGATGTTATGGCTTAAATGATATCATTTGAACAGCCCGTGGTGGCATAGT 2260
QY 2232 GATATGAAGATGTGATGGTCTGGAATGACATCATCGAAGAGGCGCGTGGTGGCACAGT 2291
Db 2261 CGTGCTATGTAAACAGGTG-----AGGACGATGAGGAAGAT 2296
QY 2292 CGGCAACCGATCGCGGTGTCTCGCTTACTATTTCACACAGAGGAGATGACGAGAT 2351

Db 2297 GGTCCACACATTCAGGACATCGCCCTCGAATATATCCTTAAAGGCATCGAAATCTTTGT 2356
QY 2352 GGGCCGACGTTCAAAGACAAAGCAGCTCGAAGTGATCCTCAAAGGCATCGATGTTTTGT 2411
Db 2357 GTATGGGACTGTGTGGGTGTGGTTGAAATTTTCAGGAATGGGTGCTCTCAATGTGTTTC 2416
QY 2412 GTGTGGGACTGTGTGGGTGTGGTTGAAATTTTCAGGAGTGGGTATCGCTCATCGTCTTC 2471
Db 2417 GATCCATTCGTGGAGCTCTTCATTTACCCCTGTGTTGCTGCTCAATACATGTTTCATGGCC 2476
QY 2472 GATCCCTTCGTGAGCTCTTCATCAGCTGTGCAITGTGTCAACACGATGTTTCATGGCA 2531
Db 2477 ATGGATCATCAGACATGAATCCGGAATTTGAGAGAGTGCTGAAAAGTGGTAACATATTTTC 2536
QY 2532 ATGGATCACCACGATATGAACAAGGAGATGGAAGCGTCTCAAGAGTGGCAACATATTTTC 2591
Db 2537 TTCACGGCCACATTTTGCATTTGAGGCCACATGAACACTGATGGCCATGAGCCGGAAGTAC 2596
QY 2592 TTACCGCCACCTTTTGCCATCGAGGCCACATGAAGCTAATGCCATGAGCCCAAGTAC 2651
Db 2597 TACTTCCAGAAAGGCTGGAACATTTTCGATTTTCATTTATTTGSCCTTGCTCTGCTGGAA 2656
QY 2652 TATTTCCAGAGAGGCTGGAACATCTTCGACTTCATTTATCGTGCCCTATCGCTATTTGGAA 2711
Db 2657 TTGGGCTCGAGGGTGTCCAGGGCTGTCCGGTGTGAGAAAGTTTTCGTTTGTCTCGTGA 2716
QY 2712 CTGGGACTCGAGGGTGTCCAGGGTGTCCGTTATTCGGTTCTCTTCGATTCGCGTGA 2771
Db 2717 TTCAAATTTGGCAAAATCATGGCCACACTGAATTTACTCATTTTCGATTTATGGCCGAGCA 2776
QY 2772 TTCAAATCGCCAAAGTCTTGGCCACACTTAATTTACTCATTTTCGATTTATGGGACACC 2831
Db 2777 ATGGGTGCAATGGGTAACTGCAATTTGACTTTTGCATTTATCATCTTCATCTTTGCGGTG 2836
QY 2832 ATGGGCGCTTTGGGTAACTGACATTTGACTTTGCTTTGCTTTGCTTTGCTTTGCGGTG 2891
Db 2837 ATGGGAATGCAACTTTTTCGGAAGAACTATATTGACCAAGGATCGCTTTCAGGACCAT 2896
QY 2892 ATGGGAATGCAACTGTTCGGAAGAAATTTATCATGATCACAAGGACCGCTTTCGGATGCG 2951
Db 2897 GAATTAACCGCGTGGAAATTTTACCAGCTTCATGACAGCTTCATGATTTGTGTTCCAGTG 2956
QY 2952 GACTCCCGCGTGGAACTTACCGACTTTATGACAGCTTCATGATCTGTTTCGCGGTG 3011
Db 2957 CTGTGGGAGAGTGGATCGAGTCCATGTGGGACTGATGTGTTGGGCGATGTGTCAGCTGT 3016
QY 3012 CTGTGGGAGATGGATCGAGTCCATGTGGGACTGCAATGTGAGTGGGCGATGTTCTCGTG 3071
Db 3017 ATACCCCTTCTTGTGCCACCGTGTGATCGGCAATCTTGTGTTCTTAACTTTTCTTA 3076
QY 3072 ATTCCCTTCTTGTGCCACCGTGTGATCGGCAATCTTGTGTAATTAACCTTTTCTTA 3131
Db 3077 GCTTTCGTTTTGTCCAACCTCGGTTTCATCTAGTTTATAGCCCCGACTGCCGACAAATGAT 3136
QY 3132 GCCTTCTTTTGTCCAATTTTGGCTCATCTAGCTTATCAGCGCGACTGCCGATTAACGAT 3191
Db 3137 ACCAATAAATAGCAGAGCGCTTCAATCTGATTTGCTGTTTAAAGAACTGGGTGAAACGT 3196
QY 3192 ACGAAATAAATAGCCGAGCGCTTCAATCGAATTTGGCCGATTTAAAGTTGGGTAAAGCGT 3251
Db 3197 AATATTGCCGATGTTTTAAGTTAATTTGAAATAAATTGACAAATCAATAAGTGCACCA 3256
QY 3252 AATATTGCTGATGTTTCAAGTTAATACGTAAACAAATGACAAATCAATAAGTGCACCA 3311
Db 3257 CATCAG-----A--CA-----TGG--CGAT--A--ATG----- 3278
QY 3312 CCATCAGGTGAGAGGACCAACCGCATCAGTTGGATTTGGAGCGAAGAGCATGGTGCACAC 3371
Db 3279 -AACTGGAGTTGGTTCATGACGAAATCATGGGCGATGGCTTGTATCAAAAGGATGTAAG 3337
QY 3372 GAACTGGAGCTGGGCCACGACGAGATCTCGCGGACGGCTCATCAAGAAAGGAGATCAAG 3431

Qy	5589	CTCTCATACCTAGTTATAAGCTTTTGGATAGTATTATTAATATGATACATTGCTGCTATCTC	5648
Db	5558	CAGAACTATACCCAGGCTACGAGGATGTCAGAGAGGCTCTACCGGACGAGGATACGAT	5617
Qy	5649	GAGAACTATAGTCAGGACCCAGGAGGCTGCAAGAGGCTCTAACCGGACGAGCTAGCAC	5708
Db	5618	ATGTACTACGAGATTGTGCAACAATTCGATCCGAGGAGCCACCCAGTACATACGATACGAC	5677
Qy	5709	ATGTACTATGAGTCTGCACACATTCGATCCGAGGAGCCACCCAGTACATACGCTATGAT	5768
Db	5678	CAGCTGTCGCGAGTTCTGGACGCTGCTGGAGCGCCGCTGACAGATCCACAGCCGAAACAAG	5737
Qy	5769	CAGCTGTCGCGAATTCCTGGACGCTACTGGAGCGCCGCTGACAGATCCACAAACCCGAAACAAG	5828
Db	5738	TACAAATCATATCGATCGACATCCGATATGTCGGGCGACATGATCTACTGCTGCTGAT	5797
Qy	5829	TACAAATCATATCGATCGACATCCCATCTGTCGGGTGACCTCATGCTACTGCTGCTGAC	5888
Db	5798	ATATTGGATGCGCTGACCAAGGACTTCTTTGCGGCGAAGGCTAATCCGATCGAGGAGACG	5857
Qy	5889	ATCCTCGAGCCCTTACGAAAGACTTCTTTGCGGCGAAGGCAATCCGATAGAGGAGACG	5948
Db	5858	GGTGAATTTGGTGAATTCGCGCGCGCGCGGACACCGAGGCGCTATGATCCCGTCTGCTCG	5917
Qy	5949	GGTGAATTTGGTGAATTCGCGCGCGCGCGGATACGAGGCGCTATGATCCCGTCTGCTCA	6008
Db	5918	ACACTGTGCGCGCCAGCGTGAGGAGTACTGCGCGAAGCTGATACAGAAATGCGTGGCG	5973
Qy	6009	ACCGTGTGCGGTCAGCGTGAGGAGTACTGCGCGCGGCTAATCCAGCAGCGCTGCGG	6064
RESULT	7		
LOCUS	MDU38814	6315 bp mRNA	INV 19-FEB-1997
DEFINITION	Musca domestica insecticide-resistant strain voltage-sensitive sodium channel mRNA, complete cds.		
ACCESSION	U38814		
NTD	g1842213		
KEYWORDS	house fly.		
SOURCE	Musca domestica		
ORGANISM	Eukaryotes; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Muscoidea; Muscidae; Musca.		
REFERENCE	1 (bases 1 to 6315)		
AUTHORS	Knipple,D.C., Doyle,K.E., Marsella-Herrick,P.A. and Soderlund,D.M.		
TITLE	Tight genetic linkage between the kdr insecticide resistance trait and a voltage-sensitive sodium channel gene in the house fly		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2483-2487 (1994)		
MEDLINE	94195766		
REFERENCE	2 (bases 1 to 6315)		
AUTHORS	Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.		
TITLE	Characterization of voltage-sensitive sodium channel gene coding sequences from insecticide-susceptible and knockdown-resistant house fly strains		
JOURNAL	Insect Biochem. Mol. Biol. 26 (4), 319-326 (1996)		
MEDLINE	96245434		
REFERENCE	3 (bases 1 to 6315)		
AUTHORS	Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-OCT-1995) Dave M. Soderlund, Entomology, New York State Agricultural Experiment Station, Cornell University, Castle Street, Geneva, NY 14456, USA		
REFERENCE	4 (bases 1 to 6315)		
AUTHORS	Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-JAN-1997) Dave M. Soderlund, Entomology, New York State Agricultural Experiment Station, Cornell University, Castle Street, Geneva, NY 14456, USA		
REMARK	Nucleotide and protein update by submitter		
FEATURES	Location/Qualifiers		
SOURCE	1. .6315 /organism="Musca domestica" /strain="kdr"		

/note="insecticide-resistant reference strain"	
/db_xref="taxon:7370"	
/chromosome="3"	
CDS	1. .6315
/codon_start=1	
/product="voltage-sensitive sodium channel"	
/db_xref="PID:g1842214"	
/translation="WTESDSISEERSLSRPFPTRESLLQIEQRIAEHEKELERKR	
AAEGEOIRYDDEDEGPDPPTLEQGVPIPRVMQGSFPPELSTPLEDIDPFFSNVL	
TAEVTSKGDIFRESASKMLLDPNPIRVAIVLVHPLSLFITTITLNCILMI	
MPTPTVESTVETIGIYTFESAVKVARGELICPFTYLRDANWLDVVLAYAVTM	
GIDGNLAALRTFVRLAKTVAIVPGTKTIVAGVIESVKNLRYIILTMESLSVFL	
MGLQIVGLVTKCKIKRPLDGSNGLDENFHLNSNSNMTENDGESYPVCGNVL	
CGAGGEDIVCLOGFGPNPDYTFSDFSWAFLSAFELMTQDFWEDIVQVLAQAG	
WHMLFFIIVIFLGSFYLVNLILAIVAMSYDELQKKAEEEAEEAIEAEEAATAA	
KLPERNAVAQAADAADAAAALHPKMAKSPYSCISYELFVGKGRGSDNNKEM	
STRSEVESVSVTORPATPATKRVKSTTSLPGSPENLRGSRSSHKYTI	
RNGRFGIPGSDRKLVIQYQDQQLHPYADDSNATVPMSENGAIIIVPAYCNG	
SHSYTSYSHQSIYTSYSHGDLGGAAGMAGSTMTKSLRSRNTNQSIGAATNGSS	
TAGGGYPDANHKERDYEMGDYTDGAKIKHNDNPFIEPVOTOTVDMKDMVLDNI	
TEQAAGRHSRASERGEDDEDPPTFKDALEYILKGIKIFCVWDCWVWLKQEWVS	
IVDPFVELFTICIVVNTMFMAMDHMDNPELEKVLKSGNYFTATFAISAKMLA	
MSPKYFQEGWNIIDFIIVALSLLLEGLGVQLSVLRSFRLRLRVKLRKLSWPTLNL	
IVSINGRTMGALNLTFLVLCILIFAYVMOLGCKNYIDKDRKDFHLPWNTDEM	
HSFMIVRVLCGEWIESWDCMVGDVSCIFPFLATVYVIGNFVNLALALLSNFGS	
SSLSATADNNTKIAEAFNRIAREKNWKNRIADCFKLIRKLNQISDQPSHGDN	
ELELGHDEIMGDLIKKMGKGTQLEVAIGDMETIHGDMKNKPKSKTINNTMI	
GNSINHQNRLPEHLNRLGSLQDDDTASINSYSHKRPKDESHKSAETIEGEEK	
RVDSKEDLDELDEEAGDEGDLGDIILHAQNDELIDDYPADCFDPSYKKFPI	
LAGDESPFWQWGNRLKTLQILNKYETAVITMLMSSIALALEVDHLPDRVMO	
DILYINDRIFTVIFLEMLIKWALGFKVYFTNACWLDVIVMLSLNLVAVHSGLN	
DIAYFRSMRTLRLALPLRAVSMWGVVVALVQAFISFNVLVLILFLWIFAIM	
VOLFAKYFKCKDNDVTLSHEIIPNRACKSENITWENSAMFEDHGNVLCFQVA	
TFKGTQIMDAIDREVDKQIRETNIYMYLVFVFFIFGSEFTLNFIVLIDNFN	
EOKKAGGSLEMETEDOKKYVNAKMGSKKPLKAIPRWRPOAIVFVITDKKFD	
IIMLPIGLMETWLDYDASEAVNNVLDKNGLVFVIFSGECLKIFALRYHYKE	
PWNLDVVVVVLSLGLVLSLIEKIFVSPILLRVVRVAKVGRVLRVLRKAGKIRLL	
FALMSLPALFNICILLFLMFIFAIGMSFFHVKESGINAVNFKTFGSGMILLF	
OMTSAGMDGVLDIAINEDCDPPDNGCGPGNCGSATVITFLSLVLSLVINM	
YIATILENSQATEDVEGLTDDDYMEIWOQDFPBTQYIRYDQSLSEFIDVLEPP	
LOIHPNKYKIIISMDPICRGDMYCDILDATKDFPAGNPTIEETGEIEAARP	
DTREGYDVPSTLWROEEYCAKIQNAWRKYKNGPOEGDEGAAGGDEGAGGGEG	
GSGGGDDGGSATAGATPTDPAAGEDAGSAGSGGGLSPGCVSGSGNSRQIATV	
VESDGFVTKHNRHVHSRSPITSTADY"	
BASE COUNT	1711 a 1344 c 1595 g 1665 t
ORIGIN	
Query Match	56.3%; Score 3664; DB 14; Length 6315;
Best Local Similarity	84.8%; Pred. No. 0.00e+00;
Matches	4980; Conservative 0; Mismatches 812; Indels 84; Gaps 21;
Db	151 ATACGATATGATGACGAGGACGAGATGAAGTCCACAGCGGATCCACACTTGAACAG 210
Qy	207 ATCCGATATGATGACGAGGACGAGGATGAAGTCCACACCGGATCTACACTTGAACAG 266
Db	211 GGTGTGCTTATACCTGTTTCGAAATGCGAGGCGAGCTTCCCGCGGAATGGCTCCACTCT 270
Qy	267 GGTGTGCCAATACCTGTTCCGATTCGAGGCGAGCTTCCCGCGGAATGGCTCCACTCT 326
Db	271 CTCGAGGATATCGATCCCTCTTACAGTAATGTACTGACATTTGTAGTAATAAGTAAAGGA 330
Qy	327 CTCGAGGATATCGATCCCTACTACAGCAATGTACTGACATTCGTAGTTGTAACCAAGGA 386
Db	331 AAGGATATTTTCGTTTTTTCGCTCAAAAGCAATGTGGTGTGATTCGATTCATTCACG 390
Qy	387 AAAGATATTTTCGTTTTTTCGCTCAAAAGCAATGTGGATGCTGATTCATTCATTCACG 446
Db	391 ATACGTCGTAGCCATTATATTTTACGTGCATCCCTTGTTCGTTTATTCATTATCACC 450
Qy	447 ATACGTCGTGTGCCATTATACATTTACTGTGCATTCATATTTTCCCTATTTCATCATCACC 506
Db	451 ACTATTCTAACTAATTTGATTTTAAATGATAATGCGCAACGCCCGGTCGATTCACCA 510

QY 507 ACAATTCTCGTCAACTGCATCCCTGATGATTAATGCCGACACGCCACGGTTGAGTCCACT 566
Db 511 GAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCAGGAGGT 570
QY 567 GAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCAGGAGGT 636
Db 571 TTCAATTTATGCCCGTTTAGTATCTTAGAGATGCATGGAATTGGCTGGACTTCGTAGTA 630
QY 627 TTCAATTTATGCCCGTTTAGTATCTTAGAGATGCATGGAATTGGCTGGACTTCGTAGTA 686
Db 631 ATAGCTTTAGCTTATGTGACCATGGGCATAGATTTAGTAAATCTCGCAGCTTTGAGAACA 690
QY 687 ATAGCTTTAGCTTATGTGACCATGGGTATAGATTTAGTAAATCTAGCAGCCCTGCGNACG 746
Db 691 TTTAGGTACTGCGAGCTCTGAACACCGTAGCCATTGTGCCAGGTCTAAACACCATTTGTC 750
QY 747 TTTAGGTGCTGCGAGCGCTTAAACACCGTAGCCATTGTGCCAGGTCTGAAGACCATCGTC 806
Db 751 GGTGCTGCTAATTAATCTGTAATAAATCTACGCGATGTGATAATTTTGACAATGTTTCC 810
QY 807 GCGCGCGTCAATCGAATCGGTGAAGATCTCGCGGATGTGAATTCCTGACCATGTTCTCC 866
Db 811 CTGTGCGTGTTCGCGTGTATGGGCTTACAAATCTATATGGGTGTCTTAACACAAAAGTGC 870
QY 867 CTGTGCGTGTTCGCGTGTATGGGCTTACAGATCTATATGGGCGTGTCTACCGAGAGTGC 926
Db 871 ATTAAGCATTTCCCGCTGGACGAGTTGGGCAATCTGACCGATGAATACTGTTTCTA 930
QY 927 ATCAAGAAGTTCCCGCTGGACGCTTCTCGGGCAATCTGACCGACGAGAACTGGGACTAT 986
Db 931 CACAATAGCAACAGTTCCCAATTTGGTTTACGAGAACAGATGGCGAGTCAATTCGGTGTGC 990
QY 987 CACAATGCGAATAGTCCCAATTTGGTATTTCCGAGGACGAGGCACTCATTTCCGTTATGC 1046
Db 991 GGAATGATATCCGCTGGGCGACAAATGGCGGAAGATACCTCTGCTGCGAGGCTTCGCG 1050
QY 1047 GGAATATATCCGCTGGGCGCAATGGCGAGCATTTACGTGTGCTGCGAGGGGTGTTG 1106
Db 1051 CCAATCCCAACTACGACTACACAGTTTCGAGCTCAATTCGTTGGGCTTTTCCTGTGGCG 1110
QY 1107 CCGAATCCGAATATGCTACACAGCTTCGATTCGATCGTTCCGATGGGCTTTCTCGGCC 1166
Db 1111 TTTGCTCTATGACCCCAAGATTTCTGGGAGGATCTGTATCAGCACGTCGTGCAAGCAGCT 1170
QY 1167 TTCGGCTGATGACAGAGGACTTCTGGGAGGATCTGTACCAGCTGGTGTGCGCGCGCC 1226
Db 1171 GGACCTGCGACATGTTGTTCTTTATAGTCATCATCTTCCTAGGTTCAATCTATCTTGTG 1230
QY 1227 GGACCATGGCACATGCTGTTCTTTATAGTCATCATCTTCCTAGGTTCAATCTATCTTGTG 1286
Db 1231 AATTGATTTTGGCCATGTTGGCATGCTTATGACCAATTCGAAAGAGAGGCGCGAAGAA 1290
QY 1287 AATTGATTTTGGCCATGTTGGCATGCTGATGACCAATTCGAAAGAGAGGCGCGAAGAA 1346
Db 1291 GAGAGGCTCGGAGGAGGAGGCGATCCGAGAGCTGAAGAGCGGCGAGCGCAAGCGC 1350
QY 1347 GAGAGGCTCGGAGGAGGAGGCGATACGTGAAGCGGAAGAGCTGCGCGCGCGCAAGCG 1406
Db 1351 GCCAAATCGGAGGAGGCGCGCAATGTAGCAGCTCAAGCGCTCAGGATGCGAGGATGCC 1410
QY 1407 GCCAAGCTGGAGGAGGCGCGCAATGCCAGGCTCAGCAGCAGCGGCTGCGGCTGCCGCC 1466
Db 1411 GCTCGCGCAGCTCTGCATCCGAGATGGCAAGAGTCCCGAGTCTCTGCTAGTAT 1470
QY 1467 GAAGAGCTGCATGCAATCCGGAATGGCCAAAGTCCGACGATTTCTGCATCAGCTAT 1526
Db 1471 GAATGTTTGTGGCGCGAGAGGCGAAGCATGACAAACAAAGAGAGAGATGTCGATA 1530
QY 1527 GAGCTATTTGTGGCGGAGAGGCGAAGCATGACAAACAAAGAGAGAGATGTCATT 1586
Db 1531 CGCAGCTCGAAGTGAATCGGAGTCGGTGAGCGTTTATACAAGACAAACGACACCTACC 1590
QY 1587 CGGAGCTCGAGGTGGAGTCGGAGTCGGTGAAGCGTTTATACAAGACAAACGACACCTACC 1646

Db 1591 ACAGCAC-CC--GCTACTAAAGTCCGTAAGTTAGCAGCACTTCCTTATCCTTACCTGGT 1647
QY 1647 ACAGCACACCAAGCTACCAAGTTCGTAAGTGCAGCAGACATCCTTATCCTTACCTGGT 1706
Db 1648 TCACCAATTTAACTAGCCGCGGATCAGCTAGTTTACACAAAGTACACAATACGAATGGG 1707
QY 1707 TCACCGTTTAAACATCGCAGGGGATCAGCTAGTTTCTCAAAAGTACAGTACGGAACGGA 1766
Db 1708 CGTGGACGTTTGGTATACAGGTAGCTAGCAGCCATTCGTAAGTTCGTAACATATCAG 1767
QY 1767 CGTGGCGCTTTGGTATACCCGGTACGATCTGAAGCCATTCGTAAGTTCGTAACATATCAG 1826
Db 1768 GATGCCACAGAGATTTGCCCTATGCCGATGACTCGAATTCGCGTAACACCAATGTCCGAA 1827
QY 1827 GATGCCACAGAGCACTTGCCCTATGCCGAGCTCGAATTCGCGTACCCTGATGCCGAA 1886
Db 1828 GAGAATGGTGCCATTAATAGTACAGCCTACTATTGTAATTTAGGTTCTAGACATTTCTCA 1887
QY 1887 GAGAATGGGGCCATCATAGTGGCCGTACTATGGCAATCTAGGCTCCGACACTCATCG 1946
Db 1888 TATACCTCGCATCAATCAAGAATCTCGTATACATACATGGTGTATTTATGGGTGGCATG 1947
QY 1947 TATACCTCGCATCAGTCCCGAATATCGTATACCTACATGGCGATCTACTCGCGGATG 2006
Db 1948 GCGGCGCTGGTGCCAGCAATGACCAAGAGAGCAAAATTCGCGAGTCCGCAACACACGC 2007
QY 2007 GCGGCTCATGGCGTCAAGCAATGACCAAGAGAGCAAAATTCGCGCAACGCAACACACGC 2066
Db 2008 AATCAATCAATCGGTGCTGCAACCAATGGTGGCAGTAGTACGCCCGGTGGTGTATCCC 2067
QY 2067 AATCAATCAAT--GG-GC-GCCACCAATGGCGCACAC--CTGTC--TGGA--C-A--CC 2114
Db 2068 GATGCAATCAACAAGCAAAAGGATTTGAATGSGTCAGGATTTATACAGACGAGCT 2127
QY 2115 AATCAACAGTCT---GATCATCGGACTACGAAATTTGGCTGGAGTGCAGGACGAGCT 2171
Db 2128 GGCATAATTAACACCAACCAATCCTTTATCGAGCCGCTCCAAACTCAAAACAGTGGTA 2187
QY 2172 GGCAGATTAACATCATGACATCCTTTATCGAGCCGCTCCAGACACAAACGGTGT 2231
Db 2188 GACATGAAGATGTTATGTTTAAATGATATCATTTGAACACCGCTGTGTCGGCATGT 2247
QY 2232 GATATGAAGATGTGATGTTCTGTAATGACATCATGCAACAGCCGCTGTGTCGGCAGT 2291
Db 2248 CGTCTAGTGAACGAGTG-----AGCAGCATGACGAGAT 2283
QY 2292 CGGCAAGCGATCGCGGTGTCCTCGTTTACTATTTCCCAACAGAGGACGATGACGAGAT 2351
Db 2284 GGTCCACATTAAGGACATCGCCCTCGAATATATCCTTAAAGGCGATCGAAATCTTTGT 2343
QY 2352 GGCAGCGTTCACACAGAGGCACTCGAAGTATCCTCAAGGCGATCGATGTTTGT 2411
Db 2344 GTATGGACTGTTTGGTGTGGTAAATTTTCAAGATGGGTCTCTCTTTATTTGTTTC 2403
QY 2412 GTTGGGACTGTTGCTGGGTTTGGTTGAAATTTTCAAGAGTGGGTATCGCTCATCGTTC 2471
Db 2404 GATCCATTCGTGGAGCTTTCATTCCTGCTGTTATGTTGTCATACATACAAATTTTCATGGCC 2463
QY 2472 GATCCCTTGTGCGAGTCTTCATCAGCTGTGCAATTTGTTGTCACACGATGTTTCATGGCA 2531
Db 2464 ATGGATCATCACACATGAATCCGGAATTTGGAGAAGTGTCTGAAAGTGTGTAATTTTC 2523
QY 2532 ATGGATCACCAACATATGAACAAGGAGTGAACGGTGTCTCAAGAGTGGCACTATTTTC 2591
Db 2524 TTCACGCCCACTTTTCAATTTAGGCCAGCATGAAGTGTATGGCCATGAGCCCGCAAGTAC 2583
QY 2592 TTCACGCCCACTTTGCCATCGAGGCCACCATGAAGCTAATGCCATGAGCCCGCAAGTAC 2651
Db 2584 TACTTCCAGAGGCTTGAACATTTTCGATTTTCATTTATTTGTCCTTGTCTCTGCTGGAA 2643
QY 2652 TATTTCCAGGAGGCTTGAACATCTTCTGACTTTCATTTATCTGTCGCCCTATCTGCTATTGGAA 2711

Db 2644 TTGGCCTGGAGGTGTCACAGGCGCTGTCGGTGTGTGAGAAAGTTTTCGTTTTCGTTTCGTTA 2703
QY 2712 CTGGACTCGAGGTGTCAGAGGTCTGTCGATTTGGTTTCCGTTTCGATTGCTGCGTTA 2771
Db 2704 TTCAAAATGGCAAAATCATGGCCACACTGAAATTTACTCATTTTCGATTATGGCCGGACA 2763
QY 2772 TTCAAACTGGCAAGTCTTGGCCACACTTAAATTTACTCATTTTCGATTATGGAGCCACC 2831
Db 2764 ATGGGTGCATTTGGTAACTTCGACATTTGTACTTTGGCAATATATCATCTTCATCTTTTGGCGTG 2823
QY 2832 ATGGGCGCTTTGGTAACTTCGACATTTGTACTTTGGCAATATATCATCTTCATCTTTTGGCGTG 2891
Db 2824 ATGGGAATGCAACTTTTCGGAAGAACTATATTGACCACAAAGGATCGCTTCAAGGACCAT 2883
QY 2892 ATGGGAATGCAACTTTCGGAAGAAATATCATGATCACAAAGGACCGCTTTCGGATGGC 2951
Db 2884 GAAATACCGGCTGGAATTTACCGACTTCATGCACAGCTTCATGATTTGTTCCGAGTG 2943
QY 2952 GACCTGCGCGCTGGAATTTACCGGACTTTATGCACAGCTTTCATGATCGTGTTCGCGGTG 3011
Db 2944 CTGTGCGGAGATGGATCGAGTCCATGTGGGACTGCATGTATGTGGCGGATGTCAGCTGT 3003
QY 3012 CTGTGCGGAGAAATGGATCGAGTCCATGTGGGACTGCATGTATGTGGCGGATGTCAGCTGT 3071
Db 3004 ATACCTTTCTTTTGGCCACGCTCGTGTATCGGCAATTTTGTGTTCTTAATCTTTCTTA 3063
QY 3072 ATTCCTTTCTTTTGGCCACCGCTTGTATCGGCAATCTTTGTGTACTTAACTTTCTTA 3131
Db 3064 GCTTTGCTTTTGTCCAACTTCGGTTCATCTAGTTATTCAGCCCGGACTGCGGCAATGAT 3123
QY 3132 GCTTTGCTTTTGTCCAAATTTTGGCTCATCTAGTTATTCAGCCCGGACTGCGGCAATGAT 3191
Db 3124 ACCAATAAAATAGCAGAGCGCTTCAATCGTATGCTGCTTTTAAAGAACTGGGTGAAACGT 3183
QY 3192 AGCAATAAAATAGCAGAGCGCTTCAATCGAATTTGSCCGAATTTAAAGTTGSGTTAAGCGT 3251
Db 3184 AATATTGCGGATTTGTTTAAAGTTAATTCGAAATAAATGACAAATCAAAATGATGACAA 3243
QY 3252 AATATTGCTGATTTGTTCAAGTTAATACGTAACAAATTTGACAAATCAAAATGATGACAA 3311
Db 3244 CCATCAG-----A-A-CA-----TGG--CGAT-A-ATG----- 3265
QY 3312 CCATCAGGTGAGAGCAACACAGATCAGTTGGATTGGCGGAGAGCATGTTGACAAAC 3371
Db 3266 -AAGTGGATTTGGTTCATGACGAAATCATGGCGGATGCTTGTATCAAAAGGATGATGAAG 3324
QY 3372 GAATGAGCTGGGCCACGACGAGATCTCGCCGACGCGCTCATCAAGAAGGGATCAAG 3431
Db 3325 GCGGAGACCGCTGGAGTGCCCATTTGGCGATGGCATGGAGTTACCATACATGGCGAT 3384
QY 3432 GAGCAGACGCAACTGGAGGTGCCATCGGGGATCGGGATGGAATTCACGATACAGGGCGAC 3491
Db 3385 ATGAAAAACAAGCCCAAGAAATCAAAATTCATAAACAACACAAACGATGATGGAAC 3444
QY 3492 ATGAAGAACACAAAGCCGAAGAAATCCAAATATCTAATAACGCAACGATGATGGCAAC 3551
Db 3445 TCAATTAACCAACCAAGACAAATAGACTGGAACATGAGCTAAACCATAGAGGTTTGTCCATA 3504
QY 3552 TCAATTAACCAACCAAGACAAATAGACTGGAACACGAGCTAAACCATAGAGGTTTGTCCATA 3611
Db 3505 CAGGAGCATGACACTGCCAGCATTAATCTATATGTTAGCCATAAGAAATCGACCATTAAG 3564
QY 3612 CAGGAGCAGGACACTGCCAGCATTAATCTATATGTTAGCCATAAGAAATCGACCATTAAG 3671
Db 3565 GAGCAGAGCCACAAGGCGAGCGCCGAGACCATCGAGGGCGAGGAAAGCGAGCTCAGC 3624
QY 3672 GAGCAGAGCCACAAGGCGAGCGCCGAGACCATCGAGGGCGAGGAAAGCGAGCGAGC 3731
Db 3625 AAAGAGGACCTCGGCTTCGACGAGGAACCTGGACGAGGAGGCGGAGGCGGATCAGGCGCAG 3684
QY 3732 AAGGAGGATTTAGTCTCGACAGGAACTGGACGAGGAGGCGGAAATGCGGAGGAGGCGCG 3791
Db 3685 CTGGATGGTGACATCATCTTCATGCCCAAAAGGACGAGGATATTCGACGACTATCCG 3744

QY 3792 CTCGACGCTGATATCATATTATTCATGCACA---CGACGAGGATATCTCGATGAATATCCA 3848
Db 3745 GCCGACTGTTCCCGGACTCGTACTACAAGAAAGTTTCGGATCTTTGGCCGGCAGCAGGAC 3804
QY 3849 GCTGATTCGCTCCCGGATTCGTAATAAGAAATTTCCGATCTTAGCCGGTGACGATGAC 3908
Db 3805 TCGCCGTTCTGCAAGGATGGGCAATTTACGACTGAAAACTTTTCAATTAATTAAGAAAT 3864
QY 3909 TCGCCGTTCTGCAAGGATGGGCAATTTACGACTGAAAACTTTTCAATTAATTAAGAAAT 3968
Db 3865 AATATTTTGAACCGCAGTTATACATATGATTTTAATGAGTAGCTTAGCTTGGCCCTTA 3924
QY 3969 AATATTTTGAACCGCAGTTATACATATGATTTTAATGAGTAGCTTAGCTTGGCAATTA 4028
Db 3925 GAAGATGTTTCATTTACCCGATCGACCTGTCATGCAGGATATATCTACTACATGACACAGG 3984
QY 4029 GAAGATGATACATCTGCCACAAGACCCATCTGCAGGATATTTATATCTATATGACAGA 4088
Db 3985 ATATTACGGTGATATCTTTTGGAGATGTTGATCAAAATGGTTGGCCCTGGGCTTTAAG 4044
QY 4089 ATATTACGGTTATATCTTTTGGAAATGTTAATCAAGTGGTTGGCGCTCGGCTTCAAA 4148
Db 4045 GTCTACTTCCACCAATGCCGTGGTGTGGCTGGATTTGCTGATTCGATGTCATCTCGCTTATA 4104
QY 4149 GTGTACTTCCACCAACGCGGTGGTGGCTCGATTTGCGTATGTTGATGTCATGATCGCTTATC 4208
Db 4105 AATTTGGTTGCCGTTTGGTGGGCTTAAATGATATAGACGCTGTTTATAGATCAATGCGCACA 4164
QY 4209 AACTTCGTTGCTTACTTGTGGAGCTGGTGTATTAAGCCCTTCAAGACTATGCGAAGC 4268
Db 4165 CTGCGGCGCTTAAGGCCATTTGGCTGCTCTAGATGGGAGGATGATGAAGTTTGTCTGTG 4224
QY 4269 TTAAGAGACTGAGACCACTACGTGCCATGTCCCGATGTCAGGCGATGAGGCTGCTCGTT 4328
Db 4225 AATGCGCTGGTTCAAGCTATACCGTCCATCTTCAATGTCTATTGGTGTGCTGATATTT 4284
QY 4329 AATGCGCTGGTACAGCTATACCGTCCATCTTCAATGTCTATTGGTGTGCTATATTT 4388
Db 4285 TGGCTTATTTTGGCCATTTAGGAGTACAGCTTTTGGTGGAAATATTTTAAAGTGTAAA 4344
QY 4389 TGGCTAATTTTGGCCATTAATGGGTGTACAGCTTTTGGTGGAAATATTTTAAAGTGGCAG 4448
Db 4345 GATGGTAAATGACACTGCTGCTGAGCCATGAATCATACCAATCGTAATGCCCTGCAAAAGT 4404
QY 4449 GACATGAATGGCGAAGAGCTCAGCCACGAGATCATACCAATCGCAATGCCCTGCGGAGC 4508
Db 4405 GAAAACTACACCTGGGAAAATTCGCAATGAACCTCGATCATCTAGTAAATGCGTATCTC 4464
QY 4509 GAGAACTACAGTGGGTGAATTCAGCAATGAATTCGATCATGTAGTAAACGGTATCTG 4568
Db 4465 TGTCTATTTCAAGTGGCCACCTTTAAGGCTGGATCCAGATTATGAACGATGCCATTGAT 4524
QY 4569 TGGCTTTTCCAAAGTGGCCACCTTTCAAAAGCTGGATCAAAATCATGAACGATGCTATCGAT 4628
Db 4525 TCAGGAGAGTGGACAGCAGCCGATCCGAGAAACCAATCTACATGTATTTATATATTTTC 4584
QY 4629 TCAGGAGAGTGGACAGCAGCCCAATCTGCGTGAACCAACATCTACATGTATTTATATTTTC 4688
Db 4585 GTATTTCTTCAATTAATTTGGATCATTTTTCACACTCAATCTGTTTGGTGGTGTATCATTT 4644
QY 4689 GTATTTCTTCAATTAATTTGGATCATTTTTCACACTCAATCTGTTTGGTGGTGTATCATTT 4748
Db 4645 GATTAATTTTGAACAAAAGAAAGAGGAGGATGATGATGATGATGATGATGATGATGATGAT 4704
QY 4749 GATAATTTTGAAGCAAAAGAAAGAGGAGGATGATGATGATGATGATGATGATGATGATGAT 4808
Db 4705 GATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCATTTAAAAAGCC 4764
QY 4809 GATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCATTTAAAAAGCC 4868
Db 4765 ATTCAGAGCCGAGGTGGCGACCAAGCAATAGTATTCGAAATAGTTTACAGATAAAAAA 4824

QY 4869 ATTCCAAGACCAAGGTGGGACCACCAAGCAATAGTCTTTTGAATAGTAAACCATTAAGAA 4928
Db 4825 TTCGATATAATCATTTAGTTGTTTCAATGTCCTTAAACATGTTTACCATGACCCCTCGATCGG 4884
QY 4929 TTCGATATAATCATTTAGTTTATTCATTTGGTCTGAACATGTTTACCATGACCCCTCGATCGT 4988
Db 4885 TAGCAGCGCTCGGAGCGGTACAAACATGTCCTCGACAACTCAATGGGATATTCGTAGTT 4944
QY 4989 TAGCATGGCTGGACACGATATACCGCGGTCTCTAGACTATCTCAATGGCATATTCGTAGTT 5048
Db 4945 ATTTTCAGTGGCAATGCTATTAAATAATATTCGGTTTACGATACTACATTTTCAAGAG 5004
QY 5049 ATTTTCAGTTCGGAATGCTATTAAATAATATTCGGTTTACGATACTACATTTTATTGAG 5108
Db 5005 CCATGGAATTTATTTGATAGTAGTGTGATTTATCCATCTTATAGGCTTGTATCTAGC 5064
QY 5109 CCATGGAATTTATTTGATAGTAGTGTGATTTATCCATCTTATAGGCTTGTATCTAGC 5168
Db 5065 GACATCATGTAGAAGTATTTGCTATCGCGGACACTGCTCCGTGGTGAGAGTGGCCAAA 5124
QY 5169 GATATTATCGAAGTACTTCTGTGCGCGACCTGCTCCGAGTGGTGGTGGCGAAA 5228
Db 5125 GTGGGTGCTGCTCCTCGGTTTACGAGGTGCAAGGATGATCCGACGTTGCTGTTCGCG 5184
QY 5229 GTGGCGGCTGCTTCGACTGTGAGGAGGCAAGGCAATTCGACACTGCTCTTCGCG 5288
Db 5185 TTAGCCATGCTGCTGCTGCTGCTTTTCAACATTTGCTGTGCTGCTTCTGCTGATGTC 5244
QY 5289 TTGGCCATGCTGCTGCTGCTGCTTTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCT 5348
Db 5245 ATCTTGTCTATCTTTGGCATGTCCTTCTTCATGTCATGTCATGCAAGAGCAAGAGCGGCAATAAT 5304
QY 5349 ATCTTGTGCAATTTTCGGCATGTCGTTCTTCATGTCAGTGAAGGAGCAAGCGGCATTAC 5408
Db 5305 GCTGTGTATAATTTTAAGACATTTGGCCAAAGTATGATATTCGTTTCAGATGTCCTACC 5364
QY 5409 GACGCTCAACATTTCAAGACCTTTGGCCAGACGATGATCCTGCTCTTCAGATGTCGAG 5468
Db 5365 TCAGCGGTTGGATGGTGTGTAGATGCCATTAATCAATGAGGAAGATTCGATCCACCC 5424
QY 5469 TCAGCGGTTGGATGGTGTACTGGACGCCATTAATCAATGAGGAAGATTCGATCCACCC 5528
Db 5425 GACACGCAAGGGCTATCCGGGCAATTTGTTGTTAGCGACTGTTGGAATACGTTTCTC 5484
QY 5529 GACACGCAAGGGCTATCCGGGCAATTTGTTGTTAGCGACCGTTTGGAAATACGTTTCTC 5588
Db 5485 CTTCATATCTAGTTATAGCTTTTGTAGTTATTAATATGATGCTGCTGCTATCTC 5544
QY 5589 CTTCATACCTAGTTATAGCTTTTGTAGTTATTAATATGATGCTGCTGCTATCTC 5648
Db 5545 GAGAACTATAGCCAGGCTACGAGGATGTACAGGAGGTTCTCACCGACGACGACTATGAT 5604
QY 5649 GAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGTTCTAACCGACGACGACTACGAC 5708
Db 5605 ATGTACTAGGATTTGGCAACAATTCGATCGGAGGTTACCGATACATAGATACGAC 5664
QY 5709 ATGTACTAGATCTGGCAGCAATTCGATCCGGAGGCGACCCAGTACATAGCCTATGAT 5768
Db 5665 CAGCTGTCGAGCTTCTGACGCTGTGGAGCGCGCTGACATCCAAAGCCGACAG 5724
QY 5769 CAGCTGTCGAAATCTCTGGACGCTGTGGAGCGCGCTGACATCCAAAGCCGACAG 5828
Db 5725 TACAAAATCATATCATGATGACATGCGGATATGTCGGGGGACATGATGCTGCTGATG 5784
QY 5829 TACAAGATCATATCATGATGACATACCCATCTCTCGCGGTGACCTATGCTGCTGCTGAC 5888
Db 5785 ATATTGGATGCTGACCAAGGACTTTCTTTCGCGCAAGGGTAATCCGATCAGGAGAGC 5844
QY 5889 ATCTCGACGCGCTTACGAAAGACTTCTTTGCGGGAAGGGCAATCCGATAGAGGAGC 5948
Db 5845 GGTGAAATGGTGAGATTCGCGCGGACCGGACACCGGAGGCTATGATCCGTTGCTGCG 5904
QY 5949 GGTGAGATTGGTGAGATAGCGCGCGCGCGGATACGGAGGGCTACGAGCCGCTCTCATCA 6008

Db 5905 ACATGTGTGCGCGCAGCGTAGGAGTACTGCGCCCAAGCTGATACAGATTCGCTGGCG 5960
QY 6009 ACGCTGTGCGCGTAGGAGTACTGCGCCCGGCTAATCCAGCAGCGCTGGCG 6064

RESULT 8

LOCUS BG073584 6096 bp mRNA INV 19-MAR-1997
DEFINITION Blattella germanica para sodium channel mRNA, complete cds.
ACCESSION U73584
NID g1657985

KEYWORDS German cockroach.
SOURCE

ORGANISM Blattella germanica

Eukaryotes; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Orthopteroidea; Blattaria;
Blattellidae; Blattellinae; Blattella.

REFERENCE 1 (bases 1 to 6096)

AUTHORS Dong, K.

TITLE A single amino acid change in the para sodium channel protein is associated with knockdown-resistance (kdr) to pyrethroid insecticides in German cockroach

JOURNAL Insect Biochem. Mol. Biol. 27 (2), 93-100 (1997)

MEDLINE 97218596

REFERENCE 2 (bases 1 to 6096)

AUTHORS Dong, K.

TITLE Direct Submission

JOURNAL Submitted (07-OCT-1996) Entomology, Michigan State University, East Lansing, MI 48824, USA

FEATURES

source

1..6096
/organism="Blattella germanica"
/strain="Ectiban-R"
/note="pyrethroid insecticide-resistant strain"
/db_xref="taxon:6973"
1..6096
/codon_start=1
/product="para sodium channel"
/db_xref="pid:g1657986"

CDS

/translation="MSDDSSISIEEBSLFRPFTRESLAATEARIAEYAKOKELEKK
RAGEVYRDEDEDEGPQDPALEQAGAPVRMQGLPPPLASLPLEDPIDPFYHQT
FVYVSKGDIERSATDAMWLDLPFNIRRVAILVLPFLSFLLITLITNCIFMIM
PTPTIESTIEVIFTGTYFSAVKVMARGFILQFTYLRDANWLDVFWLALAVTMG
IDGNLAALTRFVRLAKTVAIVPGKTIIVGAVESVKNRLVDIITMSLSVFLAM
GLQYMGVLTKQCKINPINGSWELNDENHAFCSNNTNWPPEGAPEVPLCGNSSG
AGCTPDYTCLOGFENPNYGYTSDFTGHAFLSAFLMTQDYENLYQLVRSAGPW
HMLFFVIIIFLGFIYLVNLIIAIVAMSYDELOKAAEEDAEAEAREAEALAKRA
KKURQADKLAQELAAQELAGANLAKSPSSSSRSYELFINQKGNHNNKRENSIR
SEGDSISEHKVRVGANGTAIRKVSAAASLPGSPFNHRRGSGQSHHFTIRNGRNV
GPPGDRKPLVLTSLDAQEHLPYADDSNATPMSENGAIVVPPVYASLSRHSYV
SHASRIYTSHGDLGAGNKSOTKINOLRARSVRNPNPSONPSPYMNASADSDGAV
KAKHTDNPFIEQMOTIIVDMNDVWVNLIIEQAGQOQSRASEHGVSIYFPTDEDE
GPVYKVKLAICMRGIDIFCVCDCWLAQFQETVALLVDFPFVELEITLCIVVNTLF
MALDHDHMDKMDKALKSGNYFTATFAIEATLKIAMSPPYFQEGWNTFDFTIAL
SLELGLGVQGLSVLRFLRLKAKSWPTLNLLISIMGRVGLAGNLTVYLCII
IFIFAVGMQLFGKNYVDNRPDGMWRNFTDFMHSFIVRVLCGWEIEMWDC
MLVGDWSCIPEFLATVYIGNVNLFLALLISNFGSSNLSAPTADNKNIAFAER
MRFENWIKBSALNVAKMLAKLTNLSIDTTPDAHERDITDLTASILDADGIYVRK
KSPKQQLVAVAGDMEFTIHGDKNKLKDKLNMSTKIVIGNSLHKNRRIESDY
LHNKQEDITLSTGYSKSNRPYKDDSHKSAETMDGEKKDASKEDFDQGEDEEG
EGGPLEEDVLDAGTVMWSEYPADCCPDHCYKRFPLAGDEDSFQWQGNLRK
ITQILNKYFETAVITMILLSLALALEVHLPHRPILODILYMDRIFTVFIEML
IKWLKFKFYTNACWLDIIVMSLINFVASLVGAGGIAQFAPKWTIRLARLPLRA
MSRQGMRVVNALVQAIPISENVLLVCLIFLFIAMVQLFAGYHKCVDSNSTIL
KHEIIPRNRACIAENFTWENSPNDFHVKAYLCIFQVATFKGWIQIMDAIDREHJ
SQPIIRNTIYMLIYFVFFIIFGFTLNLFIIGVITIDNFQKKKAGSLEMFMTEDQ
KYNNMKMGSKPKLAIIPRKWRQIAVFEICTDKKDFIMLFIIGNMLTMTLDHY
QSKQFSDVLDYLNMFIVIFSSECLMIFALRYHFKFEPNLFDFVVTLSILGLVL
SDITEKYFVSTPLLVRVAVKGRVLRVKGAGIRTLLEFALMSLPALNICILFL
VMTFALFGSFFSHVVDKGLDDVYNFKTFQGSMLLFQMSAGHDGVLGDIMNEE
DCKNPNSEIGTGGCGATGATLSTLVISFLVINMYIAVILENYSATGDEVQEG
TLDVDDYIYIWOQFDPDGTQYIRYDLSDFLDVLEPPLQIHKPNKYKVSMDIPTC
KGLDMFCVIDLALTDKDFARKGNPIEESAELEGVQGRPDEVGYEPVSSTLWRREE

YCARLIQNAWRKHQKQROGAPGEDSDEAGDDPELQDRHQTAFLVSDGFVTKNGHRVV

IHSRSPSVTSRSTVD*

BASE COUNT 1615 a 1376 c 1531 g 1574 t

ORIGIN

Query Match 29.4%; Score 1912; DB 14; Length 6096;

Best Local Similarity 71.2%; Pred. No. 0.00e+00;

Matches 4180; Conservative 0; Mismatches 1578; Indels 115; Gaps 74;

Db	151	CGGTGCGATGACGAGACCAAGATGAAGCCCTCAGCGGATGCGACTCTGAGCAAGG	210
Qy	210	CGATATGATGACGAGACGAGGATGAAGTCCACAAACCGGATCCTACATTGAACAGG	269
Db	211	GCSCCATCCCTGCGAATGAAGCCCTTCCCTCCGAGCTGCCCTCTACCCCGCTC	270
Qy	270	GTGCCAATACCTGTTCCGATGAGGCGAGCTCCCGCGGAATGGCCCTCCACTCCTC	329
Db	271	GAGGACATGACCCCTCTACCAACACAGAGACATTTGGTGGTGAGCAAGGAAG	330
Qy	330	GAGGATATCGATCCCTACTACAGCAATGTACTGCAATTCGTAGTTGTAAGCAAGGA	389
Db	331	GATATTTCCGGTTCAGTGGCAGAGTGCATGTGATTTGGACCCATTCAACCGGAT	390
Qy	390	GATATTTTCGCTTTCGATCAAGCAATGTGATGCTCGATCCATCAATCCGATA	449
Db	391	CGACGGGTGCCATCTACATTTGGTTCACCCCTGTCTCTACTCTTCATCATATACC	450
Qy	450	CGTGTGTGCCATTTACATTTAGTGCATCCATTTATTTCCCTATTCATCATCACA	509
Db	451	ATTTAACCAACTGCATCTTCATGATCAGCTTACACCCCAACATAGATCCACTGA	510
Qy	510	ATTCTGCTCAACTGCTCTGTATGTAATGCCGACCAACGCCACGGTTGAGTCCACT	569
Db	511	GTAATTTTACTGCACTACACATTTGAATCGCGCTTAAGGTGATGCGAGAGGTTTC	570
Qy	570	GTGATTTACCGGAATCTACATTTGAATCAGCTTTAAAGTGATGCGACGAGTTTC	629
Db	571	ATACTTCAGCCATACAGTACCTTAGAGATGCATGGAATGGCTGGACTTCGTAGTA	630
Qy	630	ATTTTATGCCGTTTACGTATCTTAGAGATGCATGGAATTTGGCTGGACTTCGTAG	689
Db	631	GCITTAGCTTACGTACTATGGGATAGATCTAGGAACCTGCCGCTTGCGAAGCTTC	690
Qy	690	GCITTAGCTTATGGACATGGGTATAGATTTAGTAAATCTAGACCCCTCGGACGTT	749
Db	691	AGGTGCTCGGAGCTTGAAGACTGTCGCTATTGTTCCAGGTTTGAAGACCATTTTGC	750
Qy	750	AGGTGCTCGGAGGCTTAAACCGTAGCCATTTGCGCAGGCTTGAAGACCATCGTCG	809
Db	751	GCTGTGATTAATCTGTAAGAACCTCGCGGATGTGATATCTCACCATTGTTCTGCTC	810
Qy	810	GCCGTATCGAATCGGTGAAGAAATCTCGCGATGTGATTTATCTGACCATGTTCTCC	869
Db	811	TCGCTGTTTGGCTTAATGGGCTCCAGATTTACATGGGTGTCTCAGCGAAGTGCATC	870
Qy	870	TCGCTGTTTGGCTTATGGGCTACAGATCTATATGGGCGTGTCTCACCAGAGTGCAT	929
Db	871	AAAACTTCCCATTAATGTTTATGGGGGAATTTGAATGATGAGAACTGGCATGCA	930
Qy	930	AAGAATTTCCGCTGGAGGTTCTCGGGCAATCTGACCGACGAGAACTGGGACTATCA	989
Db	931	TGCAGTAAACACAGAACTGGTACTTTCCGGAAGTGCACCAGAACTCCACTGTGGG	990
Qy	990	AATCGCAATAGCTCCAATTTGATTTCCGAGACGAGGGCATCTCATTTCCGTTATGGG	1049
Db	991	AATCATCAGGAGCTGGTACATCTCCACCTGATTACACATGTCTCCAGGGCTTGGAGA	1050
Qy	1050	ATATATCCGGTGGGGCAATGCGACGACGATACGTTGCTGTCGACGAGGTTTGGTCC	1109
Db	1051	AATCCCACTATGTTACACAGTTTGCATACGTTTGGTGGGCAATTCCTCTCGCCCTTC	1110
Qy	1110	AATCCGAATTTATGCTACACAGCTTCGATTCGTTCCGATGGGCTTTCTCTCGCCCTTC	1169

Db	1111	AGACTGATGACCAGGATTTATGGGAGAACCTTTATCAGCTGGTTTTGAGATCTGCTGG	1170
Qy	1170	CGGCTGATGACACAGGACTTCTGGGAGATCTGTACCAGCTGGTTGGCGCGCGCGGA	1229
Db	1171	CCCTGGCATATGCTGTTCTTCATTGTGTCATCATCTCTTAGGCTCAATCTATCTGTGA	1230
Qy	1230	CCATGGCAGATGCTGTTCTTTATAGTCATCATCTCTTAGGTCATCTATCTGTGAAT	1289
Db	1231	TTGATTTTGGCCATTTGCGCATGTCCTACGATGAGTTGCAGAAAGCTGAGGAGAA	1290
Qy	1290	TTGATTTTGGCCATTTGCGCATGTCGATGACGAATTCGAAAGGAGGCGGAAGAA	1349
Db	1291	GAACACGCGAAGAAAGCGTTGAGGGAAGCGGAAGACAGCTCTTGCAGAAAGGCG	1350
Qy	1350	GAGCTGCCGAAGAGGCGGATACGTGAAGCGGAAGAGTCCCGCGCAAGCGGCC	1409
Db	1351	AAAAATTAAGACAAGCGGATAAACTGCG--AG--CACAAGAATTAGCAGCAGCACAGA	1407
Qy	1410	AAGCTGGAGGCGGGCAATGCCAGGCTCAGGCACGCGGATCGGCTGCCCGGAA	1469
Db	1408	CTAGCTGGCGCAATCTAGCAAAATCTCCCTCGG--GAAGT--TCGCTCTCGT--AGT	1464
Qy	1470	GAGCTGCACTGCATCCGGAATGGCCAAGAGTCCGACGATTTCTTGATCATCAGCTAG	1529
Db	1465	TTGTTTATAATCAAAAGGCGCAACAATCACAACAAAGGGAAGACATGAGCATCCG	1524
Qy	1530	CTATTTTGGCGGAGAGGGCAAGATGACAAACAAGAGAAGATGTCCATTCGG	1589
Db	1525	AGCGA--AGGCGG---GGACTCGATAAGCGA--ACACAAAGG--AAG--AGTGGGTG	1575
Qy	1590	AGCGTCGAGTTGGAGTCGGAGTCGGTATACAAAGACAACCGACCTACCACA	1649
Db	1576	GGT--ACG--GGGATCA--G---G--AAGGTGAGCGCGGAAGTTTGAAGTCTACG	1626
Qy	1650	GCACACCAAGCTACCAAGTTTCGTAAGTGAAGACGACATCTTATCTTACCTGGTTC	1709
Db	1627	CCTTTCAACCATCCCGAGTTCCTCAAGGTAGTCATCATTACAATTAGAAACGAGCT	1686
Qy	1710	CGTTTAAACATACGCGGGGATCAGTAGTTCTCAGAATGACAGTACGGAACGAGCT	1769
Db	1687	GGAAGTTTCGTGGGCGCCACCTGGTGGTATCGAAACCCCTAGTACTTCTACGTACCT	1746
Qy	1770	GSCCGCTT--TGGTAT--ACCGGTAGCGATCGTAAGCCATTGGTATTGTCAACATAC	1826
Db	1747	GATGCAAGAACAATCTTCTTATGTCAGATCAGTCAAGTCAAGTAACACCTATGTCAG	1806
Qy	1827	GATGCCAGACGACTTGCCTTATGCCGACGACTCGAATGCGCTACCCCGCATGTCCGA	1886
Db	1807	GAGAATGGAGCAATAGTTGTACCAAGTTTATACGCCAGCTCGGTTCCAGGCACTCAT	1866
Qy	1887	GAGAATGGGCGCATAGTGCCCGTGTACTATGCAATCTAGGCTCCCGACACTATCG	1946
Db	1867	TATACATCAGCGCATCCAGGATATCTACAGTCTCATGGGACCTCTCTGGGTG--CA--	1924
Qy	1947	TATACATCGCATCTCCGGAATATCGTATACCTCAGTGGCGATCTACTCGCGGCGAT	2006
Db	1925	GCAA--CAAA--C--TCAGACCA--GATCAATCA--A--C---TSCGAGCTCTGAGTGC	1974
Qy	2007	GCGCTAGTGGGCGTCAGCAATGACCAAGAGAGCAAAATTCGCAACCGCAACACAGC	2066
Db	1975	AA--CAACCTT-----CAC--A--GGTG--C--CTAA--T--TCT--ACACCATACATGA	2018
Qy	2067	ATCAATCAGTGGGCGCCCAATGCGCGCACCTCTCTGGACACCAATCACAAGCTC	2126
Db	2019	G--TCAGCA--GAC--A--GTGAT--GA--TGGAG-----CGGT--GAAA---GCAA--	2059
Qy	2127	GATCATCGGCACTAGCAAAATGGCCCTGGAGTGCAGGAGAGCTGGCAAGATTAACAT	2186
Db	2060	C--TGCAATCCATTCATGAACAAATGCAAGAACTACAATTTGTTGATATGAATCATGT	2118
Qy	2187	CATGACATCTCTTTATCGAGCCCTCCAGACACAAAGGTTGGTGTGATATGAAGATGTG	2246
Db	2119	ATGGTCTGAATGACATTTATAGAACAAGCTGCTGGACAGCAGAGTAGAGCCAGTGAAC	2178

D	b	4304	CTTTGAGCCACGAAATCAATCTCTGACAGAAATGCTTTGCAATTGCTGAAAACTACACATGGG	4363
Q	y	4465	AGCTCAGCCACGAGATCATACCAAAATCGCAATGCGCTGGGAGGAGAGAACTACACGTGGG	4524
D	b	4364	AGAACTGCCAAATGAATTTTGATCAGCTCGGCAGAAAGCTTATCTCTGCTCTTCCAAATGG	4423
Q	y	4525	TGAATTCAGCAATGAATTTGATCAATGATAGTAAAGCGGTATCTGTGCTTTTCCAATGG	4584
D	b	4424	CCACCTTCAAAGGATGGATTCAGATCATGAATGAGCGCTATAGACTCTAGAGAGCTCCATA	4483
Q	y	4585	CCACCTTCAAGGCTGGATACAATCATGAACGATGCTATCGATTACGAGAGGTGGACA	4644
D	b	4484	AGCAGCAATTCAGGAAACGAACATCTACATGTACCTCTACTTTGTGTGTTTATCATCT	4543
Q	y	4645	AGCAACCAATTCGTGAAGACGAACATCTACATGTATTTATTTTGTATTTCTTCATCAT	4704
D	b	4544	TTGCTCATTTTTTCACTCTCAACCTATTCAATTGGTGTGATCATCGACAACTTTTAATGAGC	4603
Q	y	4705	TTGATCTTTTTTCACTCAATCTGTTCAATTTGGTGTATCATTTGATTAATTTTAATGAGC	4764
D	b	4604	AAAAAGAAAGGAGGAGGGTCTCTAGACATGTTTCATGACTGAAGATCAGAGAAATTAAT	4663
Q	y	4765	AAAAAGAAAGCAGGTGGATCATTAAGAAATGTTTCATGACAGAGATCAGAAAAAGTACT	4824
D	b	4664	ACAAATGCTATGAAGAAATGGGTTGCAAAAAACCGTTAAAAGCCATCCCCAGGCGCAAGT	4723
Q	y	4825	ATAATGCTATGAAGAAAGATGGGCTCTFAAAAACCAATTAAGGCCATTCACAGACCAAGT	4884
D	b	4724	GGAGACCGCAGGCCATGTGTTTGAATCTGCACAGACAGAAATTTGACATGATCAATCA	4783
Q	y	4885	GGCAGCACAAAGCAATAGTCTTTGAATATAGTAACCGATGAAGAAATTCGATATAATCATTA	4944
D	b	4784	TGTTGTTCAATTTGCTTTAAATGTTAAACATGTTAAACATGACATCTGGATCACTATCAACAGCTGAAGC	4843
Q	y	4945	TGTTATTCATTTGGTCTGAAACATGTTTACCATGACCTCGATCGTTACGATGCGTCGGACA	5004
D	b	4844	AGTTACGCGAGCTTCTTGATTTACTTTGAACATGATCTTCATCGTCACTCTTCAGTTCCGAGT	4903
Q	y	5005	CGTATAACGCGGCTAGACTATCTCAATGCGATATTCGTAGTTATTTTCAGTTCCGAAAT	5064
D	b	4904	GTCGTATGAAGATATTCGCGCCTCAGATACCACTACTTCAAGGAAACCATGGAACTCTTTG	4963
Q	y	5065	GTCATTTAAAAAATTTGCTTTTACGATATACATATTTATTTATTTGAGCCATGGAATTTATTTG	5124
D	b	4964	ATTTGCTAGTTGTCATCTATCTATTTGGGTCCTGGTATTTGAGTGACATCATTCAGAAAT	5023
Q	y	5125	ATGTAGTAGTTGTCATTTTATCCATCTTAGTCTTTGTTACTTTAGCGATTTATTCGAGAAGT	5184
D	b	5024	ACTTTGTGTCGCTACACTGCTTCGAGTGGTGAGAGTGGCGAAGTGGGTGCGATCCCTGC	5083
Q	y	5185	ACTTCGTGTCGCGACCTGCTCCGAGTGGTGGGTGGCGAAGTGGCGCGTCTCTTC	5244
D	b	5084	GTCGTGTAAGGTGCTTAGAGGTATTCGGACATATGCTGTGTGCTGTGGCTATGTCTTTTG	5143
Q	y	5245	GACTGTGTGAAGGAGGCAAGGGCATTCGGACACTGCTCTGTGCGTTGGCCATGTGCGTGC	5304
D	b	5144	CAGCGCTCTTCAATATCTGCCCTACTACTATTTTATGTATGTTATTTTTCGCACTCTTCG	5203
Q	y	5305	CGGCGCTGTTTCAACATCTGCGTCTGCTGTTCTGCTGCTATGTTTTCATCTTTGCCATTTTCG	5364
D	b	5204	GCATGCTCTTCTTCATGCACTGCTCCGCGATAAAGGTGGCTTGTATGACGTGTACAAATTTCA	5263
Q	y	5365	GCATGTCTGTTCTTCATGCACTGTAAGGAGAGAGCGGCATTAACGACGCTCTACAACTTCA	5424
D	b	5264	AGAGCTTTGGGCACTGCATGATCCTGCTCTTCCAGATGTCCACATCACTGAGTGGGATG	5323
Q	y	5425	AGACCTTTGGCCAGAGCATGATCCTGCTCTTTTTCAGATGTGCAAGCTCAGCGGTTGGGATG	5484
D	b	5324	GTGTGTTAGATGGGATCATGAATGAGAGGACTGCAACAAACCAATAGCCAGATTTGGCT	5383
Q	y	5485	GTGTACTTGGAGCGCATTTTCAATGAGGAAGCATGCGATCCACCCGACAGCAACAAAGGCT	5544

Db	5384	ACCCGGGAGACTGTGGATCAGCTACTGTCCGATAGCTTTCTTGCTGTCATACCTCGTCA	5443
Qy	5545	ATCCGGGGCAATTGTGGTTCAGCGACCGTGTGGAATAACGTTTCTCTCTCATACCTAGTGA	5604
Db	5444	TCAGTTTCTTATTTGTTATTAACATGTACATTGCTGTCATTTTGAGAAATTAATCTCCAGG	5503
Qy	5605	TAAGCTTTTGTATAGTTATTAATATGTACATGTGCTCATTTCTCGAAGCTATAGTCAGG	5664
Db	5504	GCACAGAGGATGTGCGAGGAAGCTTTGACGGGATGATGACTACGATATGTACTATGAAATTT	5563
Qy	5665	CCACGAGGAGCTGCAAGAGGGCTTAACCGACGAGCTACGACATGTACTATGAGATCT	5724
Db	5564	GGCAGCACTTTGACCCAGATGGAGCGCAATATATTCGTCTATGACAGCTGCGGATTTCC	5623
Qy	5725	GGCAGCAATTCGATCCGGAGGGCACCCAGTACATACGCTATGATCAGCTGTCGGAATTC	5784
Db	5624	TCGACGTGCTGGAACCTCCGTGCGAGATACATAAGCCGAAAGTACAAGATAGTGTGCA	5683
Qy	5785	TGGACGTACTGGAGCCCGCTGTCAGATCCACAAACGGAAGTACAAGATCATATCGA	5844
Db	5684	TGGACATCTCCGATGTCGAAGGGGACCTCATGTTCTGTTGTCACATTTTGGATGCTTTGA	5743
Qy	5845	TGGACATACCCATCTGTGCGGTGACCTCATGTACTGCGTGCACATCTCGACGCCCTTA	5904
Db	5744	CGAAGGACTTCTTTTCAAGGAAGCAATCTTATAGAAGAGTCTCGAGAGTTGGGTGAAG	5803
Qy	5905	CGAAGACTTCTTTGCGCGGAAGGCAATCCGATAGAGAGACGGGTGAGATTGCTGAGA	5964
Db	5804	TGCAACCAAGGGGGCGGAGCAAGTGGGCTATGAGCCGTGTGCTCTACGCTGTGGCGGC	5863
Qy	5965	T---AGCGGGCGCGCGGATACGGAGGCTACGAGCGGCTCTCATCAACGCTGTGCGGTC	6021
Db	5864	AGCGAGAAGATATTGTGCGGCACTGATACAGAATGCATGGCGCAAGCACAAAG	5916
Qy	6022	AGCGTGAGAGTACTTCGCCCGCGCTTAATCCAGACGCGCTGGCGAAGCACAAAG	6074
RESULT	9		
LOCUS	BGU73583	6096 bp	mrna
DEFINITION	Blattella germanica para sodium channel mRNA, complete cds.	INV	19-MAR-1997
ACCESSION	U73583		
NID	g1657983		
KEYWORDS	German cockroach.		
SOURCE	Blattella germanica		
ORGANISM	Eukaryotes; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Orthopteroidea; Blattaria; Blattellidae; Blattellinae; Blattella.		
REFERENCE	1 (bases 1 to 6096)		
AUTHORS	Dong, K.		
TITLE	A single amino acid change in the para sodium channel protein is associated with knockdown-resistance (kdr) to pyrethroid insecticides in German cockroach		
JOURNAL	Insect Biochem. Mol. Biol. 27 (2), 93-100 (1997)		
MEDLINE	97218696		
REFERENCE	2 (bases 1 to 6096)		
AUTHORS	Dong, K.		
TITLE	Direct Submission		
JOURNAL	Submitted (07-OCT-1996) Entomology, Michigan State University, East Lansing, MI 48824, USA		
FEATURES	Location/Qualifiers		
source	1. 6096		
	/organism="Blattella germanica"		
	/strain="CSMA"		
	/note="insecticide-susceptible strain"		
	/db_xref="taxon:6973"		
CDS	1. 6096		
	/codon_start=1		
	/product="para sodium channel"		
	/db_xref="PID:g1657984"		
	/translation="MSDSSSISEERSLFRPFTRESLAAIEARAEAYAKOKELERKRAEVEGYRDEDEDEGPQALLEGAPIPVRMOGLFPPELASEPLEDIDPFYHQRNRFVYKSGKIDIFRFSGATDAMWILDPFNIRRVAILVHLPLSLFTITLNCIFMIR		

PTPTTISTEYFTGLIYFESAVKVMARGFILOQPTTYLRDANWMLDFVJALAYVTMG
IDIGNLAKEITFRKALNTAIYVGLKTIWGVAVIESYKVNLRDILITFESJVSFALM
GLQIYMGVITQKRIKFNFTWNGSGLDENWHAFCSSNTNIMYFPEGAPYCLNGSSG
AGCPDPTYCLAQFNGPNYGTPTFGWAFLLAKFAELTQDWEENLYQLVLRASQPG
HMLFVTVIFLASFYLVNLIILAVMSYDELQKAEDEEAALDEYALAEALAKEA
KLRLQADKAEQELAAQELAGLANAKSPGSSSRSELYELNOKDGNNDKNRMSIR
SEGSDSIKSHOEPVANGTAIBKVSAAISLUPGSPFNHRGSGSHFTYINRGGRFV
GPGGBRKLPLVJLYDLQAEHLPLADDSNAPVMSSEANGALVVPVYIASLGRHSST
SHASRISYTHGDLGAGNKSTQIKLQIRARSVNNQSPVSNPYMNASDDSDGGA
KAKHTNPTIEQMQTYIDMNDVNLNLIIEQAQGSNARSHGVSYYFPTDEDE
GPTVKEKVALCMRGDIFVPCWDCWLWKFQEVALLVDFPVEVFTILCVNVLTF
MALDHDMNMKMDKALKSGNYETFAIETALKLIAMSPKRYFQEGWNLFDFIVAL
SLLELGEVGQGLSVYSPRLRVPKLSNPTLNLLISITMGTVAGLNLFTVLIL
IFLWAGMGLGKKNYDINVERFPGDMPDRNLTDFPHFSWTFVCLGCKWESWMDC
ILFYVQMSGCPFFLTVYIGNVLVPLMRLNTLNSFNGSPSNAPADNETKNIEAEAF
FSRFFNIMKRSALNWKMLRALTNQISDOQTPKDHRTDLDTADRLADGIVYRDK
KSPKEQTQLEAVIGDMSEPTIHGDLNKLKDKLMMANSYIIGNSLHNDKNTIESQY
LHNRQEDTLYSGYSHKNNRYPDQSHKSGAETWDEEKDKASKEDLOGBEGEDB
EGEPLELMDYDAGTEVDMSEYPADCCPDHCYKRPFLTAGDSDSPWQWGNLRLK
TFOLINKEYFEVATWMLLSLALADEHVLPHRPLLODILYAMORIVTFIEML
IKWLAGFKFYFNACWDLDFIIVWSLINFVSLVAGGLOAQFKWTRLRULRPLRA
MSRQMGVNVNALQAPISINFVLVLFWLALMGVOLFAKGYKWCDSNSTTL
SHEIIPRDNATAEYNTWSPNSDGFNGKAYLCFLQVATFKWIGIOMTDAIDREHL
KQIIPRNTIYMLYVFFYIFLSPFDTLHGVLCTVDINENQOKKAGSLDEMFETDQK
YKNYKMGSKLNAKIPRWRKQYFVSEFCIMLQYETDKFDMILMFIGNMVLTLGLV
QKSGQSDVLVLMWTFIYFSESQALMIKFAIRYHYKEPWNLFDFVWVLSLTGLV
SDIIEKXFVSPTLIVRVYKVRVLVKGAKGIRILLFALANSLPALFNICLLFL
VMIIFALFQMSFWLVRGGGLDLYNFKTQSGMILLQNMSTAGWQVLDGIMNEE
DCKNRPSEYFGDGSATVATFLVSLYKTFQSGMILLQNMSTAGWQVLDGIMNEE
LTDYDDMYETWQDPDQGTQIRYDQSLDFLQVLEPPQLQHKPNKYKIVMSDIPIC
KGLDMLQTDIALTQDFPARGNPIESBAGLQVGPDEPVEYSPVSTLNRQREE
YCARLITONARKHQQOROGACAPDEQLQDRHOTAVLVESDGFYTKNGHVV
THSRSPSYNSRSTNY

BASE COUNT	1615 a	1374 c	1532 g	1575 t
------------	--------	--------	--------	--------

Query Match 29.3%; Score 1910; DB 14; Length 6096;

Best Local Similarity 71.2%;
Matches 4179; Conservative 0;
Mismatched 1579; Indels 115; Gaps 74;

Db 151 CCGTACGATGACGAGGACGAAGATGAAGGCCCTCAGCCGGATGCCGACTCTGGAGCAAGG 210

— — — — —

QY 210 CGATATGATGACGAGGACGAGGATGAAGGTCCACAACCGGATCCTACACTTGAACAGGGT 269

Db 211 GCGCCCATCCCTGTCCGAATGCAAGGCCTTTCCCTCCCGAGCTGCCTCTACCCCGCTC 270

—

QY 270 GTGCCAATACCTGTTTCGATTGCAGGGCAGCTTCCCGCCGGAATTGGCCTCCACTCCTCTC 329

Db 271 GAGGACATCGACCCCTTCTACCACAACCAGAGAACATTTGTGGTGAGCAAGGAAAG 330

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

QY 330 GAGGATATCGATCCCTACTACAGCAATGTACTGACATTCTAGTTGTAAAGCAAAGGAAA 389

Db 331 GATATTTCCGGTTCAGTGGACAGATGCCATGTGGATTTGGACCCATTCAACCCGATT 390

[illegible]

QY 390 GATATTTTCGCTTTCTGCATCAAAAGCAATGTGGATGCTCGATCCATTCAATCCGATA 449

db 391 CGACGGGTGCCATCTACATTTTGGTCACCCCCTTCTCTCATCTTTCATCTATCACCC 450

[illegible]

QY 450 CGTCGTGGCCATTACATTCTAGTGCATCCATTATTTCCCTATTTCATCATCACCACA 509

db 451 ATTTTAAACCAACTGCATCTTCTATCATCATGCTACACCCACACATATACACTCCACTCA 510

[illegible]

QY 510 ATTCTGTCAACTGCATCCTGATGATAATGCCGACAACGCCCGTTGAGTCCACTGAG 569

511 570

DD
JII
GATTTTACCGCATCTACACAATTGAAATCGCCGTATAAGGIGATGGCGAGAGGGTTC

QY 570 GTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCACGAGGTTTC 629

[illegible]

DB 571 ATACTTTCAGCCATTACGTAACCTTAGAGATGCA TGGAACTGGCTGGACTTCGTAGTAATA 630

QY 630 ATTTATGCCCGTTACGTATCTTAGAGATGCATGGAATTGGCTGGACTTCCTAGTAATA 689

Db 631 GCTTAGCTACGTAACCTATGGGGATAGATCTAGGAAACCTGGCCGCTTGCGAACGTTT 690

QY	690	GCTTTAGCTTATGTGACCATGGGTATAGATTTAGTAAATCTAGCAGCCCTGGGAACGTTT	749
Db	691	AGGGTGCTCCGAGCTTTGAAGACTGTGCGTATTGTTTCCAGGTTTGAAGACCATTTGTTGGC	750
QY	750	AGGGTGCTCGCAGCGCTTTAAACCGTAGCCATTGTGCCAGGCTTGAAGACCATCTGTCGCG	809
Db	751	GCTGTGATTGAATCTGTAAAGAACCTCGCGGATGTGATATCTCACCATGTTTCTGCTC	810
QY	810	GCCGTATCGAATCCGGTGAAGAATCTCGCGGATGTGATTATCTGACCATGTTCTCCCTG	869
Db	811	TCCGTGTTTGCTTTAATGCGGCTCCAGATTTACATGGGTGTCCTCAGCAGAAAGTGCATC	870
QY	870	TCCGTGTTTCCGTTTGATGGGCTACAGATCTATATGGGCTGCTCACCAGAAAGTGCATC	929
Db	871	AAAAAATCTCCCATAAATGTTTCATGGGGGAATTGAATCATCAGAACTGGCATGCAATT	930
QY	930	AGAAGTTTCCCGCTGGAGGTTCTCTGGGCAATCTGACCGACGAGAACTGGGACTATCAC	989
Db	931	TGCACTAACACAGAACTGGTACTTTTCGGAAGGTGCACAGAAAGTTCCTCACTGTGTGGG	990
QY	990	AATGCAATASCTCCAAATGTTATCCGAGSACAGGGCATCTCAITTCGTTATGCGCG	104
Db	991	AATTCATCAGAGCTGGTACATCTCCACTGTATTACACATGTCTCCAGGGCTTTGGAGAA	105
QY	1050	AATATATCCGTGCGGGCAATGCGAGCAGATTACGTGTGCTGTCGAGGGTTTGGTCGG	110
Db	1051	AATCCCAACTATGTTACACAGTTTCGATACGTTTGGTTGGGCAATCTCTCGGCCTTC	111
QY	1110	AATCCGAATTATGGCTACACAGCTTCGATTCGTTCGGATGGGCTTTCCTGTCGCGCTTC	116
Db	1111	AGACTGATGACCCAGGATTATTGGGAGAACTTTATCAGCTGGTTTGGATCTGCTGGG	117
QY	1170	CGGCTGATGACAGGACTTCTGGGAGGATCTGACAGCTGCTGTCGCGCGCCGGA	122
Db	1171	CCCTGGCATATGCTGTTCTCATTTGTCATCATCTTCTTAGGCTCATCTATCTTTGTAAC	123
QY	1230	CCATGGCACATGCTGTCTTTATAGTCATCATCTTCTTAGGTTCAATCTATCTTTGTAAT	128
Db	1231	TGTATTTTGGCCATTGTCGCATCTCTCTACGATGAGTTGTCAGAAAGAACTCAGGAGAA	129
QY	1290	TGTATTTTGGCCATTGTTGCCATCTGCTATGAGCAATTGCAAGGAAGCCGGAAGAA	134
Db	1291	GAAGCAGCGGAAGAAAGCGCTTGAGGGAAGCGGAAGACAGCTCTGCGAAAGAGCG	135
QY	1350	GAGGCTGCCGAAGAGAGGCGATACGTGAGCGGAAGAGCTGCCCGCCCAAGCGCGC	140
Db	1351	AAAAAATTAGACAAGCGGATTAACACTGGC--AG-CACAAGAAATTAGCAGCAGCACAAAGAA	140
QY	1410	AAGCTGGAGGAGCGGGCCAATGCGCAGGCTCAGCAGCAGCGGATGGGCTGCGCGCGAA	146
Db	1408	CTAGCTGCGCAATCTAGCAAAATCTCCCTCGG-GAAGT-TCGTCTCGT-AGTTATGAG	146
QY	1470	GAGGCTGCATCTGCATCCGGAATGGCCAGAGTCCGACGTATTCTTTGTCATCAGCTATGAG	152
Db	1465	TGTGTTTATAATCAAAAGGACGGCAATTAATGACAACAAAAGGAGAAACATGACATCCCG	152
QY	1530	CTATTTGTTGCGCGGAGAGGGCAACGATGACACAAAGAGAAAGATGTCCTATCCG	158
Db	1525	AGCGA--AGGCGG----GGACTCGATAGCGGA-ACACAAAGG-AAG-AGTGGGTGCAAA	157
QY	1590	AGCGTCGAGGTGGAGTCGGAGTCGGTTCGGCTGAGGCTTATACAAAGACAACAGCACCTACCA	164
Db	1576	GGT-ACG--GCGATCA-G--G-AAGGTCAGCGCGGCAAGTTTGAGTCTACCAAGCTCA	162
QY	1650	GCACACCAAGCTACCAAGTTCTGTAAGTAGGACGACATCTCTTATCTCTTACCTGGTTCA	170
Db	1627	CTTTTCAACCATCGCGAGTTTCCCAAGGTAGTCACTCACTTTTACAATTAGAAACGAGCT	168
QY	1710	CCGTTTACATACCGAGGGGATCAGTATGTTCTCACAAGTACAGGATACGGAACGAGCT	176
Db	1687	GGAAGGTTCTGTGGGCCCACTTGGTGGTATCGAAACCCCTAGTACTTCTACTGACCTC	174

QY 1770 GCGCGCTI--TGGTAT-ACCGGTAGCGATCGTAAGCCATTGGTATTGTCAACATATCAG 1826
Db 1747 GATGACAAGAACATCTTCCCTTATGCGAGATGACTCGAATGCAAGTAAACACCTATGTCTAGAG 1806
QY 1827 GATGCCAGCAGCACTTGCCTCATGCGGACGACTCGAATGCCGTACCCCGATGTCCGAA 1886
Db 1807 GAGAAATGAGCAATAGTGTACCAAGTTTATACGCCAGCCCTCGGTTCGAGCACTCATCC 1866
QY 1887 GAGAAATGGGGCAATCATAGTCCCGGTGTACTATGCGCAATCTAGGCTCCCGACACTCATCG 1946
Db 1867 TATACATCACACGCGATCAGGATATCTTACACGCTCTCATGSGGACCTCCCTGGTG-CA-G 1924
QY 1947 TATACCTCGCATAGTCCCGAATATCGTATACCTCACTGCGGATCTACTCGCGGGCATG 2006
Db 1925 GCAA-CRAAT-C-TCAGACCAA-GATCAATCA-A-C-----TGCAGAGTCTGTTCACTAGTCGC 1974
QY 2007 GCCGTATGGGCGTCAAGCAATGACCAAGGAGAGCAAAATTGCGCAACCCGCAACACACGC 2066
Db 1975 AA-CAACCCIT------CAC--A-GGTG-C-CTAA-T-TCT--ACACATACATGAATGC 2018
QY 2067 AATCAATCAGTGGGCGCCACCAATGGGGCACCACTGTCTGGACACCAATACAAAGTC 2126
Db 2019 G-TCAGCA-GAC-A-GTGAT--GA-TGAG----CGGT-GAAA----GCAA-AGCA--CA- 2059
QY 2127 GATCATCGGACTAGCAAAATTGGGCTGGAGTGACGACGAGCAAGCTGCGAAGATTAAACAT 2186
Db 2060 C-TGACAATCCATTCAATGAACAAATCAGCAAACTACAATTTGTATGATGAATGATGTA 2118
QY 2187 CATGACAATCCTTTTATCGAGCCCGTCCAGACACAAACGGTGGTTGATATGAAGATGTG 2246
Db 2119 ATGCTGTGAATGACATATAGACACAGCTCTGGACAGCAGAGTAGCCAGTGAACAT 2178
QY 2247 ATGCTGTGAATGACATATGACACAGCCCGTGTGGCACAGCTCGGGCAAGCGATCGC 2306
Db 2179 GGAGTCTCCATCTATTATTTCCGACAGACGAAGATGACGAGGTCCCAAC-A-GTT-AAA 2235
QY 2307 GGTGTCCTCGTTTACTATTTCCCAAGAGACCATGACGAGGATGGCGCACCTTCAA 2366
Db 2236 GAGAAGTGTGTAGCTATATGATCGAGGTATCGACATCTTCTCGGTGGGATGTTGC 2295
QY 2367 GACAAGCACTCGAAGTATCCTCAAAAGGCATCGATGTTTGTGTGGGACTGTGC 2426
Db 2296 TGGCTCTGGCTCAGTTCCCAAGATAGCTGCCCTCCTGTGTGTGACCCCTTTGTGGAG 2355
QY 2427 TGGTGTGGTTGAAATTCAGAGTGGGTATCGCTCATCTGCTTCGATCCCTTCGTCGAG 2486
Db 2356 TTGTTTCATCCCTTTTGCATTTGCTCAATACACTGTTATGCGCCCTCGACCACCGAC 2415
QY 2487 CTCTTCATCAGCTGTGCAATTTGGTCAACACGATGTTTCATGGCAATGGATCACCGAT 2546
Db 2416 ATGAATAAGACATGGATAAGGCTCTCAAGAGTGGCAACTATTTCTTCACAGCGACCTTT 2475
QY 2547 ATGAACAAGGAGATGGAACGGTCTCAAGAGTGGCAACTATTTCTTCACCGCCACCTTT 2606
Db 2476 GCCATTGAGGCGAGCTCAGTTGATAGCAATGAGCCCTAAGTACTACTTCCAGGAAGGA 2535
QY 2607 GCCATCAGGCGCCACCTAAGACTAATGCCATGAGCCCAAGTACTATTTCCAGGAGGCG 2666
Db 2536 TGGAAACATTTTGTATTCATCATTTGTCACCTTTCTTGTGGAATGGGTCTTGAAGGT 2595
QY 2667 TGGAAACATCTCGACTTCATTTATGCTGGCCCTATCGCTATTTGGAACCTGGGACTCGAGGT 2726
Db 2596 GTCCAAGTCTGTCGCTGCTGCTGCTTCAAGATTGTTGAGAGTCTTCAAACTTGCAGAG 2655
QY 2727 GTCCAGGCTCTGTCGATTGCGTTCTCTTTTCGATTGCTGGGTGATTTCAAACTGGCCAG 2786
Db 2656 TCTTGGCGGCGCTGATCTGCTCATTTCCATCATGAGGATGAGAACTGTTGGTCTCGGT 2715
QY 2787 TCTTGGCCCACTAATTTACTCATTTTCGATTATGGACGCGCATCGGCGCTTTGGGT 2846
Db 2716 AACTCGACCTTGTGCTTGTGATTATCATTTTTCATCTTTGCGGTCATGGGTATGCAACTC 2775
QY 2847 AATCTGACATTTGTACTTGTGCAATATCATCTCTATCTTGGGTGATGGGAATGCAACTG 2906

Db 2776 TTTGGCAAAATTTATTATGATAATGTTGACGTTTCCCTGACGGGATATGCCGAGATGG 2835
QY 2907 TTCGAAAGAATTTATCATGATCACAGGACCGTTTCCGGATGGCAGCTGCCGCGTGG 2966
Db 2836 AACTTTACGGACTTCATGCACTCATTCATGATTGTGTTCCGAGTGTGTGCGGGAGTGG 2895
QY 2967 AACTTCAACCAGCTTTATGTCACAGCTTCATGATGTTGTTCCGGGTGCTCTCGGAGAATGG 3026
Db 2896 ATAGAGTCTATGTTGGGATTTGATGCTTGTGTTGGAGACTGTTCTGTCATCCCGTTCTTCTTG 2955
QY 3027 ATCGAGTCCATGTTGGGACTGCATGATGTTGGGCGATGTCTGTCGATTCCTCTTCTTCTG 3086
Db 2956 GCCACTGTCTGCTATGTTGAAACTTGGTGTGTTGAACCTTCTTGGCTTGGCTGCTCAGC 3015
QY 3087 GCCACCGTGTCTATGTCGCACTCTTGTGGTACTTAACCTTTTCTTACGCTTGTGTTGTC 3146
Db 3016 AACTTTGGTTCATCCAATCTGTCAGCCCCAACAGCTGACAAATGAAACCAACAAGATTGCT 3075
QY 3147 AATTTTGGCTCATCTAGCTTATCAGCGCCGACTGCCGATAACGATACGAATAAAATAGCC 3206
Db 3076 GAGCATTTGAGCGTTCCTCACGATTCTTTAACTGGATAAACGTTAGCGC-GCTAAACGT 3134
QY 3207 GAGCGCTTCAATCGAATTTGGCCGATTTAAAGTTTGGGTTAAGCGTAAATTTGCTGATTGT 3266
Db 3135 GGCAAAATTTTGGTCCCAAAATTAACCAATCAGATATCCGATCAGACGCGCATGCCC- 3193
QY 3267 TTCAAGT-TAATACGTAAACAAATTGACAAATCAATTAAGTATCAACCATCAGGTGAGAG 3325
Db 3194 -ATGAGCGTGA-CAC--GGACCTTGACCTCACACGG-GATGAAATC---CTGCG-C---G 3241
QY 3326 GACCAACCAAGTATGATTTGGAGCGAAGACATGTTGACAACTGAGAGTGGAGTGGG 3385
Db 3242 --ATG--GA-ATCGT-GTATAGAG----A-CAAGAGAGTCCAAAGGAGCAGACGAGTT 3290
QY 3386 CCAGCAGGAGATCCTCGCCAGCGGCTCATCAAGAAGGGGATCAAGGAGCAGACGCAACT 3445
Db 3291 GGAGTGGCGATAGGAGTGAATGGATTCCACCATCCATGGAGATCTGAAAAACAAGCT 3350
QY 3446 GGAGTGGCCATCGGGATCGGATGGAATTCAGATACACGGCGACATGAAGAACAACAA 3505
Db 3351 GAAGAAGGACAAGCTGATGATGAACAGCAGCAAGGATGATCGGCAATTTCTTGAATCATAA 3410
QY 3506 GCCGAAAGAAATCCAAATATCTAAATAACGCAACGATGATTGGCAACTCAATTAACCAACA 3565
Db 3411 AGACAATCGATAGAA-A-GTGTGA-CTATCTACACAA-TCGG--CAGGACGAGATAC 3464
QY 3566 AGACAATAGACTGGAACACAGAGCTAAACCATAGAGTTTGTCTTACAGGACGACGAC 3625
Db 3465 TTTGAGCAGACGGTCTATATGAAAGTCAAAAAACCGTCCATACAAGGATGACAGCCATA 3524
QY 3626 TGGCAGCATTAACATCATATGTTAGCCATAGAAATCGACCATTCAGAGCAGAGCCACAA 3585
Db 3525 GGAAGTGCAGAGACTATGATGGGAGGAGAAAGAAAGATGCAAGCAAAAGATCTCGA 3584
QY 3686 GGGCAGCGCCGACGATGGAGGCGGAGGAGAAAGCGCAGCGCAGCAAGGAGGATTAGG 3745
Db 3585 TCAAGAGGAGAGGAGTGAGAAAGATGGAGAGGTGAAGGACCTCTGGAGGAGACATGTT 3644
QY 3746 TCTCGAGAGGAACTGGACGAGGAGGGCGAATCGGAGGAGGGCCCGCTCGACGGTGATAT 3805
Db 3645 ATTGGATGACGGCACT-GAGGAGCTCATGATGTCAAGATATCCGAGATTTGCTGTCCTG 3703
QY 3806 CAT-TATTATGACACGAGGAGGATATCTCGATGAATATCCAGCTGATTGCTGCCCG 3864
Db 3704 ATCACTGCTATAAGCGCTTCCCTTCTTGTCTGGAGACGAAAGTCTCTCTTTCTGCGAAG 3763
QY 3865 ATTCGACTATAAGAAATTTCCGATCTTAGCCGCTGACGATGACTGCGCCCTTCTGCGAAG 3924
Db 3764 GCTGGGCAACCTCCGACTGAAACCTTCCAACTCATTTGAGAACAAATCTTTTGAACGG 3823
QY 3925 GATGGGCAATTTACGACTGAAACCTTTTCAATTAATTGAAATAAATATTTTGAACAG 3984

KEYWORDS	Drosophila virilis.	CDS	join(<1. .29,93. .>2144)
SOURCE	Drosophila virilis.		/gene="Dvir\para"
ORGANISM	Eukaryota; mitochondrion eukaryotes; Metazoa; Arthropoda; Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		/standard_name="paralytic"
REFERENCE	1 (bases 1 to 2144)		/note="lacking alternate segment a"
AUTHORS	Thackeray,J.R. and Ganetzky,B.		/codon_start=3
TITLE	Conserved alternative splicing patterns and splicing signals in the Drosophila sodium channel gene para		/product="sodium channel protein"
JOURNAL	Unpublished (1995)		/db_xref="PID:g1110467"
REFERENCE	2 (bases 1 to 2144)		/translation="ATKVRKYSTTSLRGRFGIPGSDRKLPLVLSYQDAQOHLPIYA
AUTHORS	Thackeray,J.R. and Ganetzky,B.		DDSNVTPMSENGAIIIPVYVYGNLGRSHSSTYSHOSRISYTSHGDLGGMAVMGVST
TITLE	Developmentally regulated alternative splicing generates a complex array of Drosophila para sodium channel isoforms		MTKESKLNRNTRNQSVGATNGTTCLDTNHKVBRDYEIGLECTDEAGTKIHHNDPF
JOURNAL	J. Neurosci. 14 (5 Pt 1), 2569-2578 (1994)		TEPVQTQTVDMKDVMLNDIIIEQAAGRHSRASRGVSYFFPTDEDDGPTLKDRAL
MEDLINE	94239327		LEVILKIDVFCVWDCWVWLKFEQWVSLIVDFPFVLFITLCIVVNTFMAMDHMD
REFERENCE	3 (bases 1 to 2144)		NKEMERVLKAGNYFFATFAEATMKLMAKSPKYFQEGWNIIDFIIIVALSLELGL
AUTHORS	Thackeray,J.R. and Ganetzky,B.		GVQGLSVLSRFLRLRFLAKSWPTLNLLISIMGRTMALGALNLFVLCIIIFFAVMG
TITLE	array of Drosophila para sodium channel isoforms		MOLFKNYTHDKDRFPDGLPRWNTDFMHSFMIVFVRLGALNLFVLCIIIFFAVMG
JOURNAL	J. Neurosci. 14 (5 Pt 1), 2569-2578 (1994)		IPFFLATVYIGNLVNLFLALLSNFGSSLSAPTADNTDNKIAEAFNRIGRFSKW
MEDLINE	94239327		KRVADCFKLNRKLTNQISDQPSGERINQISWLNSEKGYCVCRLSAAHNELELGH
REFERENCE	4 (bases 1 to 2144)		INDIADGLIKKGIKEQTQLEVAIGDMFTIHGDMKNKPKRSKLTNATMIGNSINH
AUTHORS	Thackeray,J.R. and Ganetzky,B.		QDNRLHNLHNRGLSLQDDDTASINSYSHKNRPFKDESHKGSATMEGEKRDASK
TITLE	Direct Submission		DIGLDEELDEE"
JOURNAL	Submitted (04-MAY-1995) Justin R. Thackeray, Biology, Yale University, 266 Whitney Avenue, New Haven, CT 06520, USA		<1. .>2144
FEATURES	Location/Qualifiers	CDS	/gene="Dvir\para"
source	1. .2144		/standard_name="paralytic"
	/organism="Drosophila virilis"		/codon_start=3
	/note="cDNA was derived by RT-PCR; sequence compiled from 6 independent clones"		/product="sodium channel protein"
	/db_xref="taxon:7244"		/db_xref="PID:g1110462"
	/chromosome="X"		/translation="ATKVRKYSTTSLRGRFGIPGSDRKLPLVLSYQDAQOHLPIYA
	1. .2144		DDSNVTPMSENGAIIIPVYVYGNLGRSHSSTYSHOS
	/gene="Dvir\para"		RISYTSHGDLGGMAVMGVSTMTKESKLNRNTRNQSVGATNGTTCLDTNHKVBRD
	/allele=""		YEIGLECTDEAGTKIHHNDPFIEPVQTQTVDMKDVMLNDIIIEQAAGRHSRASRGV
	/db_xref="FlyBase:FBgn0015214"		SVYFFPTDEDDGPTLKDRALVILKIDVFCVWDCWVWLKFEQWVSLIVDFPVE
	join(<1. .1913,1989. .>2144)		LFITLCIVVNTFMAMDHMDMKEMERVLKAGNYFFATFAEATMKLMAKSPKYFQ
	/standard_name="paralytic"		EGWNIIDFIIIVALSLELGLGVQGLSVLSRFLRLRFLAKSWPTLNLLISIMGRM
	/note="lacking alternate segment h"		GALGNLTFVLCIIIFFAVMGMOLFQKNYHDKHDKREFDGLPRWNTDFMHSFMIVR
	/codon_start=3		VLCGWIESWDCWVGVDSVCPFFLATVYIGNLVNLFLALLSNFGSSLSAPTA
	/product="sodium channel protein"		DNDTNKIAEAFNRIGRFSKWVRNADCFKLNRKLTNQISDQPSGERINQISWLNSE
	/db_xref="PID:g1110468"		GKGVCRICSAEHGDNLELGHDEILDGLIKKGIKEQTQLEVAIGDMFTIHGDMKN
	SDRKLPLVLSYQDAQOHLPIYADDSNAVTPMSENGAIIIPVYVYGNLGRSHSSTYSHOS		NKPKRSKLTNATMIGNSINHQDNRLHNLHNRGLSLQDDDTASINSYSHKNRPFKDESHKGSATMEGEKRDASKEDIGLDEELDEE"
	RISYTSHGDLGGMAVMGVSTMTKESKLNRNTRNQSVGATNGTTCLDTNHKVBRD		join(<1. .1702,1733. .>2144)
	YEIGLECTDEAGTKIHHNDPFIEPVQTQTVDMKDVMLNDIIIEQAAGRHSRASRGV		/gene="Dvir\para"
	SVYFFPTDEDDGPTLKDRALVILKIDVFCVWDCWVWLKFEQWVSLIVDFPVE		/standard_name="paralytic"
	LFITLCIVVNTFMAMDHMDMKEMERVLKAGNYFFATFAEATMKLMAKSPKYFQ		/note="lacking alternate segment f"
	EGWNIIDFIIIVALSLELGLGVQGLSVLSRFLRLRFLAKSWPTLNLLISIMGRM		/codon_start=3
	GALGNLTFVLCIIIFFAVMGMOLFQKNYHDKHDKREFDGLPRWNTDFMHSFMIVR		/product="sodium channel protein"
	VLCGWIESWDCWVGVDSVCPFFLATVYIGNLVNLFLALLSNFGSSLSAPTA		/db_xref="PID:g1110464"
	DNDTNKIAEAFNRIGRFSKWVRNADCFKLNRKLTNQISDQPSGERINQISWLNSE		/translation="ATKVRKYSTTSLRGRFGIPGSDRKLPLVLSYQDAQOHLPIYA
	GKGVCRICSAEHGDNLELGHDEILDGLIKKGIKEQTQLEVAIGDMFTIHGDMKN		DDSNVTPMSENGAIIIPVYVYGNLGRSHSSTYSHOS
	NKPKRSKLTNATMIGNSINHQDNRLHNLHNRGLSLQDDDTASINSYSHKNRPFKDESHKGSATMEGEKRDASKEDIGLDEELDEE"		RISYTSHGDLGGMAVMGVSTMTKESKLNRNTRNQSVGATNGTTCLDTNHKVBRD
	join(<1. .1106,1269. .>2144)		YEIGLECTDEAGTKIHHNDPFIEPVQTQTVDMKDVMLNDIIIEQAAGRHSRASRGV
	/gene="Dvir\para"		SVYFFPTDEDDGPTLKDRALVILKIDVFCVWDCWVWLKFEQWVSLIVDFPVE
	/standard_name="paralytic"		LFITLCIVVNTFMAMDHMDMKEMERVLKAGNYFFATFAEATMKLMAKSPKYFQ
	/note="lacking alternate segment d"		EGWNIIDFIIIVALSLELGLGVQGLSVLSRFLRLRFLAKSWPTLNLLISIMGRM
	/codon_start=3		GALGNLTFVLCIIIFFAVMGMOLFQKNYHDKHDKREFDGLPRWNTDFMHSFMIVR
	/product="sodium channel protein"		VLCGWIESWDCWVGVDSVCPFFLATVYIGNLVNLFLALLSNFGSSLSAPTA
	/db_xref="PID:g1110463"		DNDTNKIAEAFNRIGRFSKWVRNADCFKLNRKLTNQISDQPSGERINQISWLNSE
	SDRKLPLVLSYQDAQOHLPIYADDSNAVTPMSENGAIIIPVYVYGNLGRSHSSTYSHOS		GHDNELELGHDEILDGLIKKGIKEQTQLEVAIGDMFTIHGDMKNKPKRSKLTN
	RISYTSHGDLGGMAVMGVSTMTKESKLNRNTRNQSVGATNGTTCLDTNHKVBRD		NATMIGNSINHQDNRLHNLHNRGLSLQDDDTASINSYSHKNRPFKDESHKGSATME
	YEIGLECTDEAGTKIHHNDPFIEPVQTQTVDMKDVMLNDIIIEQAAGRHSRASRGV		EGEEKRDASKEDIGLDEELDEE"
	SVYFFPTDEDDGPTLKDRALVILKIDVFCVWDCWVWLKFEQWVSLIVDFPVE		join(<1. .1662,1702. .>2144)
	LFITLCIVVNTFMAMDHMDMKEMERVLKAGNYFFATFAEATMKLMAKSPKYFQ		/gene="Dvir\para"
	EGWNIIDFIIIVALSLELGLGVQGLSVLSRFLRLRFLAKSWPTLNLLISIMGRM		/standard_name="paralytic"
	GALGNLTFVLCIIIFFAVMGMOLFQKNYHDKHDKREFDGLPRWNTDFMHSFMIVR		/note="lacking alternate segment e"
	VLCGWIESWDCWVGVDSVCPFFLATVYIGNLVNLFLALLSNFGSSLSAPTA		/codon_start=3
	DNDTNKIAEAFNRIGRFSKWVRNADCFKLNRKLTNQISDQPSGERINQISWLNSE		/product="sodium channel protein"
	GHDNELELGHDEILDGLIKKGIKEQTQLEVAIGDMFTIHGDMKNKPKRSKLTN		/db_xref="PID:g1110466"
	NATMIGNSINHQDNRLHNLHNRGLSLQDDDTASINSYSHKNRPFKDESHKGSATME		/translation="ATKVRKYSTTSLRGRFGIPGSDRKLPLVLSYQDAQOHLPIYA
	EGEEKRDASKEDIGLDEELDEE"		DDSNVTPMSENGAIIIPVYVYGNLGRSHSSTYSHOS
	join(<1. .1106,1269. .>2144)		RISYTSHGDLGGMAVMGVSTMTKESKLNRNTRNQSVGATNGTTCLDTNHKVBRD
	/gene="Dvir\para"		YEIGLECTDEAGTKIHHNDPFIEPVQTQTVDMKDVMLNDIIIEQAAGRHSRASRGV
	/standard_name="paralytic"		SVYFFPTDEDDGPTLKDRALVILKIDVFCVWDCWVWLKFEQWVSLIVDFPVE
	/note="lacking alternate segment d"		LFITLCIVVNTFMAMDHMDMKEMERVLKAGNYFFATFAEATMKLMAKSPKYFQ
	/codon_start=3		EGWNIIDFIIIVALSLELGLGVQGLSVLSRFLRLRFLAKSWPTLNLLISIMGRM
	/product="sodium channel protein"		GALGNLTFVLCIIIFFAVMGMOLFQKNYHDKHDKREFDGLPRWNTDFMHSFMIVR
	/db_xref="PID:g1110463"		VLCGWIESWDCWVGVDSVCPFFLATVYIGNLVNLFLALLSNFGSSLSAPTA
	SDRKLPLVLSYQDAQOHLPIYADDSNAVTPMSENGAIIIPVYVYGNLGRSHSSTYSHOS		DNDTNKIAEAFNRIGRFSKWVRNADCFKLNRKLTNQISDQPSGERINQISWLNSE
	RISYTSHGDLGGMAVMGVSTMTKESKLNRNTRNQSVGATNGTTCLDTNHKVBRD		GHDNELELGHDEILDGLIKKGIKEQTQLEVAIGDMFTIHGDMKNKPKRSKLTN
	YEIGLECTDEAGTKIHHNDPFIEPVQTQTVDMKDVMLNDIIIEQAAGRHSRASRGV		NATMIGNSINHQDNRLHNLHNRGLSLQDDDTASINSYSHKNRPFKDESHKGSATME
	SVYFFPTDEDDGPTLKDRALVILKIDVFCVWDCWVWLKFEQWVSLIVDFPVE		EGEEKRDASKEDIGLDEELDEE"
	LFITLCIVVNTFMAMDHMDMKEMERVLKAGNYFFATFAEATMKLMAKSPKYFQ		join(<1. .1106,1269. .>2144)
	EGWNIIDFIIIVALSLELGLGVQGLSVLSRFLRLRFLAKSWPTLNLLISIMGRM		/gene="Dvir\para"
	GALGNLTFVLCIIIFFAVMGMOLFQKNYHDKHDKREFDGLPRWNTDFMHSFMIVR		/standard_name="paralytic"
	VLCGWIESWDCWVGVDSVCPFFLATVYIGNLVNLFLALLSNFGSSLSAPTA		/note="lacking alternate segment d"
	DNDTNKIAEAFNRIGRFSKWVRNADCFKLNRKLTNQISDQPSGERINQISWLNSE		/codon_start=3
	GHDNELELGHDEILDGLIKKGIKEQTQLEVAIGDMFTIHGDMKNKPKRSKLTN		/product="sodium channel protein"
	NATMIGNSINHQDNRLHNLHNRGLSLQDDDTASINSYSHKNRPFKDESHKGSATME		/db_xref="PID:g1110463"
	EGEEKRDASKEDIGLDEELDEE"		/translation="ATKVRKYSTTSLRGRFGIPGSDRKLPLVLSYQDAQOHLPIYA
	join(<1. .1106,1269. .>2144)		DDSNVTPMSENGAIIIPVYVYGNLGRSHSSTYSHOS
	/gene="Dvir\para"		RISYTSHGDLGGMAVMGVSTMTKESKLNRNTRNQSVGATNGTTCLDTNHKVBRD
	/standard_name="paralytic"		YEIGLECTDEAGTKIHHNDPFIEPVQTQTVDMKDVMLNDIIIEQAAGRHSRASRGV
	/note="lacking alternate segment d"		SVYFFPTDEDDGPTLKDRALVILKIDVFCVWDCWVWLKFEQWVSLIVDFPVE
	/codon_start=3		LFITLCIVVNTFMAMDHMDMKEMERVLKAGNYFFATFAEATMKLMAKSPKYFQ
	/product="sodium channel protein"		EGWNIIDFIIIVALSLELGLGVQGLSVLSRFLRLRFLAKSWPTLNLLISIMGRM
	/db_xref="PID:g1110463"		GALGNLTFVLCIIIFFAVMGMOLFQKNYHDKHDKREFDGLPRWNTDFMHSFMIVR
	SDRKLPLVLSYQDAQOHLPIYADDSNAVTPMSENGAIIIPVYVYGNLGRSHSSTYSHOS		VLCGWIESWDCWVGVDSVCPFFLATVYIGNLVNLFLALLSNFGSSLSAPTA
	RISYTSHGDLGGMAVMGVSTMTKESKLNRNTRNQSVGATNGTTCLDTNHKVBRD		DNDTNKIAEAFNRIGRFSKWVRNADCFKLNRKLTNQISDQPSGERINQISWLNSE
	YEIGLECTDEAGTKIHHNDPFIEPVQTQTVDMKDVMLNDIIIEQAAGRHSRASRGV		GHDNELELGHDEILDGLIKKGIKEQTQLEVAIGDMFTIHGDMKNKPKRSKLTN
	SVYFFPTDEDDGPTLKDRALVILKIDVFCVWDCWVWLKFEQWVSLIVDFPVE		NATMIGNSINHQDNRLHNLHNRGLSLQDDDTASINSYSHKNRPFKDESHKGSATME
	LFITLCIVVNTFMAMDHMDMKEMERVLKAGNYFFATFAEATMKLMAKSPKYFQ		EGEEKRDASKEDIGLDEELDEE"
	EGWNIIDFIIIVALSLELGLGVQGLSVLSRFLRLRFLAKSWPTLNLLISIMGRM		join(<1. .1106,1269. .>2144)
	GALGNLTFVLCIIIFFAVMGMOLFQKNYHDKHDKREFDGLPRWNTDFMHSFMIVR		/gene="Dvir\para"
	VLCGWIESWDCWVGVDSVCPFFLATVYIGNLVNLFLALLSNFGSSLSAPTA		/standard_name="paralytic"
	DNDTNKIAEAFNRIGRFSKWVRNADCFKLNRKLTNQISDQPSGERINQISWLNSE		/note="lacking alternate segment d"
	GHDNELELGHDEILDGLIKKGIKEQTQLEVAIGDMFTIHGDMKNKPKRSKLTN		/codon_start=3
	NATMIGNSINHQDNRLHNLHNRGLSLQDDDTASINSYSHKNRPFKDESHKGSATME		/product="sodium channel protein"
	EGEEKRDASKEDIGLDEELDEE"		/db_xref="PID:g1110463"
	join(<1. .1106,1269. .>2144)		/translation="ATKVRKYSTTSLRGRFGIPGSDRKLPLVLSYQDAQOHLPIYA
	/gene="Dvir\para"		DDSNVTPMSENGAIIIPVYVYGNLGRSHSSTYSHOS
	/standard_name="paralytic"		RISYTSHGDLGGMAVMGVSTMTKESKLNRNTRNQSVGATNGTTCLDTNHKVBRD
	/note="lacking alternate segment d"		YEIGLECTDEAGTKIHHNDPFIEPVQTQTVDMKDVMLNDIIIEQAAGRHSRASRGV
	/codon_start=3		SVYFFPTDEDDGPTLKDRALVILKIDVFCVWDCWVWLKFEQWVSLIVDFPVE
	/product="sodium channel protein"		LFITLCIVVNTFMAMDHMDMKEMERVLKAGNYFFATFAEATMKLMAKSPKYFQ
	/db_xref="PID:g1110463"		EGWNIIDFIIIVALSLELGLGVQGLSVLSRFLRLRFLAKSWPTLNLLISIMGRM
	SDRKLPLVLSYQDAQOHLPIYADDSNAVTPMSENGAIIIPVYVYGNLGRSHSSTYSHOS		GALGNLTFVLCIIIFFAVMGMOLFQKNYHDKHDKREFDGLPRWNTDFMHSFMIVR
	RISYTSHGDLGGMAVMGVSTMTKESKLNRNTRNQSVGATNGTTCLDTNHKVBRD		VLCGWIESWDCWVGVDSVCPFFLATVYIGNLVNLFLALLSNFGSSLSAPTA
	YEIGLECTDEAGTKIHHNDPFIEPVQTQTVDMKDVMLNDIIIEQAAGRHSRASRGV		DNDTNKIAEAFNRIGRFSKWVRNADCFKLNRKLTNQISDQPSGERINQISWLNSE
	SVYFFPTDEDDGPTLKDRALVILKIDVFCVWDCWVWLKFEQWVSLIVDFPVE		GHDNELELGHDEILDGLIKKGIKEQTQLEVAIGDMFTIHGDMKNKPKRSKLTN
	LFITLCIVVNTFMAMDHMDMKEMERVLKAGNYFFATFAEATMKLMAKSPKYFQ		NATMIGNSINHQDNRLHNLHNRGLSLQDDDTASINSYSHKNRPFKDESHKGSATME
	EGWNIIDFIIIVALSLELGLGVQGLSVLSRFLRLRFLAKSWPTLNLLISIMGRM		EGEEKRDASKEDIGLDEELDEE"

```
GALGNLTFVLCIIIRIFAVMGMOLEKKNYHDHDKRFPDQDLPRWNFTDFMHSFMIIVR
VLCGWIESWDCMYGVDSVCIPFLATVIGNLVNLVFLALLSLNFGSSLSAPTA
DNDTKIAEAFNRIGRFSWVRNADCFKLRNKLNOISDOPSGKGVCRCISAEHG
DNELEIGHDEILADLIKRIKEIQOLEVAIGDGMETIHGDMKNKPKKSKYLNAT
MIGNSIHQDNRLHELNHRGLSLQDDDTASINSYGSKHNRPFKDESHKGSSETMEGE
EKRDASKEDLGDEELDEE"
join(<1..654,679..>2144)
/genes="Dvir\para"
/standard_name="paralytic"
/note="lacking alternate segment b"
/codon_start=3
/product="sodium channel protein"
/db_xref="PID:g1110465"
/translation="AKYRKVSTSLSPGSPFNRRSSRSHKHKTIRNGRGRFIPG
SRKPLVUSTYQAOQHLPYADDSNAVTPMSEENGAIIVPYIYGLNRSHSYTSQHS
RISYTSGLDLAGMAYVMTKESKLNRNRNQSVGATNGGTTCLDTHNKHVRHD
YEIGLECEAGKIKHNDNPFTEPVQOTVDMKVMYLNDIIEQAAGRHSRASDRGE
DDEEDGPTILKRALVELKIDVFCWDCQVWLKFEQWVSLIVDFPVELFITLCIV
VNTMPWMDHDMKEMERYLKAGNYFFATFAIENATMKLAMSXPYIFQEGWNIFDF
IIVALSLLEGLLEGVQGLSVLRSFRLLRVFKLAKSWPTILNLLISIMGRITMGALNLT
VLCIIIFAVMGMOLEKKNYHDHDKRFPDQDLPRWNFTDFMHSFMIIVRVLCSGWIE
SWMDMYGVDSVCIPFLATVIGNLVNLVFLALLSLNFGSSLSAPTAADNDTNKIA
EAFNRIGRFSWVRNADCFKLRNKLNOISDOPSGERIINOISWSEKGVCRCI
SAEHGDNELIGHDELADGLIKKIKETOLEVAIGDGMETIHGDMKNKPKKSKY
LNNAHWIGNSIHQDNRLHELNHRGLSLQDDDTASINSYGSKHNRPFKDESHKGS
TMEGEKRDASKEDLGDEELDEE"
30..92
exon
/genes="Dvir\para"
/note="optional segment a"
655..678
exon
/genes="Dvir\para"
/note="optional segment b"
1107..1268
variation
/genes="Dvir\para"
/note="exon c"
/replace="ctgcgtgattcaaaattggccaaatcattggccaaatgtaatttactc
aatcgtataatggcgactcggcgctcggcaatcctgacacctgctctatgca
ttataatctctattcgtctaatggcgatcagctgttggcgaactacacag"
1107..1268
exon
/genes="Dvir\para"
/note="optional segment d; exon d can be replaced by exon
c in some cDNA's"
1663..1701
exon
/genes="Dvir\para"
/note="optional segment e"
1703..1732
exon
/genes="Dvir\para"
/note="optional segment f"
1914..1988
exon
/genes="Dvir\para"

...
Note: remainder of annotations omitted.

Query Match      24.48; Score 1592; DB 14; Length 2144;
Best Local Similarity 90.68; Pred. No. 0.00e+00;
Matches 1943; Conservative 0; Mismatches 171; Indels 30; Gaps 12;

Db      1  AAGCTACCAAAGTTCTGTAAGTGAGCAGCAGATCCTTATCCTTACCTGGTTACCGTTTA 60
QY      1657 AAGCTACCAAAGTTCTGTAAGTGAGCAGCAGATCCTTATCCTTACCTGGTTACCGTTTA 1716

Db      61  ACATACGACGGGATCAGCTAGTTCACAAAGTACAGATACGTAATGGACGTGGCGGTT 120
QY      1717 ACATACGACGGGATCAGCTAGTTCACAAAGTACAGATACGTAATGGACGTGGCGGTT 1776

Db      121  TCGGGATACCTGCGACGGATCGCAAGCCTTGGTATTGTCAACATATCAGGATGCACAAC 180
QY      1777 TTGGTATACCGGTAGCGATCGTAAGCCATTTGGTATTGTCAACATATCAGGATGCCCAGC 1836

Db      181  AACACTTGCCATACGCGGTAGCTCGAATGCCGTGACGCCAATGTCTGAGGAGAATGGAG 240
QY      1837 AGCACTTGCCCTATGCGGACGACTCGAATGCCGTGACGCCAATGTCTGAGGAGAATGGAG 1896
```


Qy	900	TATATGGCGTGTCTACCCGAGAAGTGCAATCAAGAAGTTCCCGCTGGACAGGTTCTCTGGGGC	959
Db	301	GAATTGAATGATGAGAACCTGGCATGTCATTTGCAGTAACAACACGAACCTGGTACTTTCCG	360
Qy	960	AATCTGACCAGCAGAACTGGGACTATCACAAATCGCATAGCTCCAATTGGTATTCGAG	1019
Db	361	GAAGGTGCCACCAAGATTCCTCATGTGTGGGAATTCATCAGGAGCTGGTACATGTCCACCT	420
Qy	1020	GACGAGGCATCTCAATTTCCGTTATCCGGCAATATATCCGTTGGGGGCAATGCGACGAC	1079
Db	421	GTATACACATGCTCCAGGSCCTTGAGANAATCCCAACTATGTTACACCAAGTTTCGAT	480
Qy	1080	GATTAGCTGTCCCTGCAGGGGTTTGGTCGAATCCGAATATGGCTACACCAAGCTTCGAT	1139
Db	481	ACGTTGGTTGGGCATTCCTCTCGGCTTCAGACTGTAGCATGTAGCCACAGGATTAATTTGGGAGAAC	540
Qy	1140	TCGTTGGATGGCTTTCCCTGTCCGCTTCGCGCTGTATGACACAGGACTTCTGGGAGGAT	1199
Db	541	CTTTATCAGCTGGTTTTGAGATCTGTGGGCCCTGGCATATGCTGTCTTCATATGTCATC	600
Qy	1200	CTGTACCAGCTGGTGTGCGCGCGCGGACCATGGCACATGCTGTCTTTATATGTCATC	1259
Db	601	ATCTTCTTAGGCTCATCTATCTTGTGAACITGATTTTGGCCATGTGCGCATGTCTCTAC	660
Qy	1260	ATCTTCTTAGGTTTCATCTATCTTGTGAATTTGATTTTGGCCATGTGTCATGCTGAT	1319
Db	661	GATGAGTTGCAGAAGAAGCTGAGGAGGAAGAAGCAGCGGAAGAAGAGCGTTGAGGGA	720
Qy	1320	GACGAATTGCAAGGAAGGCCGAAGAAGAGGCTGCCGAAGAGGAGCGCATACGTGA	1379
Db	721	CGCGAAGAAGCAGCTCTTCGAAAAGAGCGCAAAAAATTAAGACAAAGCGGATAAATGCG-	779
Qy	1380	CGCGAAGAAGCTCCCGCCGCCAAAGCGGCCAGCTGGAGAGCGGGCCAAATGCCAGGCT	1439
Db	780	-AG-CACAGAATTAGCAGCAGCAGAAGCACTAGCTGCGCGCAATCTTAGCAAAATCTCCC	837
Qy	1440	CAGCAGCAGCGGATCGGCTCGCGCGAAGAGGCTGCACCTGCATCCGGAATGGCCAAAG	1499
Db	838	TCGG-GAAGT-TCGTCCTG-TAGTTATGAGTTGTTTATAAATCAAAGGACGGCAATAAT	894
Qy	1500	AGTCGACGTAATCTTCTTGCAATCACTATGAGCTATTGTTGGGCGGAGAGGCGACGAT	1559
Db	895	GACAACAAAAGGAGAACATGAGCATCCGACGCA--AGGCGG---GGACTCGATAAGC	948
Qy	1560	GACAACAACAAGAGAAGATGTCCATTCGAGCGCTCGAGGTGGAGTCGGAGTCGCTGAGC	1619
Db	949	GA-ACACAAGG-AAG-AGTGGGTGCAATGCT-ACG--GGATCA--G---G-AAGGTG	996
Qy	1620	GTTATACAAAAGACAACGACACCTACGACAGCACACCAGACTACCAAAAGTTTCGTAAGTG	1679
Db	997	AGCGCGCACTTTTGAGTCTACAGGCTCACCTTTCACCATCGCCGAGGTTCCCAAGTT	1056
Qy	1680	AGCAGACATCCTTATCTCTTACCTGGTTACCCTTACCGTTTACATACGACGGGATACAGTAGT	1739
Db	1057	AGTCATCACTTTTACAATTAGAACGAGCAGTGAAGGTTCTGTGGGCCCACTGTGTGGTAT	1116
Qy	1740	TC TCACAAGTACAGGATACGGAACGGACGTGCCCGCTT--TGGTAT-ACCGGTTAGCGAT	1796
Db	1117	CGAAAACCCCTAGTACTTTCTTAGTACTTCGATGCAAGCAAGAACATFTTCTTATGACAGAT	1176
Qy	1797	CGTAAGCCATTGTTATGTCAACATATCAGATGCCAGCATGCCACGACACTTGCCTATGCGCAC	1856
Db	1177	GACTCGAATCGCATACACCTATGTCAGAGGAGAAATGGAGCAATAGTTGTACCAAGTTTAT	1236
Qy	1857	GACTCGAATCGGCTACCCCGATGTCCGAAGAAATGGGGCCATCATAGTCCCGCTGTAC	1916
Db	1237	TACGCCAGCCTCGGTTCCAGGCACTCATCTATACATCACACGATCCAGGATATCTCTAC	1296
Qy	1917	TATGGGAATCTAGGCTCCGACACTCATCTATACTCGCATCAGTCCCGAATATCGTAT	1976
Db	1297	ACGTCTCATGGGACCTCTCTGGGTG-CA-GGCA--CAAA-C-TCAGACCAA-GATCAAT	1350

Qy	1977	ACCTCACAATGGCGATCTACTCGCGCGGCATGCGCGCTCATGCGGCGTCAGCACAATATGACCAAG	20303
Db	1351	CA-A-C-----TGCAGTCCGTTTCAGTGGGCAA-CAACCCCTT-----CAC--A-GGTG-C	13993
Qy	2037	GAGAGCAATTGGCAACCGCAACACACACGCAATCAATCAGTGGCGGCCACCAATGGCGGC	2096
Db	1394	-CTAA-T-TCT--ACACCATACATGAATGCG--TCAGCA-GAC-A-GTGAT--GA-TGGAG	1441
Qy	2097	ACCACCTGTCTGACACCAATACAAAGTTCGATCATCGGACTACGAAATTTGGCTGGAG	2156
Db	1442	----CGGT-CAAA--GCAA-AGCA--CA-C--TGACAATCCATTCATTGACAAATGCAG	1488
Qy	2157	TGCAGCGACGACTGGCAAGATTAAACATATGACAACTCTTTATCGAGCCGCTCCAG	2216
Db	1489	CAAACTACAATTTGATATGAATGATTAATGTGCTGAATGACATATATAGAACAAAGCT	1548
Qy	2217	ACACAACGGTGTTCATATGAAGATGTGATGGTCCCTGAATGACATCATCGRACAGGCC	2276
Db	1549	GCTGGACAGCAGATGAGCCAGTGAACATGAGGACGAAAGATGACGAGGCTTCCAAACAGTT	1608
Qy	2277	GCTGTCGGCACAGTCGGGCAAGCGATCGGCTGCTCCGTTTACTATTTCCCAACAGAG	2336
Db	1609	AAAGA-CA--AGG-TG-----TT-----AG-CTAT--A-T-----GT-ATGCG---AGGT	1641
Qy	2337	GACGATCAGCAGGATGGCGCAGCTTCAAGACAAGGCATCGAAGTGAATCTCAAAGGC	2396
Db	1642	ATCGACATCTTCGCGTGTGGGATTTGCTGGCTCTCGCTCAAGTCAAGTCTCCAAAGATAGTCT	1701
Qy	2397	ATCGATCTGTTTGTGTGGGACTGTGCTGGGTGTTGGTTGNAATTTCAGGAGTGGGTA	2456
Db	1702	GCCCTCCTTGTGTTGACCCCTTTGTGGAGTTGTTTCATCACCCCTTGCATTTGGTGGTCAAT	1761
Qy	2457	TCGCTCATCTCTTCGATCCCCTCGTGGAGCTCTTCATCACGCTGTGCATTTGGTCAAC	2516
Db	1762	ACACTGTTTCATGCGCCTCGACACACACGACATGAATAAAGACATGGATAGGCTCTCAAG	1821
Qy	2517	ACGATGTTTCATGGCAATGGATCACCACGATATGAACAAGGAGATGGAAACGCTGCTCAAG	2576
Db	1822	AGTGGCAACTATTTTTCACAGCGACCTTTGCGATTGAGGCGAGCTCAAGTTGATAGCA	1881
Qy	2577	AGTGGCAACTATTTTTCACCGCCACCTTTGCCATCGAGGCCACCATGAAGCTAATGGCC	2636
Db	1882	ATGAGCCCTAAGTACTACTTCCAGGAAGATGGAAACATTTTTGATTTTCATTCATTTGTGCA	1941
Qy	2637	ATGAGCCCAAGTACTATTTCAGGAGGCTTGGAACTCTTCGACTTCATTTATGCGGCC	2696
Db	1942	CTTTCTCTGCTGGAATTGGTCTTGAAGTGTCAAGGTCTGCTCGTGTGCGATCGTTC	2001
Qy	2697	CTATCGCTATTTGGAACATGGGACTCGAGGCTGTCAAGGCTGTCCGATTTGCGTTCCTTT	2756
Db	2002	AGATTGTTGAGAGTCTTCAAACTTGCGAAGTCTTGGCCGACGCTGAATCTGCTCATTTCC	2061
Qy	2757	CGATTGCTGGTATTCAAACTTGGCCAAGTCTTGCCCAACATTAATTTACTCATTTTCG	2816
Db	2062	ATCATGGGTAGAACTCTTGCTGCTTGGGTAACTCGACTTGTGCTTTGTATTATTCATT	2121
Qy	2817	ATTATGGACGACCACTGGSCGCTTGGGTATCTGCATTTGATTTGCAATTATCATC	2876
Db	2122	TTCACTTTTGGCTCATGGGTATGCAACTCTTTTGGCAAAAATTAATATGATAATTTGTGAA	2181
Qy	2877	TTCACTTTTGGGTATGGGAATGCAACTGTTTCGGAAAGAAATTTATCATGACACAAGGAC	2936
Db	2182	CGTTTCCCTCACGGGATATGCCGAGATGGAACCTTACGGACTTCATGCACTCATTTATG	2241
Qy	2937	CGCTTTCCGATGGCACTTGGCGGCTGGAACTTTCACCGACTTTATGACAGACTTCATG	2996
Db	2242	ATTGTTTCCGAGTGTGTGTGGAGATGGATAGAGTCTATGTGGGATTTGTATCTGTTT	2301
Qy	2997	ATCTGTGTCGGGTGCTCTCGGAGAAATGGATCGAGTCCATGTGGGACTGCATGTACGCTG	3056
Db	2302	GGAGACTGGTCTGCATCCCGTTCTTCTTGGCCACTGCTGTCATTTGGAAACTTGGTTGTG	2361
Qy	3057	GGCCATGCTCGTGCAATCCCTTCTTCTTGGCCACCGTGTGTCATCGGCAATCTGTGGTA	3116

Db	2362	TTGAACCTCTTCTGGCCTTGCTGCTCAGCAACTTTGGTTTCATCCAATCTGTGACGCCCA	2421	Db	3410	TGGTCTCACTCATAAACTTCGTAGCGACCTTGGTGGCGCTGGAGGCAATTCAGCCCTTCA	3469
Qy	3117	CTTAACCTTTTCTTAGCCTTGCTTTTGTCCAATTTTGGCTCATCTAGCTTATCAGCGCGG	3176	Qy	4195	TGGTATCGCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTGGTATTCAAGCCCTTCA	4254
Db	2422	ACAGCTGACAATGAAACCAACAGATTTGCTGAGGCAATTTGAGCGTTTTCACAGATTTCTT	2481	Db	3470	AAACTATGAGGACACTCAGGCCCTTAGGCTCTTAGGGCTATGCTAGAAATGCGAGGGGA	3529
Qy	3177	ACTGCCGATAACCATACGAATAAATAGCGAGGCCCTTCAATCGAATTTGGCCGATTAA	3236	Qy	4255	AGACTATCGCAACGTTAAGAGCACTGAGACCACCTACGTGGCATGTCCCGTATGCGAGGGA	4314
Db	2482	AACGTGAATAAAGCTAGCGC-GCTAAACGTGGCAAAATTTGGTCGTGGCCAAATTAACCAA	2540	Db	3530	TGAGGTGGTGGTGAACGCTTTGGTGAAGCCATCCCACTATCTTCAATGTGTCTCTCG	3589
Qy	3237	AGTTGGTTAAGCGTAAATATTGCTGATTTGTTTCAAGT-TAATACGTTAACAAAATTGACAA	3295	Qy	4315	TGAGGTGCTGCTTAATGCGCTGGTGAAGCTATACAGTATACCGTCCATCTTCATGTGCTATGG	4374
Db	2541	TCAGATATCGGATCAGAGCGCAGATGCC--ATGACGCTGA-CAC--GACCTTGACCTC	2595	Db	3590	TGTGTCTCATCTTCTGGCTCATCTTGGCCATCATGGGTGTGTCAGCTGTTTGTCTGGAAT	3649
Qy	3296	TCAATTAAGTGTACAACCATCAGGTGAGAGGACCAACAGATCAGTTGGATTGGAGCGA	3355	Qy	4375	TGTGTCTAATATTTTGGCTAATTTTGGCATAAATGGGTGTACAGCTTTTGTCTGGAAT	4434
Db	2596	ACAGCG-GCTGAAATC---CTGGC-C--G--ATG--GA-ATCGT-GTATAGAG----A-	2636	Db	3650	ATCATAAATGTGTGGATTCCAACTCTACCACCTTTGAGCCACGAATCATCTCTGACAGAA	3709
Qy	3356	AGAGCATGGTGACAACTGGAGCTGGGCCACGACGAGATCCTCGCCGACGGCCTCAT	3415	Qy	4435	ATTTTAAGTGGGAGACATGAATGGCAGAACTCAGCCAGGAGATCATACCAATCGCA	4494
Db	2637	CAGAAGAGTCCAAAGAGCAGACGACGTTGGAGGTGGCGATAGGAGATGGATGGAGTT	2696	Db	3710	ATGCTTTGCAATTTGCGTGAACACTACACATGGGAGAACTCGCCAAATGAATTTTGTACCGCTCG	3769
Qy	3416	CAAGAAGGGATCAAGAGCAGACGCAACTGAGGTGGCCATCGGGATCGGATGGAAAT	3475	Qy	4495	ATGCCCTGGAGAGCAGAACTACAGTGGGTGAATTCAGCAATGAATTCGATCATGTAG	4554
Db	2697	CACCATCCATGGAGATCTGAAACCAAGCTGAAGAAGGACAAGCTGATGATGAACAGCAC	2756	Db	3770	GCAAGCTTATCTCTGCCCTCTTCCAAGTGGCCACCTTCAAAAGGATGGATTCAGATCATGA	3829
Qy	3476	CACGATACCGGACATGAAGAACAACAAGCCGAGAAATCCAAATATCTAAATACGC	3535	Qy	4555	GTAAACGCTATCTGTGCTCTTTTCCAAGTGGCACCTTCAAAAGGCTGGATACAAATCATGA	4614
Db	2757	GAAGGTGATGGCAATTTCTTTGAATCATAAAGACAATTCGGATAGAA-A-GTGTGA-CTA	2813	Db	3830	ATGAGCTATAGACTCTAGAGAGCTCATAAGCAGCCCAATCAGGAAACGAACTCTACA	3889
Qy	3536	AACGATGATTGGCAACTCAATTAACCAACCAAGACAATFAGACTGGAACACGAGCTAAACCA	3595	Qy	4615	ACGATGCTATCGATTACAGAGAGGTGGACAAACCAATTCGTGAAACGAACTCTACA	4674
Db	2814	TCTACAAA-TCGG--CAGACAGGATACTTTGAGCAGACAGGTCATATCGAAGTCACAA	2870	Db	3890	TCTACTCTACTTTCTGTCTTTATCATCTTTTGGCTCATTTTCTCACTCTCAACCTATTACA	3949
Qy	3596	TAGAGTTTGTCTTTACAGCAGCAGCACTGCGCAGCATTTAACTCATATGTTAGCCATAA	3655	Qy	4675	TGTATTATATTTCTGATTTCTTCATCATATTTGGATCTTTTTCACATCTCACTCTGTTC	4734
Db	2871	AAACCGTCCATACAAAGATGACAGCCATAAGGGAAGTGCAGAGACTATGGATGGGAGGA	2930	Db	3950	TTGGTGTGATCATCGACAACTTTAATAGCAAAAAGAAAAGCAGGAGGCTCGCTAGAGA	4009
Qy	3656	GAATCGACCATTCAGACAGAGCCACAGAGGCGCCGACGAGCATGGAGGCGAGGA	3715	Qy	4735	TTGGTGTATCATCTAATTTAATAGCAAAAAGAAAAGCAGGCTGGATTCATTAGAAA	4794
Db	2931	AAAGAAAGATCAAGCAAAAGATCTCGATCAAGAAGAGAGGTTGAAGAAGATGGAGA	2990	Db	4010	TGCTCATGACTCAAGTACAGAGAAATACTCAATGCTATGAAGAAATGGTTCGAAAA	4069
Qy	3716	GAAGCGGACCCAGCAAGAGGATTTAGGTCTCGACAGGAACTTGACAGGAGGCGCA	3775	Qy	4795	TGTTATGACAGAAAGATCAGAAAAAGTACTATAATGCTATGAAGAAAGTGGCTCTAAA	4854
Db	2991	AGGTGAAGGACCTCTGGAGGAGACATGGTATTGGATGTCAGGCACT-GAGGACGTCATGA	3049	Db	4070	AACCGTTAAAGCCATCCCGAGGCCAAAGTGGAGACCAGCCAGCCCAATTTGTTTGAATCT	4129
Qy	3776	ATGCGAGGAGGCCGCTCGACGCTGATATCATTT-ATTCATGCACAGCAGGATATAC	3834	Qy	4855	AACCATTAAGGCCATTCACAGACCAAGGTGGCGACCACAAGCAATAGTCTTTGAAATAG	4914
Db	3050	TGTCAGAAATATCCGCGAGATTGCTGCTGATCACTGCTATAAGCGCTTCCCTTCCTTG	3109	Db	4130	GCACAGACAAGAAATTTGACATGATCATCTGTTGTTTCAATGGCTTTACATGTTAAACAA	4189
Qy	3835	TCGATGAATATCCAGCTGATTGCTGCCCGATTCGTACTATAAGAAATTTCCGATCTTAG	3894	Qy	4915	TAACCGATAGAATTCGATATAATCATTTATTGTTTATTGTTGATGATGATTTTACACCA	4974
Db	3110	CTGGAGCAGAGACTCTCTTCTTGGCAAGCTCGGGCAACCTCCGACTGAAACCTTCC	3169	Db	4190	TGACTCTGATCAGTATCAACAGTTCAGGACGTTTCAGGACGCTTCTTGATTTACTTGAACA	4249
Qy	3895	CCGGTGAAGATGACTCGCGCTTCTGGCAAGGATGGGCAATTTTACGACTGAAAACCTTTC	3954	Qy	4975	TGACCTCGATCGTTACGATGCGTGGACACGATATAACCGGCTCTAGACTATCTCAATG	5034
Db	3170	AACTCATTTAGAACAAATACTTTGAAGCGCTGTATCACCATCATCTGCTTAGCAGTC	3229	Db	4250	TGATCTTCATCTGCTATCTTTCAGTTCGAGTGTCTGATGAAGATATTTCGCCCTTCAGATCC	4309
Qy	3955	AATTAATTTGAATAAATATTTTGAACAGCTGTTATCATCATGATTTTAAAGTAGT	4014	Qy	5035	CGATATTCGTAGTATTTCAGTTCGGAATGCTATTAATAAATATTTCGCTTTACGATATC	5094
Db	3230	TCGCACTGGCCCTTGAGGATGTACATCTGCTCATCGCCACCAATTCCTCAGGACATCTTAT	3289	Db	4310	ACTACTTCAAGAACCATGGAACCTCTTTGATTTGCTAGTTGCTCATCTCTATCTATATGG	4369
Qy	4015	TAGCTTTGGCATAGAAGATGTACATCTGCCACAAAGACCCATATCTCAGGATATTTTAT	4074	Qy	5095	ACTATTTTATGAGCCATGGAATTTATTTGATGTAGTGTAGTGTATTTTATCCATCTTAG	5154
Db	3290	ATTACATGGATGCTATCTTCTACTGTCTATCTTCTCATTTGAGATGTTGATCAAGTGGCTGG	3349	Db	4370	GTCTGTTATGAGTGACATCATTTGAGAAATACTTTGTGCGCTACACTGCTTCGAGTGG	4429
Qy	4075	ACTATATGACAGAAATATTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGG	4134	Qy	5155	GTCTTTAGTACTAGCATATATTCGAGAACTACTTCTGTGCGCGACCTTCTCCGAGTGG	5214
Db	3350	CCCTTGGTTTCAAAAAATACTTTCAAAATGCTTGGTGTGGTGGATTCATCTATGTC	3409	Db	4430	TGAGATGGCGAAGGTGGGTGCGAGTCTCGCTGTGTGTGAAAGGTGTAAAGGTTTCGGA	4489
Qy	4135	CGCTCGGCTTCAAGTGTACTTCACCAACGCGGTGTGTGGCTCGATTCGTTGATGTCA	4194	Qy	5215	TGCGTGTGGCAAGTGGGCGGTGCTTCTCGACTGTTGAAGGGAGCAAGGCGATTCGGA	5274
				Db	4490	CATTGCTGTTCGCGCTTGGCTATGCTCTTTCGCCAGCGCTCTTCAATATCTGCCTACTACTAT	4549


```

3441 CAATGGAGGTGGCCATCGGGGATCGGATCGGAATTCACGATACACGGCGACATGAAGAAC 3500
|||||
841 AACAGCCCAAGAAATCAAAATCTTAAATAACAACAACGATGATGGAAATCAATAAAC 900
|||||
3501 AACAGCCGAAGAATCAAAATCTTAAATAACAACAACGATGATGGCAACTCAATTAAC 3560
|||||
901 CACCAAGACATAGACTGGACATGAGCTAAACCATAGAGGTTTGTCCATACAGGAGCAT 960
|||||
3561 CACCAAGACATAGACTGGACAGAGCTAAACCATAGAGGTTTGTCTTACAGGAGCAG 3620
|||||
961 GACACTGCCAGCATTAACATCATATGG 986
|||||
3621 GACACTGCCAGCATTAACATCATATGG 3646
|||||

RESULT 13
LOCUS U83874 986 bp mRNA INV 07-APR-1998
DEFINITION Haematobia irritans para-like sodium channel (HF-para-like) mRNA,
alternatively spliced, partial cds.
ACCESSION U83874
NID g2231550
KEYWORDS horn fly.
SOURCE Haematobia irritans
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Muscoidea; Muscidae; Haematobia.
1 (bases 1 to 986)
Guerrero.F.D., Jamroz.R.C., Kammlah.D. and Kunz.S.E.
Toxicological and molecular characterization of
pyrethroid-resistant horn flies, Haematobia irritans:
identification of kdr and super-kdr point mutations
Insect Biochem. Mol. Biol. 27 (8-9), 745-755 (1997)
98105586
2 (bases 1 to 986)
Guerrero.F.D., Jamroz.R.C. and Kunz.S.E.
Direct Submission
Submitted (06-JAN-1997) USDA-ARS, Knippling-Bushland Livestock
Insects Research Laboratory, 2700 Fredericksburg Road, Kerrville,
TX 78028, USA

FEATURES
source
Location/Qualifiers
1..986
/organism="Haematobia irritans"
/strain="untreated pyrethroid-resistant"
/note="propagated on a steer without pyrethroid
applications; DNA designated 'Super Res*'"
/db_xref="taxon:7368"
1..986
/gene="HF-para-like"
<1..>986
/gene="HF-para-like"
/note="similar to Drosophila para; splice variant B"
/codon_start=1
/product="para-like sodium channel"
/db_xref="PID:g2231551"
/translation="EGWNIFDIIVALSLELGLGVQGLSVLRSFLLRVFKLAKSW
PTNLISITGRMTGALGNLTFVLCIIFIFAVGMQLFGKNIIDHKDFKDELPRW
NFTDFMSEMFVFRVLCGEWTESMDCWYGVDSICPFPLATVVGNFVNLFLALL
LSNFGSSLSAPTADNTNKIAEAFNRKFNWKRNIADCKFLIRKLTNOISDOP
SGERINQISWSEHGDNELELHDDIMGDGLIKGKMEOTOLEVAIGDMETIHG
DMKNKPKAKSFLNTHNIGNSINHQNRLHEHLNRLGLSIQDDDTASINSYG"
BASE COUNT 287 a 186 c 219 g 294 t

Query Match 10.7%; Score 694; DB 14; Length 986;
Best Local Similarity 85.2%; Pred. No. 0.00e+00;
Matches 840; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

Db 1 GAGGGCTGGAATATTTCGATTTCATATCGTTGCGCTTCTTTACTGGAATTGGCGCTG 60
|||||
QY 2661 GAGGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTATCGCTATTGGAACCTGGCACTC 2720
|||||
```

```

Db 61 GAAGGTGTCACAGGCTGTGCGGTGTTAAGAACTTTTTCGTTGCTTGGTGTATTTCAAAATTG 120
|||||
QY 2721 GAGGGTGTCCAGGGTCTGTGCGGTATTTCGTTGCTTTCGATGCTGCTGATTAACAACTG 2780
|||||
Db 121 GCAAAATCTTGGCCACCTGAACCTTACTCAATTCAAATTCAGGGCCGCGACATGGTGCA 180
|||||
QY 2781 GCCAAGTCTTGGCCACACTTAATTTACTCAATTCGATTATGGAGCCACCATTGGCGCT 2840
|||||
Db 181 TTGGGTAAATCTAACATTTGTACTTTGTCATTATCATCTTTCATCTTTTCCGCTTATGGGAATG 240
|||||
QY 2841 TTGGGTAAATCTGACATTTGTACTTTGTCATTATCATCTTTCATCTTTTCCGCTGATGGAATG 2900
|||||
Db 241 CAACTTTTCGGAAGAAGAACTATATGATCAACAAGGACAAATTCAAAGATCATGAATTAACCT 300
|||||
QY 2901 CAACTCTTCGGAAGAAGAAATATCATGATCAACAAGGACCGCTTTCCGGATGGCACCTGCGG 2960
|||||
Db 301 CGATGAAATTTACCGAATTCATGCACTCCTTTATGATTGTGTCCTCGAGTGTTATGTGT 360
|||||
QY 2961 CGTGGAACTTCACCGACTTTATGACACAGCTTCATGATGCTGTCCGGGTGCTTCGCGA 3020
|||||
Db 361 GAATGAAATGAATCCCATGTGGGACTGCATGTATGTGGGCGATGTCTCTCTGTATACCATTC 420
|||||
QY 3021 GAATGATCGAGTCCATGTGGGACTGCATGTACGTGGGCGATGTCTCTGTGATTCCTTC 3080
|||||
Db 421 TCTTGGCTACTGTTCTCATCGGCAATTTTGTGTTCTTAAATCTTTTCTAGCTTTGCTT 480
|||||
QY 3081 TCTTGGCCACCGTTGTCATCGGCAATCTTGTGTTCTTAACTTTTCTTAGCTTTGCTT 3140
|||||
Db 481 TTCTCAATTTTGGTTCATCTAGTTTATCAGCACCCGACTGCGGACAAATGATACCAATAAA 540
|||||
QY 3141 TTGTCCAAATTTGGCTTCATCTAGCTTATCAGCCGCGACTGCGGATACCAATGATAGATAA 3200
|||||
Db 541 ATACGAGAGCCCTCAATCGTATTTCTCGTTTFAAGAACTGGGTGAAACGTAAATTTGCC 600
|||||
QY 3201 ATAGCCGAGGCCCTTCAATGAAATTTGGCGGATTTAAAAGTTGGGTAAAGCTAATTTGCT 3260
|||||
Db 601 GATTGTTTAAAGTTATAGCTAATAAATTCACAAATCAATAGTGACCAACCATCAGGT 660
|||||
QY 3261 GATTGTTTCAAGTTAATAGCTAATAAATTTGACAAATCAATAGTGATCAACCATCAGGT 3320
|||||
Db 661 GAGAGGATCAACAGATCAGTTGGATTGGAGGAAAGACATGGCGATATGAACCTGGAG 720
|||||
QY 3321 GAGAGGACCAACAGATCAGTTGGATTGGAGCGAAGAGCATGGTGACACGACTGGAG 3380
|||||
Db 721 TTGGGTGATGATGACATCATGCGCGATGGCCTGATCAAAAGGGAATGAAAGAGCAAAAC 780
|||||
QY 3381 CTGGGCCACACGAGATCCTTCGCCGCGGCTCATCAAGAAGGGGATCAAGGAGCAGACG 3440
|||||
Db 781 CAACTGGAGGTGGCCATGGCGATGGCGATGGAGTTCAACCATACATGGCGATATGAAGAAC 840
|||||
QY 3441 CAACTGGAGGTGGCCATGGCGGATGGGATGGGAATTCACGATACACGGCGACATGAAGAAC 3500
|||||
Db 841 AACAGCCCAAGAAATCAAAATTTCTTAAATAACAACAACGATGATTGGAAACTCAATAAAC 900
|||||
QY 3501 AACAGCCGAAGAATCAAAATATCTAATAACGCAACGATGATTGGCACTCAATTAAC 3560
|||||
Db 901 CACCAAGACATAGACTGGAACTGAGCTAAACCATAGAGTAAACCATAGAGGTTTGTCCATACAGGAGAT 960
|||||
QY 3561 CACCAAGACATAGACTGGAACTGAGCTAAACCATAGAGGTTTGTCTTACAGGAGCAG 3620
|||||
Db 961 GACACTGCCAGCATTAACATCATATGG 986
|||||
QY 3621 GACACTGCCAGCATTAACATCATATGG 3646
|||||

RESULT 14
LOCUS DMU26715 1840 bp DNA INV 30-APR-1996
DEFINITION Drosophila melanogaster sodium channel protein (para) gene,
optional segments f and h, partial cds.
ACCESSION U26715
NID g1110473
KEYWORDS fruit fly.
SOURCE
```

ORGANISM	Drosophila melanogaster Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 1840) Thackeray, J.R. and Ganetzky, B. Developmentally regulated alternative splicing generates a complex array of Drosophila para sodium channel isoforms J. Neurosci. 14 (5 Pt 1), 2569-2578 (1994) 94238327 2 (bases 1 to 1840) Thackeray, J.R. and Ganetzky, B. Conserved alternative splicing patterns and splicing signals in the Drosophila sodium channel gene para Genetics 141 (1), 203-214 (1995) 95042905 3 (bases 1 to 1840) Thackeray, J.R. and Ganetzky, B. Direct Submission Submitted (10-MAY-1995) Justin R. Thackeray, Biology, Yale University, 266 Whitney Avenue, New Haven, CT 06520, USA Location/Qualifiers 1. .1840 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /map="X; 14C7-8" /chromosome="X" 405..1674 /note="paralytic" /gene="para" /allele="" /db_xref="FlyBase:FBgn0003036" join(<405..623.1267..>1674) /gene="para" /standard_name="paralytic" /codon_start=1 /product="sodium channel protein" /db_xref="PID:g1110474" /translation="TKGKVCRCISAEHGDNELGHDETLADGLIKKIGKQTOLEY AIGDHEFTTHGDMKNNPKSKYLNATDDDTASINSGSHKNRPFKESHKGSAT KEEGLKADSDDEEGECEEGLDGDIIHAHDEIDFADPCPDSDY MKPFILAGDDSPFWGCGWNLRLKTFQLIENKYFETAVITMILMSIAL"
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
MEDLINE	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
MEDLINE	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
source	
gene	
CDS	
BASE COUNT	673 a 374 c 305 g 488 t
ORIGIN	

Query Match	7.4%	Score 485;	DB 14;	Length 1840;
Best Local Similarity 100.0%;		Pred. No. 0.00e+00;		
Matches 485;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps 0;				
Db	1191	GATGATTGGCAACTCAATTAACCAACCAAGACAATAGACTGGAAACACGAGCTAAACCATAG	1250	
Qy	3539	GATGATTGGCAACTCAATTAACCAACCAAGACAATAGACTGGAAACACGAGCTAAACCATAG	3598	
Db	1251	AGGTTTGTCTTACAGGACGACGACACTGCCAGCATTAACTCATATGTTAGCCATAAGAA	1310	
Qy	3599	AGGTTTGTCTTACAGGACGACGACACTGCCAGCATTAACTCATATGTTAGCCATAAGAA	3658	
Db	1311	TCGACCACTTCAAGGACGAGAGCCACAAGGGCAGCGCCGAGACGATGGAGGCGCAGGAGAA	1370	
Qy	3659	TCGACCACTTCAAGGACGAGAGCCACAAGGGCAGCGCCGAGACGATGGAGGCGCAGGAGAA	3718	
Db	1371	CGCGGACGCCAGCAAGGAGGATTTAGTCTCGACGAGGAACCTGGACGAGGAGGCGGAATG	1430	
Qy	3719	CGCGGACGCCAGCAAGGAGGATTTAGTCTCGACGAGGAACCTGGACGAGGAGGCGGAATG	3778	
Db	1431	CGAGGAGGCGCGCTCGACGGTGATATCATTTATCTGCACACGACGAGGATATCTCGA	1490	
Qy	3779	CGAGGAGGCGCGCTCGACGGTGATATCATTTATCTGCACACGACGAGGATATCTCGA	3838	
Db	1491	TGAATATCCAGCTGATTGCTCCCCCGATTTCGTACTATAAGAAATTTCCGCATCTTAGCCGG	1550	
Qy	3839	TGAATATCCAGCTGATTGCTCCCCCGATTTCGTACTATAAGAAATTTCCGCATCTTAGCCGG	3898	

Db	1551	TCACGATGACTCGCGGTCTCTGGCAAGGATGGGCAATTTAGACTGAAAACCTTTTCAATT	1610
Qy	3899	TGACGATGACTCGCGGTCTCTGGCAAGGATGGGCAATTTAGACTGAAAACCTTTTCAATT	3958
Db	1611	AATTGAAATAAATATTTTGAACAGCTGTTATCAGTATGATTTTAATGAGTAGCTTAGC	1670
Qy	3959	AATTGAAATAAATATTTTGAACAGCTGTTATCAGTATGATTTTAATGAGTAGCTTAGC	4018
Db	1671	TTTGG 1675	
Qy	4019	TTTGG 4023	
RESULT	15		
LOCUS	U83871	947 bp	mRNA
DEFINITION	Haematobia irritans para-like sodium channel (HF-para) mRNA, alternatively spliced, partial cds.	INV	07-APR-1998
ACCESSION	U83871		
NID	g2231544		
KEYWORDS	.		
SOURCE	horn fly.		
ORGANISM	Haematobia irritans		
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Muscoidea; Muscidae; Haematobia.		
AUTHORS	1 (bases 1 to 947)		
TITLE	Guerrero, F.D., Jamroz, R.C., Kammlah, D. and Kunz, S.E. Toxicological and molecular characterization of pyrethroid-resistant horn flies, Haematobia irritans: identification of kdr and super-kdr point mutations Insect Biochem. Mol. Biol. 27 (8-9), 745-755 (1997) 98105586		
JOURNAL	2 (bases 1 to 947)		
MEDLINE	Guerrero, F.D., Jamroz, R.C. and Kunz, S.E.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (06-JAN-1997) USDA-ARS, Knippling-Bushland Livestock Insects Research Laboratory, 2700 Fredericksburg Road, Kerrville, TX 78028, USA		
JOURNAL			
TITLE			
FEATURES	Location/Qualifiers		
source	1..947		
	/organism="Haematobia irritans"		
	/strain="pyrethroid-susceptible"		
	/note="propagated on citrated bovine blood; DNA designated 'sus*'"		
gene	/db_xref="taxon:7368"		
	1..947		
CDS	/gene="HF-para"		
	<1..>947		
	/note="similar to Drosophila para; splice variant A"		
	/codon_start=1		
	/product="para-like sodium channel"		
	/db_xref="PDB:g2231545"		
	/translation="EGNIFDFIFVALSLELEGVQGLSVLRSFLLRVFKLAKS PTFDLISIMGRMTGALGNTFVLCIIFIVAVGMQLFGKNIYIDHKDKFDHLPKRW NFDLMHSFIMVFRVLCGENTSMWDCMVGDSICPFPLATVYIGNLVNLFLAL LSNFGSSLSAPTADNDTNKMAEAFNISRKKNVKRNIADCFKLIKNKLTNQLSDQP SEQGDNELEIGHDDIMGDELIIKGMKEQTQOLEVNAIGDGMETFIHGDMKNKPKKSKFT NNTDNEILSHOHDNRUEHLNHLGSLQDDDTASINSYG"		
BASE COUNT	273 a 181 c 207 g 286 t		
ORIGIN			
Query Match	6.9%;	Score 448;	DB 14; Length 947;
Best Local Similarity	84.0%;	Pred No. 0.00e+00;	
Matches	553; Conservative	0; Mismatches 105;	Indels 0; Gaps 0;
Db	1	GAGGCTGGAATATTTTCGATTTCATTTCGTTGCTTGTCTTTACTGGAATTTGGCCTG	60
Qy	2661	GAGGCTGGAACATCTTCGACTTCATTATCTGGGCCCTATCGCTATTGGAAGTGGGACTC	2720
Db	61	GAAGGTGTCAGGGCTTTCGGTGTAAAGAGTTTTCGTTGCTGCTGATTCAAATG	120
Qy	2721	GAGGGTGTCAGGGTCTTCGGTATTCGTTGCTTCCCTGATTCGATTCGCTGCTGATTCAACTG	2780

W P S R E H
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sun Sep 13 07:20:22 1998; MasPar time 249.45 Seconds
Tabular output not generated. 1217.927 Million cell updates/sec

Title: >US-08-554-424-7
Description: (1-6513) from US08554424.seq
Perfect Score: 6513
N.A. Sequence: 1 TCTAGACGTTGGCCGATAG.....ACCGAGTATTAGCTCTAGA 6513
Comp: AGATCTGCACCGCGTATC.....TGGCCTCAATCGAGATCT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 88822 seqs, 23323279 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 10.185; Variance 5.490; scale 1.855

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	6513	100.0	6513	2	PCT-US95-1 Sequence 7, Applicatio	0.00e+00
2	6513	100.0	6513	1	US-08-337- Sequence 7, Applicatio	0.00e+00
3	6513	100.0	6513	1	US-08-724- Sequence 7, Applicatio	0.00e+00
4	6513	100.0	6513	1	US-08-338- Sequence 7, Applicatio	0.00e+00
5	6513	100.0	6513	2	PCT-US95-1 Sequence 7, Applicatio	0.00e+00
6	110	1.7	7218	1	US-08-232- Sequence 14, Applicati	2.08e-58
7	60	0.9	7218	1	US-08-232- Sequence 14, Applicati	8.52e-23
8	41	0.6	215	1	US-08-238- Sequence 5, Applicatio	2.09e-10
9	36	0.6	215	1	US-08-238- Sequence 5, Applicatio	2.27e-07
10	36	0.6	1809	2	PCT-US95-1 Sequence 1, Applicatio	2.27e-07
11	39	0.6	5904	1	US-07-745- Sequence 6, Applicatio	3.54e-09
12	37	0.6	5962	3	5386025-5 Patent No. 5386025.	5.73e-08
13	37	0.6	5975	1	US-08-404- Sequence 1, Applicatio	5.73e-08
14	37	0.6	5975	1	US-08-314- Sequence 1, Applicatio	5.73e-08
15	30	0.5	33	1	US-08-337- Sequence 1, Applicatio	6.37e-04
16	30	0.5	33	2	PCT-US95-1 Sequence 1, Applicatio	6.37e-04
17	30	0.5	33	1	US-08-724- Sequence 1, Applicatio	6.37e-04
18	30	0.5	33	2	PCT-US95-1 Sequence 1, Applicatio	6.37e-04
19	30	0.5	33	1	US-08-338- Sequence 1, Applicatio	6.37e-04
20	31	0.5	75	1	US-08-237- Sequence 6, Applicatio	1.77e-04

21	30	0.5	228	3	5482709-9	Patent No. 5482709.	6.37e-04
22	30	0.5	228	3	5273901-10	Patent No. 5273901.	6.37e-04
c	23	0.5	1213	1	US-08-276- Sequence 6, Applicatio	Sequence 6, Applicatio	6.37e-04
c	24	0.5	2256	1	US-07-794- Sequence 1, Applicatio	Sequence 1, Applicatio	4.81e-05
c	25	0.5	2256	1	US-08-001- Sequence 1, Applicatio	Sequence 1, Applicatio	4.81e-05
c	26	0.5	2721	3	5215881-2	Patent No. 5215881.	1.77e-04
c	27	0.5	4255	2	PCT-US96-0	Sequence 14, Applicati	4.81e-05
c	28	0.5	4835	2	PCT-US96-0	Sequence 9, Applicatio	4.81e-05
c	29	0.5	5775	2	PCT-US93-0	Sequence 29, Applicati	6.37e-04
c	30	0.5	8438	1	US-07-945- Sequence 1, Applicatio	Sequence 1, Applicatio	1.77e-04
c	31	0.5	8438	1	US-08-338- Sequence 6, Applicatio	Sequence 6, Applicatio	2.25e-03
c	32	0.4	32	1	US-08-337- Sequence 6, Applicatio	Sequence 6, Applicatio	2.25e-03
c	33	0.4	32	1	US-08-724- Sequence 6, Applicatio	Sequence 6, Applicatio	2.25e-03
c	34	0.4	32	2	PCT-US95-1 Sequence 6, Applicatio	Sequence 6, Applicatio	2.25e-03
c	35	0.4	32	2	PCT-US95-1 Sequence 6, Applicatio	Sequence 6, Applicatio	2.25e-03
c	36	0.4	51	1	US-08-068- Sequence 1, Applicatio	Sequence 1, Applicatio	2.25e-03
c	37	0.4	75	1	US-08-237- Sequence 5, Applicatio	Sequence 5, Applicatio	2.25e-03
c	38	0.4	105	1	US-07-855- Sequence 13, Applicati	Sequence 13, Applicati	2.25e-03
c	39	0.4	1144	1	US-08-486- Sequence 2, Applicatio	Sequence 2, Applicatio	2.25e-03
c	40	0.4	1144	1	US-08-014- Sequence 1, Applicatio	Sequence 1, Applicatio	2.25e-03
c	41	0.4	2329	2	PCT-US94-0	Sequence 9, Applicatio	2.25e-03
c	42	0.4	3086	3	5206152-1	Patent No. 5206152.	2.25e-03
c	43	0.4	7125	1	US-07-745- Sequence 1, Applicatio	Sequence 1, Applicatio	2.25e-03
c	44	0.4	10366	1	US-08-246- Sequence 5, Applicatio	Sequence 5, Applicatio	2.25e-03
c	45	0.4	10366	1	US-08-453- Sequence 5, Applicatio	Sequence 5, Applicatio	2.25e-03

ALIGNMENTS

RESULT 1
ID PCT-US95-14378-7 STANDARD; DNA; UNC; 6513 BP.
AC xxxxxx

Sequence 7, Application PC/TUS9514378
Sequence 7, Application PC/TUS9514378
GENERAL INFORMATION:

APPLICANT: Warmke, Jeffrey W.
APPLICANT: Hall, Linda
APPLICANT: Feng, Gouping
APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
TITLE OF INVENTION: PARA SODIUM CHANNEL
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:

ADDRESSEE: Roy D. Meredith
STREET: P. O. Box 2000, 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14378
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Meredith, Roy D.
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: 19332 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4678
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 6513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

Db 2101 CCTGCTCGACCAATCACAGCTCGATCATCGGACTAGCAATGGCTGGAGTCA 2160
Qy 2101 CCTGCTCGACCAATCACAGCTCGATCATCGGACTAGCAATGGCTGGAGTCA 2160
Db 2161 CGGAGAAAGCTGGCAAGATTAACATCATGACAAATCCCTTTATCGAGCCCGTCCAGACAC 2220
Qy 2161 CGGAGAAAGCTGGCAAGATTAACATCATGACAAATCCCTTTATCGAGCCCGTCCAGACAC 2220
Db 2221 AAACGGTGGTGTATGATGAAAGATGTGATGGTCTGCTGAATGACATCATCAACAGCCCGCTG 2280
Qy 2221 AAACGGTGGTGTATGAAAGATGTGATGGTCTGCTGAATGACATCATCAACAGCCCGCTG 2280
Db 2281 GTCGGCAGCTGGGCAAGCATCGCGTGTCTCGTTTACTATTTCCACACAGGAGC 2340
Qy 2281 GTCGGCAGCTGGGCAAGCATCGCGTGTCTCGTTTACTATTTCCACACAGGAGC 2340
Db 2341 ATGACGAGATGGGCGGAGCTTCAAGACAAGGCACTCGAAGTGTATCTCAAGGCACTCG 2400
Qy 2341 ATGACGAGATGGGCGGAGCTTCAAGACAAGGCACTCGAAGTGTATCTCAAGGCACTCG 2400
Db 2401 ATGTGTTTGTGTGGGACTGTGCTGGGTTTGGTTGAAATTTTCAGAGTGGGTATCGC 2460
Qy 2401 ATGTGTTTGTGTGGGACTGTGCTGGGTTTGGTTGAAATTTTCAGAGTGGGTATCGC 2460
Db 2461 TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATCAGCTGTGCATTTGTGTCAACAGCA 2520
Qy 2461 TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATCAGCTGTGCATTTGTGTCAACAGCA 2520
Db 2521 TGTTCATGGCAATGATCACCACGATATGAACAAGGAGATGGAACGCGTGTCAAGAGTG 2580
Qy 2521 TGTTCATGGCAATGATCACCACGATATGAACAAGGAGATGGAACGCGTGTCAAGAGTG 2580
Db 2581 GCAACTATTTCTACCCGCCACTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA 2640
Qy 2581 GCAACTATTTCTACCCGCCACTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA 2640
Db 2641 GCCCCAAGTACTATTTCCAGGAGGCTGGAGACTTTCGACTTCATTTATCGTGGCCCTAT 2700
Qy 2641 GCCCCAAGTACTATTTCCAGGAGGCTGGAGACTTTCGACTTCATTTATCGTGGCCCTAT 2700
Db 2701 CGCTATTGGAAGTGGAGTTCGAGGGTGTCCAGGGTGTCTGCGTATTTGCTTTTCGAT 2760
Qy 2701 CGCTATTGGAAGTGGAGTTCGAGGGTGTCCAGGGTGTCTGCGTATTTGCTTTTCGAT 2760
Db 2761 TGCTCGGTGTATTCAACTGGCCAAAGTCTTGGCCACACACTTAATTTACTCATTTTCGATTA 2820
Qy 2761 TGCTCGGTGTATTCAACTGGCCAAAGTCTTGGCCACACACTTAATTTACTCATTTTCGATTA 2820
Db 2821 TGGGACGACCATGGGCGGCTTTGGGTAATCTGACATTTGTACTTTGCAATTAATCATCTTCA 2880
Qy 2821 TGGGACGACCATGGGCGGCTTTGGGTAATCTGACATTTGTACTTTGCAATTAATCATCTTCA 2880
Db 2881 TCTTTGCGGTGATGGAATGCAACTGTTCGGAAGAATTTATCATGATCACAAGGACCGCT 2940
Qy 2881 TCTTTGCGGTGATGGAATGCAACTGTTCGGAAGAATTTATCATGATCACAAGGACCGCT 2940
Db 2941 TTCCGGATGGGACCTGCGCGCTGGAATTCACCGCACTTTATGACAGCTTCATGATCG 3000
Qy 2941 TTCCGGATGGGACCTGCGCGCTGGAATTCACCGCACTTTATGACAGCTTCATGATCG 3000
Db 3001 TGTTCGGGTGCTCTGCGGAGAAATGGATCGAGTCCATGTGGGACTGCAATGACGTGGGCG 3060
Qy 3001 TGTTCGGGTGCTCTGCGGAGAAATGGATCGAGTCCATGTGGGACTGCAATGACGTGGGCG 3060
Db 3061 ATGTCTCGTGCATCCCTTCCTTTGGCCACCGTGTGTCATCGGCAATCTTGTGGTACTTA 3120
Qy 3061 ATGTCTCGTGCATCCCTTCCTTTGGCCACCGTGTGTCATCGGCAATCTTGTGGTACTTA 3120
Db 3121 ACCTTTTCTTAGCCCTTGTGTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGGCCGCACTG 3180
Qy 3121 ACCTTTTCTTAGCCCTTGTGTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGGCCGCACTG 3180
Db 3181 CCGATAACGATACGAATAAAATAGCCGAGGCGCTTCAATCGAATTTGGCCGCTTTAAAGTT 3240

Qy 3181 CCGATAACGATACGAATAAAATAGCCGAGGCGCTTCAATCGAATTTGGCCGATTTAAAGTT 3240
Db 3241 GGGTTAAAGCGTAATATTCCTGATTGTTTCAAGTTAAATACGTAACAAATTTGCAATCAAA 3300
Qy 3241 GGGTTAAAGCGTAATATTCCTGATTGTTTCAAGTTAAATACGTAACAAATTTGCAATCAAA 3300
Db 3301 TAACTGATCAACCAATCAGGTGAGAGCAACACAGATCAGTTGGATTGGAGCGAAGAGC 3360
Qy 3301 TAACTGATCAACCAATCAGGTGAGAGCAACACAGATCAGTTGGATTGGAGCGAAGAGC 3360
Db 3361 ATGCTGCAACGAATCTGGAGCTGGCCACGACGAGATCTCTGCCGACGGCTCATCAAGA 3420
Qy 3361 ATGCTGCAACGAATCTGGAGCTGGCCACGACGAGATCTCTGCCGACGGCTCATCAAGA 3420
Db 3421 AGGGGATCAAGGAGCAGACGCAACTGGAGTGGCCATCGGGGATCGGATGGAATTCACGA 3480
Qy 3421 AGGGGATCAAGGAGCAGACGCAACTGGAGTGGCCATCGGGGATCGGATGGAATTCACGA 3480
Db 3481 TACACGGCGACATGAAGAACAACCAAGCGGAAGAAATCCAAATATCTAAATTAACCAACGA 3540
Qy 3481 TACACGGCGACATGAAGAACAACCAAGCGGAAGAAATCCAAATATCTAAATTAACCAACGA 3540
Db 3541 TGATTGGCAACTCAATTAACCAACCAACACATAGACTGGAAACAGAGCTAAACCATAGAG 3600
Qy 3541 TGATTGGCAACTCAATTAACCAACCAACACATAGACTGGAAACAGAGCTAAACCATAGAG 3600
Db 3601 GTTTGTCTTACAGGACGACGACACTGCCAGCTTAATCTATGATGATGATGATGATGATGATG 3660
Qy 3601 GTTTGTCTTACAGGACGACGACACTGCCAGCTTAATCTATGATGATGATGATGATGATGATG 3660
Db 3661 GACCATTCAAGGACGAGAGCCACAAGGCGCAGCGGAGACGATGGAGGCGGAGGAGAGC 3720
Qy 3661 GACCATTCAAGGACGAGAGCCACAAGGCGCAGCGGAGACGATGGAGGCGGAGGAGAGC 3720
Db 3721 GCGAGCGCCCAAGGAGGATTTAGTCTCGAGGAGAACTGCGAGGAGGCGGCAATGCG 3780
Qy 3721 GCGAGCGCCCAAGGAGGATTTAGTCTCGAGGAGAACTGCGAGGAGGCGGCAATGCG 3780
Db 3781 AGGAGGCGCCCTCGAGGTGATATCATTTATTCATGACACGACGAGGATATCTCGATG 3840
Qy 3781 AGGAGGCGCCCTCGAGGTGATATCATTTATTCATGACACGACGAGGATATCTCGATG 3840
Db 3841 AATATCCAGCTGATTGCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGCTG 3900
Qy 3841 AATATCCAGCTGATTGCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGCTG 3900
Db 3901 ACGATGACTCCCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAAACTTTTCAATTA 3960
Qy 3901 ACGATGACTCCCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAAACTTTTCAATTA 3960
Db 3961 TTGAAATAAATATTTGAAACAGCTGTTATCTACTATGATTTAATGATGATGATGATGATG 4020
Qy 3961 TTGAAATAAATATTTGAAACAGCTGTTATCTACTATGATTTAATGATGATGATGATGATG 4020
Db 4021 TGGCATTAGAAGATGTACATCTGCCAAGACCCACTACTCAGGATATTTTACTATA 4080
Qy 4021 TGGCATTAGAAGATGTACATCTGCCAAGACCCACTACTCAGGATATTTTACTATA 4080
Db 4081 TGGCAGAAATATTTACGGTTATATCTTTTGGAAATGTTAATCAAGTGGTGGCGCTCG 4140
Qy 4081 TGGCAGAAATATTTACGGTTATATCTTTTGGAAATGTTAATCAAGTGGTGGCGCTCG 4140
Db 4141 GCTTCAAGTGTACTTCCACACCGGCTGTTGGCTCGATTTCTGATGATGATGATGATGATG 4200
Qy 4141 GCTTCAAGTGTACTTCCACACCGGCTGTTGGCTCGATTTCTGATGATGATGATGATGATG 4200
Db 4201 CGCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTGGTATTAAGCCCTTCAAGACTA 4260
Qy 4201 CGCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTGGTATTAAGCCCTTCAAGACTA 4260
Db 4261 TGGCAACGCTTAAGAGCACTGAGACCACTACGTGCCATGCTCCCGTATGCGAGGCGATGAGGG 4320

QY 4261 TCGACGTTAAGACACTGAGCACCTACGTGCCATGTCCTCGTATGACGGCATGAGG 4320
Db 4321 TCGTCGTTAATCGGTGGTACAAAGCTATACCGTCCATCTTCAATGTGCTATTTGGTGTG 4380
QY 4321 TCGTCGTTAATCGGTGGTACAAAGCTATACCGTCCATCTTCAATGTGCTATTTGGTGTG 4380
Db 4381 TATATTTTGGCTAATTTTGGCTAATGAGGTGACAGCTTTTCTGCGAAATATTTTA 4440
QY 4381 TATATTTTGGCTAATTTTGGCTAATGAGGTGACAGCTTTTCTGCGAAATATTTTA 4440
Db 4441 AGTGCAGGACATGAATGCGAAGCTCAGCCAGAGATACAAATCGCAATGCT 4500
QY 4441 AGTGCAGGACATGAATGCGAAGCTCAGCCAGAGATACAAATCGCAATGCT 4500
Db 4501 GCAGAGCGAAGACTACAGTGGGTGAATTCAGCATGAATTCGATCATGTAGTAAAG 4560
QY 4501 GCAGAGCGAAGACTACAGTGGGTGAATTCAGCATGAATTCGATCATGTAGTAAAG 4560
Db 4561 CGTATCTGTCCTTTTCCAAAGTGGCCACCTTCAAAGCTGGATACAAATCATGAACGATG 4620
QY 4561 CGTATCTGTCCTTTTCCAAAGTGGCCACCTTCAAAGCTGGATACAAATCATGAACGATG 4620
Db 4621 CTATCGAATCACGAGAGTGGACAGCAACCAATTCGTGAAGGACATCTACATGATT 4680
QY 4621 CTATCGAATCACGAGAGTGGACAGCAACCAATTCGTGAAGGACATCTACATGATT 4680
Db 4681 TATATTCGATTTTCATCATATTTGGATCCTTTTTCACACTCAATCTTTCATTTGGTG 4740
QY 4681 TATATTCGATTTTCATCATATTTGGATCCTTTTTCACACTCAATCTTTCATTTGGTG 4740
Db 4741 TTATCATTTGATAATTTAATGAGCAAAAGAAAAGCAGGTGGATCATTAGAAATGTTCA 4800
QY 4741 TTATCATTTGATAATTTAATGAGCAAAAGAAAAGCAGGTGGATCATTAGAAATGTTCA 4800
Db 4801 TGACAGAAAGTACAGAAAGTACTATATCTATGAAAGAGTGGCTCTTAAAAAACCAT 4860
QY 4801 TGACAGAAAGTACAGAAAGTACTATATCTATGAAAGAGTGGCTCTTAAAAAACCAT 4860
Db 4861 TAAAGCCATTCCAAAGACCAAGTGGCGACCAAGCAATAGTCTTGAATAGTAAACG 4920
QY 4861 TAAAGCCATTCCAAAGACCAAGTGGCGACCAAGCAATAGTCTTGAATAGTAAACG 4920
Db 4921 ATAAGAAATTCGATATAATCAATATGTTATTCATTTGGTCTGAACATGTTTCAACATGACCC 4980
QY 4921 ATAAGAAATTCGATATAATCAATATGTTATTCATTTGGTCTGAACATGTTTCAACATGACCC 4980
Db 4981 TCGATCGTTACGATCGCTCGGACACGTATACGGGCTCTAGACTATCTCAATGCCATAT 5040
QY 4981 TCGATCGTTACGATCGCTCGGACACGTATACGGGCTCTAGACTATCTCAATGCCATAT 5040
Db 5041 TCGTAGTTATTTTCAGTTCCGAATGCTATTAATAAATATTCGCTTTACGATATCACTATT 5100
QY 5041 TCGTAGTTATTTTCAGTTCCGAATGCTATTAATAAATATTCGCTTTACGATATCACTATT 5100
Db 5101 TTATTGACCATGAAATTTTATGATAGTATGTTGCTATTTATCCATCTTAGTCTTG 5160
QY 5101 TTATTGACCATGAAATTTTATGATAGTATGTTGCTATTTATCCATCTTAGTCTTG 5160
Db 5161 TACTTAGCGATATTATCAGAAAGTACTTCGTGTCGCGACCTGCTCCGAGTGGTGGTG 5220
QY 5161 TACTTAGCGATATTATCAGAAAGTACTTCGTGTCGCGACCTGCTCCGAGTGGTGGTG 5220
Db 5221 TGGCGAAAGTGGGCGGTGTCCTTCGACTGTTGAAAGGAGCCAAAGGATTCGACATGCG 5280
QY 5221 TGGCGAAAGTGGGCGGTGTCCTTCGACTGTTGAAAGGAGCCAAAGGATTCGACATGCG 5280
Db 5281 TCTTCGCGTTGGCCATGTCGCTGCGGCCCTGTTCAACATCTGCTGCTGTTCTCTGG 5340
QY 5281 TCTTCGCGTTGGCCATGTCGCTGCGGCCCTGTTCAACATCTGCTGCTGTTCTCTGG 5340
Db 5341 TCATGTTTCATCTTTGCCATTTTTCGCGATGTCGTTCTTTCATGCAAGTGAAGAGAGCG 5400
QY 5341 TCATGTTTCATCTTTGCCATTTTTCGCGATGTCGTTCTTTCATGCAAGTGAAGAGAGCG 5400

Db 5401 GCATTAAACGAGCTTACAACTTCAAGACCTTTGGCCAGAGCATGATCTCTGCTCTTTTCAGA 5460
QY 5401 GCATTAAACGAGCTTACAACTTCAAGACCTTTGGCCAGAGCATGATCTCTGCTCTTTTCAGA 5460
Db 5461 TGTGCGAGTCAAGCGGTTGGGATGGTGTACTGGACGCCATTATCAATGAGGAAGCATGCG 5520
QY 5461 TGTGCGAGTCAAGCGGTTGGGATGGTGTACTGGACGCCATTATCAATGAGGAAGCATGCG 5520
Db 5521 ATCCACCCGACAGCAAAAGCTATCCGGGCAATTTGGTTCAGCGACCGTTTGAATATA 5580
QY 5521 ATCCACCCGACAGCAAAAGCTATCCGGGCAATTTGGTTCAGCGACCGTTTGAATATA 5580
Db 5581 CGTTTCTCTCTCATACCTAGTTTATAAGCTTTTGTAGTATTAATAATGATGATGCTG 5640
QY 5581 CGTTTCTCTCTCATACCTAGTTTATAAGCTTTTGTAGTATTAATAATGATGATGCTG 5640
Db 5641 TCATTCTCGAAGACTATAGTCAGGCCACCCAGGACGTCGAAGGGTCTAACCCAGCAGC 5700
QY 5641 TCATTCTCGAAGACTATAGTCAGGCCACCCAGGACGTCGAAGGGTCTAACCCAGCAGC 5700
Db 5701 ACTAGCATGATCTACTATGAGATCTGCGAGCAATTCGATCCGAGGGCACCAGTACATAC 5760
QY 5701 ACTAGCATGATCTACTATGAGATCTGCGAGCAATTCGATCCGAGGGCACCAGTACATAC 5760
Db 5761 GCTATGATCAGCTGTCCGAATTCCTGACGCTACTGAGCCCCCTCGATCCCAAAAC 5820
QY 5761 GCTATGATCAGCTGTCCGAATTCCTGACGCTACTGAGCCCCCTCGATCCCAAAAC 5820
Db 5821 CGAACAGTACAAGATCATATCGATGGACATACCCATCTGTGCGGGTGAACCTCATGTACT 5880
QY 5821 CGAACAGTACAAGATCATATCGATGGACATACCCATCTGTGCGGGTGAACCTCATGTACT 5880
Db 5881 CGCTCGACATCTCGACGCCCTTACGAAAGACTTCTTTGCGCGAAGGGCAATCCGATAG 5940
QY 5881 CGCTCGACATCTCGACGCCCTTACGAAAGACTTCTTTGCGCGAAGGGCAATCCGATAG 5940
Db 5941 AGGAGCGGTGAGATTGGTGAGATAGCGGCCCGCCGGATACGGAGGGTACAGGCCCG 6000
QY 5941 AGGAGCGGTGAGATTGGTGAGATAGCGGCCCGCCGGATACGGAGGGTACAGGCCCG 6000
Db 6001 TCTCATCAACGCTGTGGCGTGAAGAGTACTGCGCCCGCTATTCAGCACGCGCT 6060
QY 6001 TCTCATCAACGCTGTGGCGTGAAGAGTACTGCGCCCGCTATTCAGCACGCGCT 6060
Db 6061 GCGGAAAGCAAGCGCGCGGAGGAGTGGTCTTTGAGCCGGATACGATCATG 6120
QY 6061 GCGGAAAGCAAGCGCGCGGAGGAGTGGTCTTTGAGCCGGATACGATCATG 6120
Db 6121 GCGATGGCGGTGATCCGGATCCGGGACCCGCGCCCGATGAAGCAACGACGCGCATG 6180
QY 6121 GCGATGGCGGTGATCCGGATCCGGGACCCGCGCCCGATGAAGCAACGACGCGCATG 6180
Db 6181 CGCCCGCTGGTGGAGATGTTTAAAGTACTGCAAGAGGAGTCCCGATGCCGATG 6240
QY 6181 CGCCCGCTGGTGGAGATGTTTAAAGTACTGCAAGAGGAGTCCCGATGCCGATG 6240
Db 6241 AGAGTAAATGATAGTCCGGTGAAGTACGCGCGCGCGGACGACGACGACGACGAG 6300
QY 6241 AGAGTAAATGATAGTCCGGTGAAGTACGCGCGCGCGGACGACGACGACGACGAG 6300
Db 6301 CGCGCGCGCGGACGACGACGCGGGGAGTCCGCGAGCGGGTAGCGCCGGGCGACAGA 6360
QY 6301 CGCGCGCGCGGACGACGACGCGGGGAGTCCGCGAGCGGGTAGCGCGGGGCGACAGA 6360
Db 6361 CGCGCGCTTCTGTTGAGAGCGAGGGTTCGTGACGAGAACCGGCCACAGGTGGTCACTC 6420
QY 6361 CGCGCGCTTCTGTTGAGAGCGAGGGTTCGTGACGAGAACCGGCCACAGGTGGTCACTC 6420
Db 6421 ACTTCGCGATCGCGAGCATCAGTCCGCGACGCGGATGCTGAGCAGCGCTCGCCCCC 6480
QY 6421 ACTTCGCGATCGCGAGCATCAGTCCGCGACGCGGATGCTGAGCAGCGCTCGCCCCC 6480

Db 6481 CCTCCAAAGATCGACGGAGTATTAGCTCTAGA 6513
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 6481 CCTCCAGATCGACGGAGTATTAGCTCTAGA 6513
RESULT 2
ID US-08-337-339-7 STANDARD; DNA; UNC; 6513 BP.
AC xxxxxx
DT
DE Sequence 7, Application US/08337339
CC Sequence 7, Application US/08337339
CC Patent No. 5593864
CC GENERAL INFORMATION:
CC APPLICANT: Warmke, Jeffrey W.
CC APPLICANT: Hall, Linda
CC APPLICANT: Feng, Gouping
CC APPLICANT: Van Der Ploeg, Leonardus
CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
CC TITLE OF INVENTION: PARA SODIUM CHANNEL
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: John W. Wallen III
CC STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CC CITY: Rahway
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07065-0900
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/337,339
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Wallen III, John W.
CC REGISTRATION NUMBER: 35,403
CC REFERENCE/DOCKET NUMBER: 19332
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (908) 594-3905
CC TELEFAX: (908) 594-4720
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6513 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC SEQUENCE 6513 BP; 1661 A; 1548 C; 1702 G; 1582 T; 0 OTHER.

Query Match 100.0%; Score 6513; DB 1; Length 6513;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TCTAGACGTTGGCCGATAGACAAATGACAGAAGATTCGACTCGATATCTGAGGAAGAAC 60
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 1 TCTAGACGTTGGCCGATAGACAAATGACAGAAGATTCGACTCGATATCTGAGGAAGAAC 60

Db 61 GCAGTTTGTTCGTCCTTACCCCGCAATCATTTGGTCAATCGAACAAAGCATTCGCG 120
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 61 GCAGTTTGTTCGTCCTTACCCCGCAATCATTTGGTCAATCGAACAAAGCATTCGCG 120

Db 121 CTGAACATGAAAGCAGAGGAGCTGGAAGAAAGAGAGCCGAGGAGAGTGCAGCAT 180
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 121 CTGAACATGAAAGCAGAGGAGCTGGAAGAAAGAGAGCCGAGGAGAGTGCAGCAT 180

Db 181 ATGTGCGCAAGAAAAACAAAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGTGC 240
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 181 ATGTGCGCAAGAAAAACAAAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGTGC 240

Db 241 CACAACCCGATCCTACATCTGACAGGCTGTGCCAATACCTGTCGATTGCGAGGCGAGCT 300
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

QY 241 CACAACCCGATCCTACACTTGAACAGGCTGCAATACCTGTTTCGATTGCGAGGCGAGCT 300
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 301 TCCCGCGGAATGGCCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 301 TCCCGCGGAATGGCCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 361 TGACATTGCTAGTTGTAAGCAAGAAAGATATTTTCGCTTTTCTGCAATCAAAAGCAA 420
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 361 TGACATTGCTAGTTGTAAGCAAGAAAGATATTTTCGCTTTTCTGCAATCAAAAGCAA 420
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 421 TGTGATGCTCGATCCATTCATCCGATCGTCTGCGGCAATTTACATTTCTAGTGCATC 480
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 421 TGTGATGCTCGATCCATTCATCCGATCGTCTGCGGCAATTTACATTTCTAGTGCATC 480
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 481 CATTATTTTCCCTATTTCATCATCAACCAATTCCTCGTCAACTGCTGATGATAATGC 540
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 481 CATTATTTTCCCTATTTCATCATCAACCAATTCCTCGTCAACTGCTGATGATAATGC 540
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 541 CGACAAGCCACCGTTGAGTCCACTGAGTGATATTCACCGGAATCTACACATTTGAAT 600
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 541 CGACAAGCCACCGTTGAGTCCACTGAGTGATATTCACCGGAATCTACACATTTGAAT 600
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 601 CAGCTGTTAAAGTATGACGACGAGTTTCATTTTATGCCGTTTACGTATCTTAGAGATG 660
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 601 CAGCTGTTAAAGTATGACGACGAGTTTCATTTTATGCCGTTTACGTATCTTAGAGATG 660
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 661 CATGGAATTGGCTGACTTCGTAGTAAATAGCTTTAGCTTATGACCATGGTATAGATT 720
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 661 CATGGAATTGGCTGACTTCGTAGTAAATAGCTTTAGCTTATGACCATGGTATAGATT 720
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 721 TAGTAATCTAGCAGCCCTCGAAGCGTTTAGGGTCTGCGAGCGCTTAAACACCTAGCCA 780
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 721 TAGTAATCTAGCAGCCCTCGAAGCGTTTAGGGTCTGCGAGCGCTTAAACACCTAGCCA 780
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 781 TTGTGCCAGGCTTGAAGACCATCTCGCGCCGCTATCGAATCGGTGAAGAAATCTGCGCG 840
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 781 TTGTGCCAGGCTTGAAGACCATCTCGCGCCGCTATCGAATCGGTGAAGAAATCTGCGCG 840
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 841 ATGTGATTATCTGACCATGTTCTCCCTGTCGGTGTTCGGCTTATGGCTACAGATCT 900
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 841 ATGTGATTATCTGACCATGTTCTCCCTGTCGGTGTTCGGCTTATGGCTACAGATCT 900
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 901 ATATGGCGTCTCACCGAGAAGTGCATCAAGAAGTTCCCGCTGGAGCGTTCTTGGGSCA 960
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 901 ATATGGCGTCTCACCGAGAAGTGCATCAAGAAGTTCCCGCTGGAGCGTTCTTGGGSCA 960
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 961 ATCTGACGAGCAACTGGGACTATCACATCCCAATAGCTCCCAATGTTATCCGAGG 1020
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 961 ATCTGACGAGCAACTGGGACTATCACATCCCAATAGCTCCCAATGTTATCCGAGG 1020
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 1021 ACAGGGCATCTCATTTCCGTTATCGGCAATATATCCGGTGGGCAATGCGGAGCAGC 1080
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 1021 ACAGGGCATCTCATTTCCGTTATCGGCAATATATCCGGTGGGCAATGCGGAGCAGC 1080
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 1081 ATTACGTTGCTCGAGGGTTTGGTCCGAATCCGAATTTATGGCTACACCAAGCTTCGATT 1140
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 1081 ATTACGTTGCTCGAGGGTTTGGTCCGAATCCGAATTTATGGCTACACCAAGCTTCGATT 1140
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 1141 CGTTCGATGGCTTTTCTGTCGCCCTTCGGCTGATGACACAGACTTCTGAGGAGATC 1200
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 1141 CGTTCGATGGCTTTTCTGTCGCCCTTCGGCTGATGACACAGACTTCTGAGGAGATC 1200
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 1201 TGTACAGCTGGTCTGCGCGCCCGGACCATGGACATGCTCTTCTTTATAGTCATCA 1260
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 1201 TGTACAGCTGGTCTGCGCGCCCGGACCATGGACATGCTCTTCTTTATAGTCATCA 1260
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 1261 TCTTCCCTAGGTTCTATCTTCTGTAATTTGATTTTGGCCATTGTTGCCATGTCGTATG 1320
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
QY 1261 TCTTCCCTAGGTTCTATCTTCTGTAATTTGATTTTGGCCATTGTTGCCATGTCGTATG 1320
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Db 1321 ACGAATTCGAAGGAGGCGGAAGAAAGAGGCTGCCGAAGAGGAGGCGGATCGTGAAG 1380
CC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

QY 1321 ACGAATTGCAAGGAGCGCCGAAGAAGAGAGCTGCCGAAGAGGAGCGCATACGTGAAG 1380
Db 1381 CGGAAGAAGCTCCGCGCCGAAGCGGCCAAGCTGAGAGAGCGGCCAATGCGCAGGCTC 1440
QY 1381 CGGAAGAAGCTCCGCGCCGAAGCGGCCAAGCTGAGAGAGCGGCCAATGCGCAGGCTC 1440
Db 1441 AGGCAGCAGCGATCGGGCTCGCGCGGAAGAGAGCTGCACTGCGGAAATGGCCAAGA 1500
QY 1441 AGGCAGCAGCGATCGGGCTCGCGCGGAAGAGAGCTGCACTGCGGAAATGGCCAAGA 1500
Db 1501 GTCCGACGATATCTTCATCAGCTATGAGCTATTTGTTGGCGCGGAGAGGCAACGATG 1560
QY 1501 GTCCGACGATATCTTCATCAGCTATGAGCTATTTGTTGGCGCGGAGAGGCAACGATG 1560
Db 1561 ACAACAACAAGAGAAGATGTCCATTCCGAGCGTCGAGGTGAGAGTCGGGTGAGCG 1620
QY 1561 ACAACAACAAGAGAAGATGTCCATTCCGAGCGTCGAGGTGAGAGTCGGGTGAGCG 1620
Db 1621 TTATACAAGACAAACAGCAGCACTACACAGACACACCAAGCTACCAAAAGTTCTGAAGTGA 1680
QY 1621 TTATACAAGACAAACAGCAGCACTACACAGACACACCAAGCTACCAAAAGTTCTGAAGTGA 1680
Db 1681 GCACGACATCCTTATCCTTTACCTGTGTTACCGTCTTAAACATACGCAAGGGATCACGTAGT 1740
QY 1681 GCACGACATCCTTATCCTTTACCTGTGTTACCGTCTTAAACATACGCAAGGGATCACGTAGT 1740
Db 1741 CTCACAAGTACAGTACGGAACGAGCGTGGCGCTTTGGTATACCCGGTAGCGATCGTA 1800
QY 1741 CTCACAAGTACAGTACGGAACGAGCGTGGCGCTTTGGTATACCCGGTAGCGATCGTA 1800
Db 1801 AGCCATTGGTATGTCAACATATCAGGATGCCAGCAGCACTTGCCCTATGCCGAGCACT 1860
QY 1801 AGCCATTGGTATGTCAACATATCAGGATGCCAGCAGCACTTGCCCTATGCCGAGCACT 1860
Db 1861 CGAATCCGCTACCCCGATGTCGGAAGAGATGGGCCATCATAGTCCCGGTACTATG 1920
QY 1861 CGAATCCGCTACCCCGATGTCGGAAGAGATGGGCCATCATAGTCCCGGTACTATG 1920
Db 1921 GCAATCTAGGCTCCCGACACTCATCGTATACCTCGCATCAGTCCCGAATATCGTATACCT 1980
QY 1921 GCAATCTAGGCTCCCGACACTCATCGTATACCTCGCATCAGTCCCGAATATCGTATACCT 1980
Db 1981 CACATGGCGATCTACTCGCGCGCATGGCGTATGGCGCTCAGCACAATGACCAAGGAGA 2040
QY 1981 CACATGGCGATCTACTCGCGCGCATGGCGTATGGCGCTCAGCACAATGACCAAGGAGA 2040
Db 2041 GCAAAATTGGCAACCGCAACACACGCAATCAATCAGTGGCGCCACCAATGGCGGACCA 2100
QY 2041 GCAAAATTGGCAACCGCAACACACGCAATCAATCAGTGGCGCCACCAATGGCGGACCA 2100
Db 2101 CCGTCTGGACACCAATCAAGCTCGATCATCGGACTACGAAATGGCCCTGGAGTGA 2160
QY 2101 CCGTCTGGACACCAATCAAGCTCGATCATCGGACTACGAAATGGCCCTGGAGTGA 2160
Db 2161 CGGACCAAGCTGGCAAGATTAAACATCATGACAATCCTTTTATCGAGCCCGTCCAGACAC 2220
QY 2161 CGGACCAAGCTGGCAAGATTAAACATCATGACAATCCTTTTATCGAGCCCGTCCAGACAC 2220
Db 2221 AAACGGTGGTGTATGAAGATGTGATGGTCTGAATGACATCATCGAACAAGCGCGCTG 2280
QY 2221 AAACGGTGGTGTATGAAGATGTGATGGTCTGAATGACATCATCGAACAAGCGCGCTG 2280
Db 2281 GTCGGCACAGTCGGGCAAGCGATCGCGGTGTCTCCGTTTACTATTTCGAACAGAGGAG 2340
QY 2281 GTCGGCACAGTCGGGCAAGCGATCGCGGTGTCTCCGTTTACTATTTCGAACAGAGGAG 2340
Db 2341 ATGACAGAGATGGCGCGAGCTTCAAGACAAAGCACTCGAAGTGAATTCGAAAGGCGATCG 2400
QY 2341 ATGACAGAGATGGCGCGAGCTTCAAGACAAAGCACTCGAAGTGAATTCGAAAGGCGATCG 2400
Db 2401 ATGTGTTTTGTGTGGGACTGTGTCTGGGTTTGGTTGAAATTTACGAGTGGGTATCCG 2460
QY 2401 ATGTGTTTTGTGTGGGACTGTGTCTGGGTTTGGTTGAAATTTACGAGTGGGTATCCG 2460

Db 2461 TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATCACGCTGTGCATTTGGTCAACACGA 2520
QY 2461 TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATCACGCTGTGCATTTGGTCAACACGA 2520
Db 2521 TGTTCATGGCAATGGATCACCACGATATGAACAAGGAGATGAACGCGTGTCAAGAGTG 2580
QY 2521 TGTTCATGGCAATGGATCACCACGATATGAACAAGGAGATGAACGCGTGTCAAGAGTG 2580
Db 2581 GCAACTATTTCTTACCCTCCACCTTTGCGATCGAGGCCACCATGAAGCTAATGGCCATGA 2640
QY 2581 GCAACTATTTCTTACCCTCCACCTTTGCGATCGAGGCCACCATGAAGCTAATGGCCATGA 2640
Db 2641 GCGCCAAAGTACTATTTCCAGGAGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTAT 2700
QY 2641 GCGCCAAAGTACTATTTCCAGGAGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTAT 2700
Db 2701 CGCTATTGGAACTGGGACTCGAGGCTGTCAGGGTCTCTCGTATTTGGTTCCTTTCCGAT 2760
QY 2701 CGCTATTGGAACTGGGACTCGAGGCTGTCAGGGTCTCTCGTATTTGGTTCCTTTCCGAT 2760
Db 2761 TGCTCGTGTATTCAAACTGGCCAACTCTTGCCCCACACTTAATTTACTCATTTCCGATTA 2820
QY 2761 TGCTCGTGTATTCAAACTGGCCAACTCTTGCCCCACACTTAATTTACTCATTTCCGATTA 2820
Db 2821 TGGGACGACCATGGGCGCTTTGGGTAATCTGACATTTTGTACTTTTGCATTATCATCTTCA 2880
QY 2821 TGGGACGACCATGGGCGCTTTGGGTAATCTGACATTTTGTACTTTTGCATTATCATCTTCA 2880
Db 2881 TCTTTGCGGTGATGGGAATGCAACTGTTTCGGAAGAATTTATCATGATCACAAGGACCGCT 2940
QY 2881 TCTTTGCGGTGATGGGAATGCAACTGTTTCGGAAGAATTTATCATGATCACAAGGACCGCT 2940
Db 2941 TTCGGATGGCGACCTGCGCGCTGGAACCTTCACCGACTTATGCGACAGCTTCATGATCG 3000
QY 2941 TTCGGATGGCGACCTGCGCGCTGGAACCTTCACCGACTTATGCGACAGCTTCATGATCG 3000
Db 3001 TGTTCGCGGTGCTCTGCGGAGAAATGGATCGAGTCCATGCGGACTGCTACGCGGCGG 3060
QY 3001 TGTTCGCGGTGCTCTGCGGAGAAATGGATCGAGTCCATGCGGACTGCTACGCGGCGG 3060
Db 3061 ATGTCTCGTGTATCCCTTCCTTTGGCCACCGTTGTCATGGCAATCTTTGGTACTTA 3120
QY 3061 ATGTCTCGTGTATCCCTTCCTTTGGCCACCGTTGTCATGGCAATCTTTGGTACTTA 3120
Db 3121 ACCTTTTCTTAGCCCTTGCTTTTGTCCAATTTTGGCTCATCTAGCTTATCAGCGCGACTG 3180
QY 3121 ACCTTTTCTTAGCCCTTGCTTTTGTCCAATTTTGGCTCATCTAGCTTATCAGCGCGACTG 3180
Db 3181 CGGATAACGATACGAATAAAATAGCCGAGGCTTCAATCGAATTTGCGCGATTAAAAAGTT 3240
QY 3181 CGGATAACGATACGAATAAAATAGCCGAGGCTTCAATCGAATTTGCGCGATTAAAAAGTT 3240
Db 3241 GGGTTAAAGCGTAATTTGCTGATTGTTTCAAGTTAATACGTAACAAATGACAAATCAAA 3300
QY 3241 GGGTTAAAGCGTAATTTGCTGATTGTTTCAAGTTAATACGTAACAAATGACAAATCAAA 3300
Db 3301 TAAAGTATCAACCATCAGGTGAGAGGACCAACAGATCAGTTGGATTGGAGCGAAGAGC 3360
QY 3301 TAAAGTATCAACCATCAGGTGAGAGGACCAACAGATCAGTTGGATTGGAGCGAAGAGC 3360
Db 3361 ATGTGTACAACGAACCTGGAGCTGGGCCACGACGAGATCCTCGCCGACGCGCTCATCAAGA 3420
QY 3361 ATGTGTACAACGAACCTGGAGCTGGGCCACGACGAGATCCTCGCCGACGCGCTCATCAAGA 3420
Db 3421 AGGGATCAAGGAGCAGACGCAACTGGAGGTGGCCATCGGGGATCGGATGGAATTCAGA 3480
QY 3421 AGGGATCAAGGAGCAGACGCAACTGGAGGTGGCCATCGGGGATCGGATGGAATTCAGA 3480
Db 3481 TACACGGGACATGAAGAACCAACAGCCGAAGAAATCCAAATATCTAAATACGCAACGA 3540
QY 3481 TACACGGGACATGAAGAACCAACAGCCGAAGAAATCCAAATATCTAAATACGCAACGA 3540

Db 3541 TGATTGGCAACTCAATTAACCAACCAAGACAAATAGACTGGACAGGAGCTAAACCATAGAG 3600
QY 3541 TGATTGGCAACTCAATTAACCAACCAAGACAAATAGACTGGACAGGAGCTAAACCATAGAG 3600
Db 3601 GTTTGTCTCTACAGGACGACGACACTGCCAGCATTAACCTCATATGTTAGGACATAAGAAATC 3660
QY 3601 GTTTGTCTCTACAGGACGACGACACTGCCAGCATTAACCTCATATGTTAGGACATAAGAAATC 3660
Db 3661 GACCATTCAAGGACGAGAGCCACAAGGCGAGCGCCGAGAGGATGGAGGGGAGGAGAAGC 3720
QY 3661 GACCATTCAAGGACGAGAGCCACAAGGCGAGCGCCGAGAGGATGGAGGGGAGGAGAAGC 3720
Db 3721 GCGACGCCACGACGAGGATTTAGTCTCGACGAGGAACCTGGACGAGGAGGCGCAATGCG 3780
QY 3721 GCGACGCCACGACGAGGATTTAGTCTCGACGAGGAACCTGGACGAGGAGGCGCAATGCG 3780
Db 3781 AGGAGGCCCGCTCGACGGGTGATATCATTTATTCATGCACACGACGAGGATATCTCGATG 3840
QY 3781 AGGAGGCCCGCTCGACGGGTGATATCATTTATTCATGCACACGACGAGGATATCTCGATG 3840
Db 3841 AATATCCAGCTGATTTGCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTG 3900
QY 3841 AATATCCAGCTGATTTGCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTG 3900
Db 3901 ACGATGACTGCCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAACACTTTTCAATATA 3960
QY 3901 ACGATGACTGCCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAACACTTTTCAATATA 3960
Db 3961 TTGAAATAAATATTTTGAACACGCTGTATCATCTATGATTTAATGAGTAGCTTAGCTT 4020
QY 3961 TTGAAATAAATATTTTGAACACGCTGTATCATCTATGATTTAATGAGTAGCTTAGCTT 4020
Db 4021 TGGCATTAGAAGATGTACATCTGCCCAAAAGACCCACTACTCAGGATATTTTATACATA 4080
QY 4021 TGGCATTAGAAGATGTACATCTGCCCAAAAGACCCACTACTCAGGATATTTTATACATA 4080
Db 4081 TGGACAGAAATTTACGGTTATATCTTCTTGGAAATGTTAATCAAGTGGTGGCGCTCG 4140
QY 4081 TGGACAGAAATTTACGGTTATATCTTCTTGGAAATGTTAATCAAGTGGTGGCGCTCG 4140
Db 4141 GCTTCAAGTGTACTTCAACCAACGCTGGTGTGGCTGCTGATTTGCTGATTCGTATGCTAT 4200
QY 4141 GCTTCAAGTGTACTTCAACCAACGCTGGTGTGGCTGCTGATTTGCTGATTCGTATGCTAT 4200
Db 4201 CGCTTATCAACTCGTTGCTTCACTTGTGGAGCTGGTGGTATTCAAGCCCTTCAAGACTA 4260
QY 4201 CGCTTATCAACTCGTTGCTTCACTTGTGGAGCTGGTGGTATTCAAGCCCTTCAAGACTA 4260
Db 4261 TGGCAAGCTTAAAGACACTGAGACCACTACGTGCCATGTCCCGTATGAGGGCATGAGGG 4320
QY 4261 TGGCAAGCTTAAAGACACTGAGACCACTACGTGCCATGTCCCGTATGAGGGCATGAGGG 4320
Db 4321 TCGTCGTTAATGCGCTGTACAACTATACCGTCCATCTTCAATGCTATTTGCTGTC 4380
QY 4321 TCGTCGTTAATGCGCTGTACAACTATACCGTCCATCTTCAATGCTATTTGCTGTC 4380
Db 4381 TAATATTTTGGCTAATTTTGGCCATAATGGGTACAGCTTTTGGTGGAAATATTTTA 4440
QY 4381 TAATATTTTGGCTAATTTTGGCCATAATGGGTACAGCTTTTGGTGGAAATATTTTA 4440
Db 4441 AGTGGAGGACATGAATGGCAGAGCTACGAGCTACGAGATCATACCAATCGCAATGCGCT 4500
QY 4441 AGTGGAGGACATGAATGGCAGAGCTACGAGCTACGAGATCATACCAATCGCAATGCGCT 4500
Db 4501 GCGAGAGGAGAACTACACGCTGGGTGAATTCAGCAATGAATTTCCATCATCTAGGTAAACG 4560
QY 4501 GCGAGAGGAGAACTACACGCTGGGTGAATTCAGCAATGAATTTCCATCATCTAGGTAAACG 4560
Db 4561 CGTATCTGCTCTTTTCCAACTGGCCACTTCAAGGCTGGATCAAAATCATGAACGATG 4620
QY 4561 CGTATCTGCTCTTTTCCAACTGGCCACTTCAAGGCTGGATCAAAATCATGAACGATG 4620
Db 4621 CTATCGATTACGAGAGGTGGACAAGCAACCAATTCGTGAAACGAACATCTACATGTATT 4680

QY 4621 CTATCGATTACGAGAGGTGGACAAGCAACCAATTCGTGAAACGAACATCTACATGTATT 4680
Db 4681 TATATTTCTGATTTCTTCATCATATTTGGATCTCTTTTCACACCAATCTCTTCATTGGTG 4740
QY 4681 TATATTTCTGATTTCTTCATCATATTTGGATCTCTTTTCACACCAATCTCTTCATTGGTG 4740
Db 4741 TATATTTCTGATTTCTTCATCATATTTGGATCTCTTTTCACACCAATCTCTTCATTGGTG 4800
QY 4741 TATATTTCTGATTTCTTCATCATATTTGGATCTCTTTTCACACCAATCTCTTCATTGGTG 4800
Db 4801 TGACAGAAATTCAGAAAGTACTATACTGCTATGAAAAAGATGGGCTCTAAAAAACCAT 4860
QY 4801 TGACAGAAATTCAGAAAGTACTATACTGCTATGAAAAAGATGGGCTCTAAAAAACCAT 4860
Db 4861 TAAAGCCATTTCCAAGACCAAGGTGGCGACCAAGCAATAGTCTTTGAAATAGTAACCG 4920
QY 4861 TAAAGCCATTTCCAAGACCAAGGTGGCGACCAAGCAATAGTCTTTGAAATAGTAACCG 4920
Db 4921 ATAGAAATTCGATATAATCATTTATTTATTTGCTGTAACATGTTCCACCATGACC 4980
QY 4921 ATAGAAATTCGATATAATCATTTATTTATTTGCTGTAACATGTTCCACCATGACC 4980
Db 4981 TCGATCGTTACGATGCGTCCGACACGATATAACGGGTCTTAGACTATCTCAATGCGGAT 5040
QY 4981 TCGATCGTTACGATGCGTCCGACACGATATAACGGGTCTTAGACTATCTCAATGCGGAT 5040
Db 5041 TCGTAGTATTTTTCAGTTCCGAATGCTATTTAAAAATATTTCGCTTTACGATATCACATTT 5100
QY 5041 TCGTAGTATTTTTCAGTTCCGAATGCTATTTAAAAATATTTCGCTTTACGATATCACATTT 5100
Db 5101 TTTATGACCATGGAATTTATTTGATGATGATGTTGTCATTTTATTCATCTTAGGCTTG 5160
QY 5101 TTTATGACCATGGAATTTATTTGATGATGATGTTGTCATTTTATTCATCTTAGGCTTG 5160
Db 5161 TACTTAGCGATATATCGAAGTACTTCTGTCGCGACCCCTGCTCCGAGTGGTGGTG 5220
QY 5161 TACTTAGCGATATATCGAAGTACTTCTGTCGCGACCCCTGCTCCGAGTGGTGGTG 5220
Db 5221 TGGGAAAGTGGGCGGTCTCTTCGACTGTTGAAGGAGCAAGGGCATTCGGACACTGC 5280
QY 5221 TGGGAAAGTGGGCGGTCTCTTCGACTGTTGAAGGAGCAAGGGCATTCGGACACTGC 5280
Db 5281 TCTTCGCGTTGGCCATGCTGCTGCCGCCCTGTTTCAACATCTGCTGCTGCTCTG 5340
QY 5281 TCTTCGCGTTGGCCATGCTGCTGCCGCCCTGTTTCAACATCTGCTGCTGCTCTG 5340
Db 5341 TCATGTTTCATCTTTGGCCATTTTGGCCATGCTGCTTTCATGCGAGTGAAGAGAGCG 5400
QY 5341 TCATGTTTCATCTTTGGCCATTTTGGCCATGCTGCTTTCATGCGAGTGAAGAGAGCG 5400
Db 5401 GCATTAACGACGCTACAACCTTCAAGACCTTGGCCAGAGCATGATCCTGCTCTTTCAGA 5460
QY 5401 GCATTAACGACGCTACAACCTTCAAGACCTTGGCCAGAGCATGATCCTGCTCTTTCAGA 5460
Db 5461 TGTGCGAGCTCAGCGGTTGGGATGTTGCTGAGCGCCATTTCAATGAGGAAACATGCG 5520
QY 5461 TGTGCGAGCTCAGCGGTTGGGATGTTGCTGAGCGCCATTTCAATGAGGAAACATGCG 5520
Db 5521 ATCCACCCGACGAGCAAAAGGCTATCCGGCAATTTGTTGTCAGCGACCGTTTGAATAA 5580
QY 5521 ATCCACCCGACGAGCAAAAGGCTATCCGGCAATTTGTTGTTTCCAGCGACCGTTTGAATAA 5580
Db 5581 CGTTTCTCTCTCATCTCTATAGTATTAAGCTTTTGTAGTATTAATATGATGCTGCTG 5640
QY 5581 CGTTTCTCTCTCATCTCTATAGTATTAAGCTTTTGTAGTATTAATATGATGCTGCTG 5640
Db 5641 TCATTTCTCGAACTATAGTCAGGCCACCGAGGAGTGAAGAGGCTTAACCCAGCAGC 5700
QY 5641 TCATTTCTCGAACTATAGTCAGGCCACCGAGGAGTGAAGAGGCTTAACCCAGCAGC 5700
Db 5701 ACTACGACATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGCGACCGATACATAC 5760

QY 5701 ACTAGACATGTACTATGAGATCTGGCAGCAATTCCGATCCGAGGGCACCAGTACATAC 5760
Db 5761 GCTATGATCAGCTGTCCGAATTCCTGGACGTAGGAGCCCGCTGCAGATCCACAAAC 5820
QY 5761 GCTATGATCAGCTGTCCGAATTCCTGGACGTAGGAGCCCGCTGCAGATCCACAAAC 5820
Db 5821 CGAACAGTACAGATCATATCGATGGACATACCCATCTGTCCGGGTGACCTCATGTACT 5880
QY 5821 CGAACAGTACAGATCATATCGATGGACATACCCATCTGTCCGGGTGACCTCATGTACT 5880
Db 5881 GCGTCGACATCTCCAGCCCTTACGAAGACTTCTTTCGCGGGAAGGSCAATCCGATAG 5940
QY 5881 GCGTCGACATCTCCAGCCCTTACGAAGACTTCTTTCGCGGGAAGGSCAATCCGATAG 5940
Db 5941 AGGAGACGGGTGAGATTGGTGAAGTAGGGCCCGCCGCGATACGAGGGCTACGAGCCCG 6000
QY 5941 AGGAGACGGGTGAGATTGGTGAAGTAGGGCCCGCCGCGATACGAGGGCTACGAGCCCG 6000
Db 6001 TCTCATCAACGCTGTGGGTGACGTGAGGAGTACTTGGCCCGGGCTAATCCAGACGGCT 6060
QY 6001 TCTCATCAACGCTGTGGGTGACGTGAGGAGTACTTGGCCCGGGCTAATCCAGACGGCT 6060
Db 6061 GCGCAAGCACAAAGCGCGCGGAGGAGTGGTCTTTGAGCCGGATACGGATCATG 6120
QY 6061 GCGCAAGCACAAAGCGCGCGGAGGAGTGGTCTTTGAGCCGGATACGGATCATG 6120
Db 6121 GCGATGGCGGTGATCCGGATCCGGGACCCGGCCCGCGATGAAGCAACGAGCGCGATG 6180
QY 6121 GCGATGGCGGTGATCCGGATCCGGGACCCGGCCCGCGATGAAGCAACGAGCGCGATG 6180
Db 6181 GCGCCGCTGGTGGATGGTAGTGTAACTGAGTACTGAGAGGAGCTGCCGATGCCGATG 6240
QY 6181 GCGCCGCTGGTGGATGGTAGTGTAACTGAGTACTGAGAGGAGCTGCCGATGCCGATG 6240
Db 6241 AGAGTAATGTAATAGTCCGGGTGAGGATGCAAGCGCGCGCGCAGCAGCAGCAGCAG 6300
QY 6241 AGAGTAATGTAATAGTCCGGGTGAGGATGCAAGCGCGCGCGCAGCAGCAGCAGCAG 6300
Db 6301 CGCGCGCGCGCGGACGACGAGCGCGGGAAGTCCGCGAGCGGGTACGCGCGCGGACAGA 6360
QY 6301 CGCGCGCGCGCGGACGACGAGCGCGGGAAGTCCGCGAGCGGGTACGCGCGCGGACAGA 6360
Db 6361 CGCGCGGTCTCGTGAGAGCGAGGGTTCGTGACCAAGAACGGCCACAGGTGTCATCC 6420
QY 6361 CGCGCGGTCTCGTGAGAGCGAGGGTTCGTGACCAAGAACGGCCACAGGTGTCATCC 6420
Db 6421 ACTCGGATCGCGGAGCATCAGTCGCGCAGCGCGGATGCTTGAGCCAGGCTCCGCCCC 6480
QY 6421 ACTCGGATCGCGGAGCATCAGTCGCGCAGCGCGGATGCTTGAGCCAGGCTCCGCCCC 6480
Db 6481 CCTCCAGATCGCGGAGTATTAGCTCTAGA 6513
QY 6481 CCTCCAGATCGCGGAGTATTAGCTCTAGA 6513

RESULT 3
ID US-08-724-095-7 STANDARD; DNA; UNC; 6513 BP.
AC xxxxxx

DE Sequence 7, Application US/08724095
CC Sequence 7, Application US/08724095
CC Patent No. 5688917

CC GENERAL INFORMATION:
CC APPLICANT: Warmke, Jeffrey W.
CC APPLICANT: Hall, Linda
CC APPLICANT: Feng, Gouping
CC APPLICANT: Van Der Ploeg, Leonardus
CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: J. Mark Hand - Merck & Co., Inc.
CC STREET: P.O. Box 2000 - 126 E. Lincoln Avenue

CC CITY: Rahway
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07065-0907
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: FASTseq. Version #1.d5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/724,095
CC FILING DATE:
CC CLASSIFICATION: 536
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hand, J. Mark
CC REGISTRATION NUMBER: 36,545
CC REFERENCE/DOCKET NUMBER: 19332DA
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (908) 594-3905
CC TELEFAX: (908) 594-4720
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6513 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.

Query Match 100.0%; Score 6513; DB 1; Length 6513;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TCTAGAGCTTGGCCGCGATAGCAATGACAGAAAGATTCGACTCGATATCTGAGGAAGAAC 60
QY 1 TCTAGAGCTTGGCCGCGATAGCAATGACAGAAAGATTCGACTCGATATCTGAGGAAGAAC 60
Db 61 GCAGTTTGTTCGCTCCCTTTACCCGCGAATCATTTGGTGCATAATCGAAACACGCAATTGCCG 120
QY 61 GCAGTTTGTTCGCTCCCTTTACCCGCGAATCATTTGGTGCATAATCGAAACACGCAATTGCCG 120
Db 121 CTGAACATGAAGAACAGAGGAGCTGGAAGAAAGAGAGCGGAGAGGAGTGCGCGCAT 180
QY 121 CTGAACATGAAGAACAGAGGAGCTGGAAGAAAGAGAGCGGAGAGGAGTGCGCGCAT 180
Db 181 ATGTCTCGCAAGAAAACAAAAGAAATCCGATATGATGACGAGGACGAGGATCAAGGTC 240
QY 181 ATGTCTCGCAAGAAAACAAAAGAAATCCGATATGATGACGAGGACGAGGATCAAGGTC 240
Db 241 CACAACCGGATCCCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTGCGAGGACGCT 300
QY 241 CACAACCGGATCCCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTGCGAGGACGCT 300
Db 301 TCCCGCGGAAATTCGCTCCACTCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360
QY 301 TCCCGCGGAAATTCGCTCCACTCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360
Db 361 TGACATTCGTAGTTGTAAGCAAGAAAAGATAATTTTCGCTTTTCTGCATCAAAAGCAA 420
QY 361 TGACATTCGTAGTTGTAAGCAAGAAAAGATAATTTTCGCTTTTCTGCATCAAAAGCAA 420
Db 421 TGTGGATGCTCGATCCATTCATCCGATACGTCGTGGGCCATTTACATTTCTAGTGTATC 480
QY 421 TGTGGATGCTCGATCCATTCATCCGATACGTCGTGGGCCATTTACATTTCTAGTGTATC 480
Db 481 CATTATTTTCCCTATTCATCATCAACCAATTCCTCGCACTGCTGCTGATGATATGC 540
QY 481 CATTATTTTCCCTATTCATCATCAACCAATTCCTCGCACTGCTGCTGATGATATGC 540
Db 541 CGACAAGCCCGGTTGAGTCCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600
QY 541 CGACAAGCCCGGTTGAGTCCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600

QY 2761 TGCTGCTGATTCAAACTGCCAAAGTCTTGCGCCACACTTAATTTACTCATTTTCGATTA 2820
Db 2821 TGGACCAACCATGGCGCTTTGGGTAAATCTGACATTTGACATTTGCTATATCATCTTCA 2880
QY 2821 TGGACCAACCATGGCGCTTTGGGTAAATCTGACATTTGACATTTGCTATATCATCTTCA 2880
Db 2881 TCTTTGCGGTGATGGGAATCAACTGTTCGGAAGAAATTAATCATGATCAACAAGACCGCT 2940
QY 2881 TCTTTGCGGTGATGGGAATCAACTGTTCGGAAGAAATTAATCATGATCAACAAGACCGCT 2940
Db 2941 TTCCGGATGGGACCTCGCGCTTGGAACTTACCAGACTTTATGCGACAGCTTTCATGATCG 3000
QY 2941 TTCCGGATGGGACCTCGCGCTTGGAACTTACCAGACTTTATGCGACAGCTTTCATGATCG 3000
Db 3001 TGTTCGGGTGCTCTGCGGAGATGGATCGAGTCCATGTGGACTGCATGATAGTGGCG 3060
QY 3001 TGTTCGGGTGCTCTGCGGAGATGGATCGAGTCCATGTGGACTGCATGATAGTGGCG 3060
Db 3061 ATGTCTCGTGATTCCTTCTTTGCGCACCGTTGTCTAGCTTATCAGCGCCGACTG 3120
QY 3061 ATGTCTCGTGATTCCTTCTTTGCGCACCGTTGTCTAGCTTATCAGCGCCGACTG 3120
Db 3121 ACCTTTCTTAGCCCTTGGTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCGCCGACTG 3180
QY 3121 ACCTTTCTTAGCCCTTGGTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCGCCGACTG 3180
Db 3181 CCGATAACGATACGAATAAAATACCGAGGCTTCAATCGAATTTGGCGGATTTAAAGATT 3240
QY 3181 CCGATAACGATACGAATAAAATACCGAGGCTTCAATCGAATTTGGCGGATTTAAAGATT 3240
Db 3241 GGGTTAAGCGTAATTTGCTGATTTGTTCAAGTTTAATACGTAACAAATGACAAATCAAA 3300
QY 3241 GGGTTAAGCGTAATTTGCTGATTTGTTCAAGTTTAATACGTAACAAATGACAAATCAAA 3300
Db 3301 TAAGTGATCAACCATCAGGTGAGAGGACCAACAGATCAGTTGATTTGGAGCGAAGCG 3360
QY 3301 TAAGTGATCAACCATCAGGTGAGAGGACCAACAGATCAGTTGATTTGGAGCGAAGCG 3360
Db 3361 ATGTTGACAAAGCTGAGCTGGGCCACAGAGATCTTCCGCGAGGCGCTCATCAAGA 3420
QY 3361 ATGTTGACAAAGCTGAGCTGGGCCACAGAGATCTTCCGCGAGGCGCTCATCAAGA 3420
Db 3421 AGGGATCAAGGACGACGCAACTGGAGTGGCCATCGGGGATCGGATGGAATTCACGA 3480
QY 3421 AGGGATCAAGGACGACGCAACTGGAGTGGCCATCGGGGATCGGATGGAATTCACGA 3480
Db 3481 TACAGCGGACATGAAGAACCAACAGCGGAATAATCTAAATTAACGCAACGA 3540
QY 3481 TACAGCGGACATGAAGAACCAACAGCGGAATAATCTAAATTAACGCAACGA 3540
Db 3541 TGATTTGCAACTCAATTAACCAACCAAGCAATAGACTGGAAACAGGCTAAACCATAGAG 3600
QY 3541 TGATTTGCAACTCAATTAACCAACCAAGCAATAGACTGGAAACAGGCTAAACCATAGAG 3600
Db 3601 GTTTGCTCTTACAGACGACGACACTGCCAGTAACTCATATGTTAGCCATAGATC 3660
QY 3601 GTTTGCTCTTACAGACGACGACACTGCCAGTAACTCATATGTTAGCCATAGATC 3660
Db 3661 GACCAATTAAGGACGAGGACCAAGGCGAGCGGACGATGGAGGCGGAGGAGCG 3720
QY 3661 GACCAATTAAGGACGAGGACCAAGGCGAGCGGACGATGGAGGCGGAGGAGCG 3720
Db 3721 GCGAGCCGACGAGGAGGATTTAGTCTCGACGAGGAACTGGACGAGGAGGCGGAATGCG 3780
QY 3721 GCGAGCCGACGAGGAGGATTTAGTCTCGACGAGGAACTGGACGAGGAGGCGGAATGCG 3780
Db 3781 AGGAGGCGCGCTCAGCGGTGATATCATTTATGATGACAGGAGGATATCTCGATG 3840
QY 3781 AGGAGGCGCGCTCAGCGGTGATATCATTTATGATGACAGGAGGATATCTCGATG 3840
Db 3841 AATATCCAGCTGATTTGCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTG 3900
QY 3841 AATATCCAGCTGATTTGCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTG 3900

3901 ACGATCACTCGCGCTTGGCAAGGATGGGCAATTTACGACTGAAAACTTTTCAATTA 3960
QY 3901 ACGATCACTCGCGCTTGGCAAGGATGGGCAATTTACGACTGAAAACTTTTCAATTA 3960
Db 3961 TTGAAAAATAATATTTTGAACAGCTGTTATCACHATATGATTTAATGAGTAGCTTAGCTT 4020
QY 3961 TTGAAAAATAATATTTTGAACAGCTGTTATCACHATATGATTTAATGAGTAGCTTAGCTT 4020
Db 4021 TGGCATTAGAAGATGATACATCTGCCACAAAGACCCATCTGCAGGATATTTTATATACTATA 4080
QY 4021 TGGCATTAGAAGATGATACATCTGCCACAAAGACCCATCTGCAGGATATTTTATATACTATA 4080
Db 4081 TGGCAGAAATATTTACGGTTATATCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG 4140
QY 4081 TGGCAGAAATATTTACGGTTATATCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG 4140
Db 4141 GCTTCAAGTGTACTTCAACCAAGCGTGGTGTGGCTCGATTTCTGATTTGTCATGGTAT 4200
QY 4141 GCTTCAAGTGTACTTCAACCAAGCGTGGTGTGGCTCGATTTCTGATTTGTCATGGTAT 4200
Db 4201 CGCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTGGTATTCAGGCTTCAAGACTA 4260
QY 4201 CGCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTGGTATTCAGGCTTCAAGACTA 4260
Db 4261 TGGCAACGTTAAGAGCAGCTGAGACCACTACGTGCCATGTCCCGTATGCGAGGCGATGAGG 4320
QY 4261 TGGCAACGTTAAGAGCAGCTGAGACCACTACGTGCCATGTCCCGTATGCGAGGCGATGAGG 4320
Db 4321 TGTCTCTTAATGGCTGGTACAGCTATACCGTCCATCTTCAATGTCTATTTGGTGTGTC 4380
QY 4321 TGTCTCTTAATGGCTGGTACAGCTATACCGTCCATCTTCAATGTCTATTTGGTGTGTC 4380
Db 4381 TAATATTTTGGCTAAATTTTGGCAATGGTGTACAGCTTTTGTGCAAAATATTTTA 4440
QY 4381 TAATATTTTGGCTAAATTTTGGCAATGGTGTACAGCTTTTGTGCAAAATATTTTA 4440
Db 4441 AGTGGAGGACATGAATGGCAGAACTCAGCCACGAGATCATACCAATTCGCAATGCT 4500
QY 4441 AGTGGAGGACATGAATGGCAGAACTCAGCCACGAGATCATACCAATTCGCAATGCT 4500
Db 4501 GCAGAGCGAGACTACAGTGGTGAATTCAGCAATGAATTCGATCATGTAGGTAAGC 4560
QY 4501 GCAGAGCGAGACTACAGTGGTGAATTCAGCAATGAATTCGATCATGTAGGTAAGC 4560
Db 4561 CGTATCTGTGCTTTTCCAAAGTGGCCACCTTCAAAGGCTGGATACAAATCATGAACGATG 4620
QY 4561 CGTATCTGTGCTTTTCCAAAGTGGCCACCTTCAAAGGCTGGATACAAATCATGAACGATG 4620
Db 4621 CTATCGATTCACGAGGTTGGACAACCAATTCGTGAACGCAACATCTACATGTT 4680
QY 4621 CTATCGATTCACGAGGTTGGACAACCAATTCGTGAACGCAACATCTACATGTT 4680
Db 4681 TATATTCGTATTCATCATATTTGGATCTTTTACACCTCAATCTGTTTCAATTTGGTG 4740
QY 4681 TATATTCGTATTCATCATATTTGGATCTTTTACACCTCAATCTGTTTCAATTTGGTG 4740
Db 4741 TTATCTTGATAATTTTATGACAAAAGAAAAAGCAGGTGGATCATTTAGAAATGTTC 4800
QY 4741 TTATCTTGATAATTTTATGACAAAAGAAAAAGCAGGTGGATCATTTAGAAATGTTC 4800
Db 4801 TGACAGAGATCAGAAAAAGTACTATTAATGCTATGAAAAGATGGGCTCTAAAAAACCAT 4860
QY 4801 TGACAGAGATCAGAAAAAGTACTATTAATGCTATGAAAAGATGGGCTCTAAAAAACCAT 4860
Db 4861 TAAAGCCATTCAGAACCAAGGTGGCGACCAAGCAATAGTCTTTGAATAGTAACCG 4920
QY 4861 TAAAGCCATTCAGAACCAAGGTGGCGACCAAGCAATAGTCTTTGAATAGTAACCG 4920
Db 4921 ATAAGAAATTCGATATAATCATTTATGTTATTTGCTTGAACATGTTCCACCATGACCC 4980
QY 4921 ATAAGAAATTCGATATAATCATTTATGTTATTTGCTTGAACATGTTCCACCATGACCC 4980

Db 4981 TCGATCGTTACGATCGCTCGGACACGTTATACGCGGTCCCTAGACATATCTCAATCCGATAT 5040
QY 4981 TCGATCGTTACGATCGCTCGGACACGTTATACGCGGTCCCTAGACATATCTCAATCCGATAT 5040
Db 5041 TCGTAGTATTTTCAGTTCGGAATGCTATTAAATAATTCGCTTTACGATATACATATT 5100
QY 5041 TCGTAGTATTTTCAGTTCGGAATGCTATTAAATAATTCGCTTTACGATATACATATT 5100
Db 5101 TTATTGACCATGGAATTTATTGATAGTAGTGTGTCATTTTATCCATCTTAGGCTCTTG 5160
QY 5101 TTATTGACCATGGAATTTATTGATAGTAGTGTGTCATTTTATCCATCTTAGGCTCTTG 5160
Db 5161 TACTTACGATATATTCGAGAAGTACTTCGTGTCGCGACCCCTGCTCCGAGTGTGCGTG 5220
QY 5161 TACTTACGATATATTCGAGAAGTACTTCGTGTCGCGACCCCTGCTCCGAGTGTGCGTG 5220
Db 5221 TGGCGAAGTGGGCGGTGCTTCGACTGTGTGAAGGAGCCCAAGGCATTTCGGACACTGC 5280
QY 5221 TGGCGAAGTGGGCGGTGCTTCGACTGTGTGAAGGAGCCCAAGGCATTTCGGACACTGC 5280
Db 5281 TCTTCGCGTTGGCCATGTCGCTGCGGCGCCTGTTCAACATCTGCTGCTGCTTCCTGG 5340
QY 5281 TCTTCGCGTTGGCCATGTCGCTGCGGCGCCTGTTCAACATCTGCTGCTGCTTCCTGG 5340
Db 5341 TCATGTTCACTTTTGCCATTTTCGCGATGTCGTTCTTCATCGCAGTGAAGGAGAAGCG 5400
QY 5341 TCATGTTCACTTTTGCCATTTTCGCGATGTCGTTCTTCATCGCAGTGAAGGAGAAGCG 5400
Db 5401 GCATTACGAGCTCTACAACCTTCAAGACCTTTGGCCAGAGCATCTGCTCTTTTCAGA 5460
QY 5401 GCATTACGAGCTCTACAACCTTCAAGACCTTTGGCCAGAGCATCTGCTCTTTTCAGA 5460
Db 5461 TGTCCAGCTACGCGGTTGGGATGGTGTACTGGACGCGCATTTCAATGAGGAACATCGC 5520
QY 5461 TGTCCAGCTACGCGGTTGGGATGGTGTACTGGACGCGCATTTCAATGAGGAACATCGC 5520
Db 5521 ATCCACCGCAGCGACAAAGGCTATCGGGAATTTGTTGTCAGCAGCCTTGGATATA 5580
QY 5521 ATCCACCGCAGCGACAAAGGCTATCGGGAATTTGTTGTCAGCAGCCTTGGATATA 5580
Db 5581 CGTTTCTCTCTACCTACTGTTATAGCTTTTGTAGTATTATTAATGTACATTGCTG 5640
QY 5581 CGTTTCTCTCTACCTACTGTTATAGCTTTTGTAGTATTATTAATGTACATTGCTG 5640
Db 5641 TCATTCTCGAAGCTATAGTCAGGCGCCAGGAGCGTCAAGAGGGTCTAACCCAGCAGC 5700
QY 5641 TCATTCTCGAAGCTATAGTCAGGCGCCAGGAGCGTCAAGAGGGTCTAACCCAGCAGC 5700
Db 5701 ACTACGACATCTACTATGAGATCTGGCAGCAATTCGATCCGGAGGCGACCCAGTACATAC 5760
QY 5701 ACTACGACATCTACTATGAGATCTGGCAGCAATTCGATCCGGAGGCGACCCAGTACATAC 5760
Db 5761 GCTATGATCAGCTCTCGAATTTCTGGACGTTACTGGAGCCCCCGCTCGAGATCCACAAC 5820
QY 5761 GCTATGATCAGCTCTCGAATTTCTGGACGTTACTGGAGCCCCCGCTCGAGATCCACAAC 5820
Db 5821 CGAACAGTACAAGATCATATCGATGGACATACCATCTGTCGGGGTGACCTCATGTACT 5880
QY 5821 CGAACAGTACAAGATCATATCGATGGACATACCATCTGTCGGGGTGACCTCATGTACT 5880
Db 5881 CGCTCGACATCTCGACGCCCTTACGAAAGACTTCTTTGCGCGGAAGGCGCAATCCGATAG 5940
QY 5881 CGCTCGACATCTCGACGCCCTTACGAAAGACTTCTTTGCGCGGAAGGCGCAATCCGATAG 5940
Db 5941 AGGAGAGGGTGAATTTGGTGAATAGCGGCGCCCGCGGATACGAGGGCTACGAGCCCG 6000
QY 5941 AGGAGAGGGTGAATTTGGTGAATAGCGGCGCCCGCGGATACGAGGGCTACGAGCCCG 6000
Db 6001 TCTCATCAACGCTGTGGGCTGAGGTGAGGAGTACTGCGCCCGGCTAATCCAGCAGCCT 6060
QY 6001 TCTCATCAACGCTGTGGGCTGAGGTGAGGAGTACTGCGCCCGGCTAATCCAGCAGCCT 6060
Db 6061 GCGGAAAGCACAAAGCGCGCGGAGGAGGTGGGTCTCTTTGAGCCGATACGGATCATG 6120

QY 6061 GGGCAAAACGACAAAGCGCGCGAGGAGGTGGTCTTTGAGCCGATACGGATCATG 6120
Db 6121 GCATGCGCGTGTATCCGATGTCGCGGACCCGCGCCCGATGAAGCAACGAGCGCGCATG 6180
QY 6121 GCATGCGCGTGTATCCGATGTCGCGGACCCGCGGCGCGGATGAAGCAACGAGCGCGCATG 6180
Db 6181 CGCCCGCTGTGGAGATGTTAGTGTAAACGTTACTGCAGAAAGAGCTGCCGATGCCCGATG 6240
QY 6181 CGCCCGCTGTGGAGATGTTAGTGTAAACGTTACTGCAGAAAGAGCTGCCGATGCCCGATG 6240
Db 6241 AGAGTAATGTAATAGTCCCGGTGAGGATCAGGGGCGCGGAGCAGCAGCAGCAGCAG 6300
QY 6241 AGAGTAATGTAATAGTCCCGGTGAGGATCAGGGGCGCGGAGCAGCAGCAGCAGCAGCAG 6300
Db 6301 CGCGCGCGCGGACGACGCGGGAAGTCCCGGAGCGGTAGCGCGGCGGACAGCAGCAGCAG 6360
QY 6301 CGCGCGCGCGGACGACGCGGGAAGTCCCGGAGCGGTAGCGCGGCGGACAGCAGCAGCAGCAG 6360
Db 6361 CGCGCGTCTCTGAGAGCAGCGGTTCTGACGAAGAAGCCCAAGGTGGTCTATCC 6420
QY 6361 CGCGCGTCTCTGAGAGCAGCGGTTCTGACGAAGAAGCCCAAGGTGGTCTATCC 6420
Db 6421 ACTCGGATCCGCGAGCATCAGTCCGCGACGCGGAGTGTCTGAGCCAGGCTCGCCCCC 6480
QY 6421 ACTCGGATCCGCGAGCATCAGTCCGCGACGCGCGGATGTCTGAGCCAGGCTCGCCCCC 6480
Db 6481 CCTTCCAAGATGACGCGAGTATTAGCTCTAGA 6513
QY 6481 CCTTCCAAGATGACGCGAGTATTAGCTCTAGA 6513

RESULT 4
ID US-08-338-702-7 STANDARD; DNA; UNC; 6513 BP.
AC xxxxxx
DT

Sequence 7, Application US/08338702
Sequence 7, Application US/08338702
CC Patent No. 5550049
CC

GENERAL INFORMATION:
CC APPLICANT: Warnke, Jeffrey W.

CC APPLICANT: Van Der Ploeg, Leonardus

CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE

CC TITLE OF INVENTION: PARA SODIUM CHANNEL

CC NUMBER OF SEQUENCES: 7

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: John W. Wallen III

CC STREET: P.O. Box 2000, 126 E. Lincoln Avenue

CC CITY: Rahway

CC STATE: New Jersey

CC COUNTRY: USA

CC ZIP: 07065-0900

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/338,702

CC FILING DATE:

CC CLASSIFICATION: 435

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Wallen III, John W.

CC REGISTRATION NUMBER: 35,403

CC REFERENCE/DOCKET NUMBER: 19338

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (908) 594-3905

CC TELEFAX: (908) 594-4720

CC INFORMATION FOR SEQ ID NO: 7:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 6513 base pairs

CC TYPE: nucleic acid

CC STRANDEDNESS: single

[illegible]

QY 2041 GCAATTTGCCAACCGCAACACACAGGCNATCAATCAGTGGCGGCCACCAATGGCGGCACCA 2100
Db 2101 CTTGTCTGGACACAAATCACAAGCTCGATCATCGCGACTACGAAATTTGGCCTGGAGTGCA 2160
QY 2101 CTTGTCTGGACACAAATCACAAGCTCGATCATCGCGACTACGAAATTTGGCCTGGAGTGCA 2160
Db 2161 CGGACGAAGCTGCGCAAGATTAAACATCATCATCAATCCTTTTATCGAGCCCGTCCAGACAC 2220
QY 2161 CGGACGAAGCTGCGCAAGATTAAACATCATCATCAATCCTTTTATCGAGCCCGTCCAGACAC 2220
Db 2221 AAACGGTGGTTGATATGAAGAATGTGATGCTCTGAATGACATCATCAAGACGCGCGTG 2280
QY 2221 AAACGGTGGTTGATATGAAGAATGTGATGCTCTGAATGACATCATCAAGACGCGCGTG 2280
Db 2281 GTCCGCAAGTCCGGGCAAGCGATCGCGGTGCTCCGTTTACTATTTTCCCAACAGAGACG 2340
QY 2281 GTCCGCAAGTCCGGGCAAGCGATCGCGGTGCTCCGTTTACTATTTTCCCAACAGAGACG 2340
Db 2341 ATGACGAGGATGGCGGACGTTTCAAGACAAAGGCACTCGAAGTGATCTCAAGGCAATCG 2400
QY 2341 ATGACGAGGATGGCGGACGTTTCAAGACAAAGGCACTCGAAGTGATCTCAAGGCAATCG 2400
Db 2401 ATGTGTTTGTGTGGGACTGTTGCTGGGTTTGGTTTGAATTTTCAGGATGGGTATCGC 2460
QY 2401 ATGTGTTTGTGTGGGACTGTTGCTGGGTTTGGTTTGAATTTTCAGGATGGGTATCGC 2460
Db 2461 TCATCGCTTTCGATCCCTTCGTCAGCTCTTCATCGAGCTGTGCTATGCTGCTCAACACGA 2520
QY 2461 TCATCGCTTTCGATCCCTTCGTCAGCTCTTCATCGAGCTGTGCTATGCTGCTCAACACGA 2520
Db 2521 TGTTCATGGCAATGGATCACCAGATATGAACAAGGAGATGGAACGGCTGCTCAAGAGTG 2580
QY 2521 TGTTCATGGCAATGGATCACCAGATATGAACAAGGAGATGGAACGGCTGCTCAAGAGTG 2580
Db 2581 GCAACTATTTCTCACCGCCACCTTTGCCATCGAGGCCACCATGAAGCTAATGCCATGA 2640
QY 2581 GCAACTATTTCTCACCGCCACCTTTGCCATCGAGGCCACCATGAAGCTAATGCCATGA 2640
Db 2641 GCCCAAGTACTATTTCCAGGAGGCTGGAACATCTTCGACTTCATTATCGTGCCCTAT 2700
QY 2641 GCCCAAGTACTATTTCCAGGAGGCTGGAACATCTTCGACTTCATTATCGTGCCCTAT 2700
Db 2701 CGCTATTTGGAACCTGGAGCTCGAGGCTCGAGGCTCGTCCGATATTCGTTTCTTCGAT 2760
QY 2701 CGCTATTTGGAACCTGGAGCTCGAGGCTCGAGGCTCGTCCGATATTCGTTTCTTCGAT 2760
Db 2761 TGCTGCGTGTATTCAAACTGSCCAAGTCTTGGCCACACTTAATTTACTCATTTTCGATTA 2820
QY 2761 TGCTGCGTGTATTCAAACTGSCCAAGTCTTGGCCACACTTAATTTACTCATTTTCGATTA 2820
Db 2821 TGGGACCCACATGGGGCTTTGGGTAATCTGACATTTGTACTTTGCAATTCATCTTCA 2880
QY 2821 TGGGACCCACATGGGGCTTTGGGTAATCTGACATTTGTACTTTGCAATTCATCTTCA 2880
Db 2881 TCTTTGCGGTGATGGGAATGCAACTGTTTCGGAAGAATATCATGATCACAAGACCGCT 2940
QY 2881 TCTTTGCGGTGATGGGAATGCAACTGTTTCGGAAGAATATCATGATCACAAGACCGCT 2940
Db 2941 TTCCGGATGGGACCTCGCGGCTTGGAACTTCACCGACTTTATGACAGCTTCATGATCG 3000
QY 2941 TTCCGGATGGGACCTCGCGGCTTGGAACTTCACCGACTTTATGACAGCTTCATGATCG 3000
Db 3001 TGTTCGGGTGCTCTCGGGAGAAATGGATCGAGTCCATGTGGGACTGCATGTACGTGGCG 3060
QY 3001 TGTTCGGGTGCTCTCGGGAGAAATGGATCGAGTCCATGTGGGACTGCATGTACGTGGCG 3060
Db 3061 ATGTCCTGTCATCCCTTCTTCTTGGCCACCGTTGTCATCGGCAATCTTGTGCTACTTA 3120
QY 3061 ATGTCCTGTCATCCCTTCTTCTTGGCCACCGTTGTCATCGGCAATCTTGTGCTACTTA 3120
Db 3121 ACCTTTTCTAGCCTTGTCTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCCGCGACTG 3180
QY 3121 ACCTTTTCTAGCCTTGTCTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCCGCGACTG 3180

Db 3181 CCGATAACGATACGAATAAATAAGCCGAGGCCCTTCAATCGAATTTGCCGATTTAAAAGTT 3240
QY 3181 CCGATAACGATACGAATAAATAAGCCGAGGCCCTTCAATCGAATTTAAAAGTT 3240
Db 3241 GGGTTAAGCGTATATGCTGATGTTTCAAGTTAATAGCTACAAATTCGACAAATCAAA 3300
QY 3241 GGGTTAAGCGTATATGCTGATGTTTCAAGTTAATAGCTACAAATTCGACAAATCAAA 3300
Db 3301 TAAGTATCAACCATCAGGTGAGAGGACCAACAGATCAGTTGATTTGGAGGCAAGAGC 3360
QY 3301 TAAGTATCAACCATCAGGTGAGAGGACCAACAGATCAGTTGATTTGGAGGCAAGAGC 3360
Db 3361 ATGGTGACAAACGAACTGGAGCTGGGCCACGACGAGATCTCTCGCCGACGGCCTCATCAAG 3420
QY 3361 ATGGTGACAAACGAACTGGAGCTGGGCCACGACGAGATCTCTCGCCGACGGCCTCATCAAG 3420
Db 3421 AGGGGATCAAGGAGCAGACCAACTGGAGTGGCCATCGGGGATCGGATGGAATTCACGA 3480
QY 3421 AGGGGATCAAGGAGCAGACCAACTGGAGTGGCCATCGGGGATCGGATGGAATTCACGA 3480
Db 3481 TACACGGCGACATGAAGAACAACCAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA 3540
QY 3481 TACACGGCGACATGAAGAACAACCAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA 3540
Db 3541 TGATTGGCAACTCAATTAACCAACAGACAAATAGACTTGAACACAGACTAAACCATAGAG 3600
QY 3541 TGATTGGCAACTCAATTAACCAACAGACAAATAGACTTGAACACAGACTAAACCATAGAG 3600
Db 3601 GTTTGTCTTTACAGGACGACGACATGCGCAGCAATTAACATCATATGTTAGCCATTAAGAATC 3660
QY 3601 GTTTGTCTTTACAGGACGACGACATGCGCAGCAATTAACATCATATGTTAGCCATTAAGAATC 3660
Db 3661 GACCATTCAAGGACGAGAGCCACAAGGCGCCGAGAGATGGAAGGCGGAGGAGAAC 3720
QY 3661 GACCATTCAAGGACGAGAGCCACAAGGCGCCGAGAGATGGAAGGCGGAGGAGAAC 3720
Db 3721 GCACGCCACGACAGGAGGATTTAGGTCTCGACGAGGAACCTGGACGAGGAGGCGGAATGCG 3780
QY 3721 GCACGCCACGACAGGAGGATTTAGGTCTCGACGAGGAACCTGGACGAGGAGGCGGAATGCG 3780
Db 3781 AGGAGGCCCGCTCGAGGCTGATATCATTTATTCATGACACAGCAGGATATCTCGATG 3840
QY 3781 AGGAGGCCCGCTCGAGGCTGATATCATTTATTCATGACACAGCAGGATATCTCGATG 3840
Db 3841 AATATCCAGCTGATTCGTCGCCGATTCGTTACTATAGAAATTTCCGATCTTAGCCGGTG 3900
QY 3841 AATATCCAGCTGATTCGTCGCCGATTCGTTACTATAGAAATTTCCGATCTTAGCCGGTG 3900
Db 3901 ACATGACTCGCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTA 3960
QY 3901 ACATGACTCGCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTA 3960
Db 3961 TTGAAAATAAATTTTGAACAGCTGTTTACTACTATGATTTTAAAGTAGCTTAGCTT 4020
QY 3961 TTGAAAATAAATTTTGAACAGCTGTTTACTACTATGATTTTAAAGTAGCTTAGCTT 4020
Db 4021 TGGCATTAGAGATGTACATCTGCCACAAGACCCACTACTGCAGGATATTTTACTATA 4080
QY 4021 TGGCATTAGAGATGTACATCTGCCACAAGACCCACTACTGCAGGATATTTTACTATA 4080
Db 4081 TGGACAGAATATTTAGCGTTATATTTCTTGGAAATGTTAACTAGTGTGGCGCTG 4140
QY 4081 TGGACAGAATATTTAGCGTTATATTTCTTGGAAATGTTAACTAGTGTGGCGCTG 4140
Db 4141 GCTTCAAGTGTACTTACCAACCGCTGTTGGCTCGATTTTCGTTGATTTGCTGATG 4200
QY 4141 GCTTCAAGTGTACTTACCAACCGCTGTTGGCTCGATTTTCGTTGATTTGCTGATG 4200
Db 4201 CGCTTATCAACTTCGTTGCTTCACTTGTGAGCTGTTGAGTATTAAGCCCTTCAAGACTA 4260
QY 4201 CGCTTATCAACTTCGTTGCTTCACTTGTGAGCTGTTGAGTATTAAGCCCTTCAAGACTA 4260

QY 6421 ACTCGGATCGCGAGCATCAGTCGCGCAGCGGAGTGCTGAGCCAGGCTCGCCCCC 6480
Db 6481 CCTCCTAAGATGACGCGAGTATAGTCTAGA 6513
QY 6481 CCTCCTAAGATGACGCGAGTATAGTCTAGA 6513
RESULT 5
ID PCT-US95-14262-7 STANDARD; DNA; UNC; 6513 BP.
AC xxxxxx
DE Sequence 7, Application PC/TUS9514262
CC Sequence 7, Application PC/TUS9514262
CC GENERAL INFORMATION:
CC APPLICANT: Warmke, Jeffrey W.
CC APPLICANT: Van Der Ploeg, Leonardus
CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
CC TITLE OF INVENTION: PARA SODIUM CHANNEL
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Jack L. Tribble
CC STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CC CITY: Rahway
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07065-0907
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/14262
CC FILING DATE:
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Tribble, Jack L.
CC REGISTRATION NUMBER: 32,633
CC REFERENCE/DOCKET NUMBER: 19338 PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (908) 594-5321
CC TELEFAX: (908) 594-4720
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6513 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear.
CC MOLECULE TYPE: cDNA
CC SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.
Query Match 100.0%; Score 6513; DB 2; Length 6513;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 TCTAGAGTTGGCGCATAGACAAATCCGACTCGATATCTGAGGAAGAAC 60
QY 1 TCTAGAGTTGGCGCATAGACAAATCCGACTCGATATCTGAGGAAGAAC 60
Db 61 GCAGTTGTTCCGTCCTTTACCGCGGAATCTGGTGAATTCGAACACGATTCGCG 120
QY 61 GCAGTTGTTCCGTCCTTTACCGCGGAATCTGGTGAATTCGAACACGATTCGCG 120
Db 121 CTGAACATGAAGACGAGAGCTGGAAAGAGAGAGCGGAGAGGTCGCCCGAT 180
QY 121 CTGAACATGAAGACGAGAGCTGGAAAGAGAGAGCGGAGAGGTCGCCCGAT 180
Db 181 ATGGTCGAAGAAAAACAAAGAAATCCGATATGATGACGAGGACGAGATGAAGTC 240
QY 181 ATGGTCGAAGAAAAACAAAGAAATCCGATATGATGACGAGGACGAGATGAAGTC 240
Db 241 CACAACCGGATCTACACTTTGAACAGGGTGCCCAATACCTGTTTCGATTCGAGGAGCT 300
QY 241 CACAACCGGATCTACACTTTGAACAGGGTGCCCAATACCTGTTTCGATTCGAGGAGCT 300
Db 301 TCCCGCCGGAATTTGGCTCCACTCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360
QY 301 TCCCGCCGGAATTTGGCTCCACTCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360
Db 361 TGACATTCGTAGTTGTAGCAAGAAAGATATTTTCGCTTTTCTGCAATCAAAAGCAA 420
QY 361 TGACATTCGTAGTTGTAGCAAGAAAGATATTTTCGCTTTTCTGCAATCAAAAGCAA 420
Db 421 TGTGGATGCTCGATCAATTCATCCGATACGTCGTCGTCGTCGTCGTCGTCGTCGTC 480
QY 421 TGTGGATGCTCGATCAATTCATCCGATACGTCGTCGTCGTCGTCGTCGTCGTCGTC 480
Db 481 CATTTATTTCCCTATTTCATCATCACCACAAATTCCTCGTCAACTGCATCTCTGATGATAATGC 540
QY 481 CATTTATTTCCCTATTTCATCATCACCACAAATTCCTCGTCAACTGCATCTCTGATGATAATGC 540
Db 541 CGACAACGCCACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600
QY 541 CGACAACGCCACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 600
Db 601 CAGCTGTTAAAGTGATGGCAGGAGTTTCATTTTATGCCCCGTTTACGTATCTTAGAGATG 660
QY 601 CAGCTGTTAAAGTGATGGCAGGAGTTTCATTTTATGCCCCGTTTACGTATCTTAGAGATG 660
Db 661 CATGGAATTTGGCTGGACTTCGTAGTAATAGCTTTAGCTTTATGTGACCATGGGTATAGATT 720
QY 661 CATGGAATTTGGCTGGACTTCGTAGTAATAGCTTTAGCTTTATGTGACCATGGGTATAGATT 720
Db 721 TAGGTAATCTAGACGCCCTGCGAAGCTTTAGGGTGCTGCGAGCGCTTAAACCGTAGCCA 780
QY 721 TAGGTAATCTAGACGCCCTGCGAAGCTTTAGGGTGCTGCGAGCGCTTAAACCGTAGCCA 780
Db 781 TTGTGCCAGGCTTGAAGACCATCGTGGCGCGCTCATCGAATCGGTGAGAAATCTCGCG 840
QY 781 TTGTGCCAGGCTTGAAGACCATCGTGGCGCGCTCATCGAATCGGTGAGAAATCTCGCG 840
Db 841 ATGTGATTTATCTGACCATGTTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 841 ATGTGATTTATCTGACCATGTTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 901 ATATGGGCTGCTCACCGGAGAGTGCATCAAGAAGTTCCCGCTGGACGGTTCTCTGGGCA 960
QY 901 ATATGGGCTGCTCACCGGAGAGTGCATCAAGAAGTTCCCGCTGGACGGTTCTCTGGGCA 960
Db 961 ATCTGACCCAGCAGAACTGGGACTATCAAAATCGCAATAGCTCCCAATTTGGTATTCGAGG 1020
QY 961 ATCTGACCCAGCAGAACTGGGACTATCAAAATCGCAATAGCTCCCAATTTGGTATTCGAGG 1020
Db 1021 ACGAGGCGATCTCATTTCCGTTTATGCGCAATATATCCCGTGGCGGCAATGCGAGCAGC 1080
QY 1021 ACGAGGCGATCTCATTTCCGTTTATGCGCAATATATCCCGTGGCGGCAATGCGAGCAGC 1080
Db 1081 ATTACGTGTCCCTGACAGGGTTTGGTCCGAATCCGAATTTATGGCTACACAGCTTCGATT 1140
QY 1081 ATTACGTGTCCCTGACAGGGTTTGGTCCGAATCCGAATTTATGGCTACACAGCTTCGATT 1140
Db 1141 CGTTCGGATGGGTTTCTGTCGCGCTTCCGGCTGATGACACAGGACTTCTGGGAGATC 1200
QY 1141 CGTTCGGATGGGTTTCTGTCGCGCTTCCGGCTGATGACACAGGACTTCTGGGAGATC 1200
Db 1201 TGTACCGAGTGTGTTGCGCGCGCGGACCATGGCACATGCTGTTCTTTATAGTCATCA 1260
QY 1201 TGTACCGAGTGTGTTGCGCGCGCGGACCATGGCACATGCTGTTCTTTATAGTCATCA 1260
Db 1261 TCTTCTTAGGTTCAATCTATCTTGTGAATTTGATTTGGCCATTGTTGCGCATGCTGATG 1320
QY 1261 TCTTCTTAGGTTCAATCTATCTTGTGAATTTGATTTGGCCATTGTTGCGCATGCTGATG 1320
Db 1321 ACGAATTCGAAGGAGCGCCGAAGAGAGGCTGCCGAAGAGGAGCGGATACGTTGAAG 1380
QY 1321 ACGAATTCGAAGGAGCGCCGAAGAGAGGCTGCCGAAGAGGAGCGGATACGTTGAAG 1380

||||| 3541 TGNATGGCAACTCAATTAAACCACCAAGACATATAGACTGGAACACAGGCTTAAACCATAGAG 3600
Db 3601 GTTGTTCCTTACAGGACGACGACTGCCAGCATTAACATCATATGGTAGCCCAAGAATC 3660
Qy 3601 GTTGTTCCTTACAGGACGACGACTGCCAGCATTAACATCATATGGTAGCCCAAGAATC 3660
Db 3661 GACCATTCAAGCAGAGACCCACAGGGCAGGCCGAGACGATGAGGGCGAGGAGAAC 3720
Qy 3661 GACCATTCAAGCAGAGACCCACAGGGCAGGCCGAGACGATGAGGGCGAGGAGAAC 3720
Db 3721 GCGACCCACGACGAGGAGGATTTAGGTCTCGACGAGAACTGGACGAGGAGGCGAATGCG 3780
Qy 3721 GCGACCCACGACGAGGAGGATTTAGGTCTCGACGAGAACTGGACGAGGAGGCGAATGCG 3780
Db 3781 AGGAGGCCCGCTCGACGGTGATATCATTTATCATGCACACGAGGATATACCTCGATG 3840
Qy 3781 AGGAGGCCCGCTCGACGGTGATATCATTTATCATGCACACGAGGATATACCTCGATG 3840
Db 3841 AATATCCAGCTGATTCGTCGCCGGATTCGTACTATGAAGAAATTCGGATCTTAGCGGGTG 3900
Qy 3841 AATATCCAGCTGATTCGTCGCCGGATTCGTACTATGAAGAAATTCGGATCTTAGCGGGTG 3900
Db 3901 ACGATGACTCGCGTCTCGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTA 3960
Qy 3901 ACGATGACTCGCGTCTCGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTA 3960
Db 3961 TTGAAATAAATATTTGAAACAGCTGTTATCACTATGATTTAATAGTAGCTTAGCTT 4020
Qy 3961 TTGAAATAAATATTTGAAACAGCTGTTATCACTATGATTTAATAGTAGCTTAGCTT 4020
Db 4021 TGGCATTTAGAAGATGATATCTGCCACAAAGACCCATCTCGAGGATATTTTATACATA 4080
Qy 4021 TGGCATTTAGAAGATGATATCTGCCACAAAGACCCATCTCGAGGATATTTTATACATA 4080
Db 4081 TGGACAGAAATTTACGGTTATATCTCTGGAATGTTAATCAAGTGGTGGGCGCTCG 4140
Qy 4081 TGGACAGAAATTTACGGTTATATCTCTGGAATGTTAATCAAGTGGTGGGCGCTCG 4140
Db 4141 GCTTCAAGATGTAATTCACCAACGCGTGTGTTGGCTCGATTTCTGATTTGTCATGGTAT 4200
Qy 4141 GCTTCAAGATGTAATTCACCAACGCGTGTGTTGGCTCGATTTCTGATTTGTCATGGTAT 4200
Db 4201 CGCTTATCAACTTCGTTGCTTCACTTTGGAGCTGGTGGTATTCGAAGCCTTCAAGACTA 4260
Qy 4201 CGCTTATCAACTTCGTTGCTTCACTTTGGAGCTGGTGGTATTCGAAGCCTTCAAGACTA 4260
Db 4261 TGGCAACGTTAAGACGACTGAGACCACTACGTGCCATGTCCCGTATGCAAGGCGATGAGGG 4320
Qy 4261 TGGCAACGTTAAGACGACTGAGACCACTACGTGCCATGTCCCGTATGCAAGGCGATGAGGG 4320
Db 4321 TCGTCGTTAATGGCTGGTACAAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTC 4380
Qy 4321 TCGTCGTTAATGGCTGGTACAAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTC 4380
Db 4381 TAATATTTGGCTTAATTTTGGCATAATGGGTACAGCTTTTGGTGGAAATATTTTA 4440
Qy 4381 TAATATTTGGCTTAATTTTGGCATAATGGGTACAGCTTTTGGTGGAAATATTTTA 4440
Db 4441 AGTGCAGGACATGATGGCAGCAAGCTCAGCCACGAGATCATACCANAATCGCAATGCGCT 4500
Qy 4441 AGTGCAGGACATGATGGCAGCAAGCTCAGCCACGAGATCATACCANAATCGCAATGCGCT 4500
Db 4501 GCGAGACGCAAGAACTACAGCTGGGTGAATTCAGCAATGAATTTGATCATGTAGGTAAAG 4560
Qy 4501 GCGAGACGCAAGAACTACAGCTGGGTGAATTCAGCAATGAATTTGATCATGTAGGTAAAG 4560
Db 4561 CGTATCTGTGCCCTTTCCAAAGTGGCCACCTTCAAGGCTGGATACAAATCATGAACGATG 4620
Qy 4561 CGTATCTGTGCCCTTTCCAAAGTGGCCACCTTCAAGGCTGGATACAAATCATGAACGATG 4620
Db 4621 CTATCCATTCACGAGGTGGACAAAGCAATTCGTGAAGCAACATCTACATGTATT 4680
|||||

Qy 4621 CTATCCATTACGAGAGGTGGACAAAGCAACCAATTCGTGTAACGACATCTACATGTATT 4680
Db 4681 TATATTTCCGTATTTCTTCATCATATTTGGATCCTTTTTCACACTCAATCTGTTCAATGGTG 4740
Qy 4681 TATATTTCCGTATTTCTTCATCATATTTGGATCCTTTTTCACACTCAATCTGTTCAATGGTG 4740
Db 4741 TTATCATTTGATAATTTTAAATGAGCAAAAAGAAAAGAGAGGTGGATCATTAGAATGTTCA 4800
Qy 4741 TTATCATTTGATAATTTTAAATGAGCAAAAAGAAAAGAGAGGTGGATCATTAGAATGTTCA 4800
Db 4801 TGACAAAGATTCAGAAAAAGTACTATAATGCTATGAAAAAGATGGCTCTTAAAAAACCAT 4860
Qy 4801 TGACAAAGATTCAGAAAAAGTACTATAATGCTATGAAAAAGATGGCTCTTAAAAAACCAT 4860
Db 4861 TAAAAAGCCATTCCAAAGACCAAGGTGGCGACCAAGCAATAGTCTTTGAAATAGTAACCG 4920
Qy 4861 TAAAAAGCCATTCCAAAGACCAAGGTGGCGACCAAGCAATAGTCTTTGAAATAGTAACCG 4920
Db 4921 ATAAGAAATTCGATATATCATATATGTTTATTCATTTGGTCTGAACATGTTACCATGAGCC 4980
Qy 4921 ATAAGAAATTCGATATATCATATATGTTTATTCATTTGGTCTGAACATGTTACCATGAGCC 4980
Db 4981 TCGATCGTTACGATCGTCGGACAGTATAAGCGGTCTAGACTATCTCAATGGCATAT 5040
Qy 4981 TCGATCGTTACGATCGTCGGACAGTATAAGCGGTCTAGACTATCTCAATGGCATAT 5040
Db 5041 TCGTAGTTATTTTCCAGTTCGGAATGCTATTAATAATATTCGCTTTAGCATATCACTATT 5100
Qy 5041 TCGTAGTTATTTTCCAGTTCGGAATGCTATTAATAATATTCGCTTTAGCATATCACTATT 5100
Db 5101 TTATTTAGCCCATGGAATTTATTTGATGATAGTGTGTCATTTATTCATCTTAGGTCGTTG 5160
Qy 5101 TTATTTAGCCCATGGAATTTATTTGATGATAGTGTGTCATTTATTCATCTTAGGTCGTTG 5160
Db 5161 TACTTTAGCGATATATTCGAGAACTACTTCGTCTCCGACCCCTGCTCCAGTGGTGGCGTG 5220
Qy 5161 TACTTTAGCGATATATTCGAGAACTACTTCGTCTCCGACCCCTGCTCCAGTGGTGGCGTG 5220
Db 5221 TGGCGAAAGTGGCGCGTGTCTTCGACTGGTGAAGGAGCAAGGCAATTCGACACTGCG 5280
Qy 5221 TGGCGAAAGTGGCGCGTGTCTTCGACTGGTGAAGGAGCAAGGCAATTCGACACTGCG 5280
Db 5281 TCTTCGCGTGGCCATGTCGTCGCGGCCCTGTTCAACATGTCGCTGCTGTCGTTCCCTGG 5340
Qy 5281 TCTTCGCGTGGCCATGTCGTCGCGGCCCTGTTCAACATGTCGCTGCTGTCGTTCCCTGG 5340
Db 5341 TCATCTTCATCTTTGCCATTTTCGGCATGTCGTTCTTCATGCACGTGAAGGAGAGAGCG 5400
Qy 5341 TCATCTTCATCTTTGCCATTTTCGGCATGTCGTTCTTCATGCACGTGAAGGAGAGAGCG 5400
Db 5401 GCATTTAAACGACGCTTACAACTTCAAGACTTTGGCCAGAGCATGATCCTGCTCTTTTACA 5460
Qy 5401 GCATTTAAACGACGCTTACAACTTCAAGACTTTGGCCAGAGCATGATCCTGCTCTTTACA 5460
Db 5461 TGTGACGCTACGCGGTTGGGATGCTGAGCGCCATTTCAATGAGGAAGCATGCG 5520
Qy 5461 TGTGACGCTACGCGGTTGGGATGCTGAGCGCCATTTCAATGAGGAAGCATGCG 5520
Db 5521 ATCCACCCGACAGCAGCAAGGCTATCGGGCAATTTGGTTACGACCGCTTGGAAATAA 5580
Qy 5521 ATCCACCCGACAGCAGCAAGGCTATCGGGCAATTTGGTTACGACCGCTTGGAAATAA 5580
Db 5581 CGTTTCTCTCTCATACCTAGTTAAGCTTTTTCATAGTTTATTAATATGATGATGCTG 5640
Qy 5581 CGTTTCTCTCTCATACCTAGTTAAGCTTTTTCATAGTTTATTAATATGATGATGCTG 5640
Db 5641 TCATTTCTCGAGAACTATAGTCAGGCCACCGAGGAGGTGCAAGAGGCTTCAACCGACGAG 5700
Qy 5641 TCATTTCTCGAGAACTATAGTCAGGCCACCGAGGAGGTGCAAGAGGCTTCAACCGACGAG 5700
Db 5701 ACTAGACATGTACTATGATGATCTGGCAGCAATTCGATCCGAGGCGACCCAGTACATAC 5760
Qy 5701 ACTAGACATGTACTATGATGATCTGGCAGCAATTCGATCCGAGGCGACCCAGTACATAC 5760
|||||

Db	5761	GCTATGATCAGCTGCTCGAATTCTTGGACGTACTGGAGCCCCCGCTGCAGATCCACAAC	5820
Qy	5761		
Db	5761	GCTATGATCAGCTGCTCGAATTCTTGGACGTACTGGAGCCCCCGCTGCAGATCCACAAC	5820
Qy	5761		
Db	5821	CGAACAGTACAAAGTATATCGATGGACATACCCATCTGTGCGGTGACCTCATGTACT	5880
Qy	5821		
Db	5821	CGAACAGTACAAAGTATATCGATGGACATACCCATCTGTGCGGTGACCTCATGTACT	5880
Qy	5821		
Db	5881	GCCTCGACATCCTCGAGCCCTTACAAAGACTTCTTTGCCGGAAGGCAATCCGATAG	5940
Qy	5881		
Db	5881	GCCTCGACATCCTCGAGCCCTTACAAAGACTTCTTTGCCGGAAGGCAATCCGATAG	5940
Qy	5881		
Db	5941	AGGAGACGGGTGAGATTGTTGATAGCGGCCGCCGGATACGAGGGGTACGAGCCCG	6000
Qy	5941		
Db	5941	AGGAGACGGGTGAGATTGTTGATAGCGGCCGCCGGATACGAGGGGTACGAGCCCG	6000
Qy	5941		
Db	6001	TCTCATCAACGCTGTGGCGTCAAGCTGAGGAGTACTGCGCCCGCTAATCCAGCACGCT	6060
Qy	6001		
Db	6001	TCTCATCAACGCTGTGGCGTCAAGCTGAGGAGTACTGCGCCCGCTAATCCAGCACGCT	6060
Qy	6001		
Db	6061	GGGAAAGCACAAAGCCGCGGAGGAGTGGTCTTTGACCGGGATACGGATCATG	6120
Qy	6061		
Db	6061	GGGAAAGCACAAAGCCGCGGAGGAGTGGTCTTTGACCGGGATACGGATCATG	6120
Qy	6061		
Db	6121	GCATGCGGTGATCCGAGTCCGGGACCCGGCGCCCGATGAAGCAACGAGCGCGATG	6180
Qy	6121		
Db	6121	GCATGCGGTGATCCGAGTCCGGGACCCGGCGCCCGATGAAGCAACGAGCGCGATG	6180
Qy	6121		
Db	6181	CGCCCGCTGTGGAGATGTTAGTGTAAACGTTACTGCAGAAGGAGCTGCCGATCCGATG	6240
Qy	6181		
Db	6181	CGCCCGCTGTGGAGATGTTAGTGTAAACGTTACTGCAGAAGGAGCTGCCGATCCGATG	6240
Qy	6181		
Db	6241	AGAGTAATGTAATAGTCCGGGTGAGGATGCAGCGCGCGCGACAGCAGCAGCAG	6300
Qy	6241		
Db	6241	AGAGTAATGTAATAGTCCGGGTGAGGATGCAGCGCGCGCGACAGCAGCAGCAGCAG	6300
Qy	6241		
Db	6301	CGGCGCGCGCGCACAGCAGCGCGGGGAAGTCCCGGAGCGGGTAGCGCCGGGCGACAG	6360
Qy	6301		
Db	6301	CGGCGCGCGCGCACAGCAGCGCGGGGAAGTCCCGGAGCGGGTAGCGCCGGGCGACAG	6360
Qy	6301		
Db	6361	CCGCGCTTCGTGTGAGAGCGAGGGTTCGTACGAAGAAGCGCCACAAGTGGTCAATC	6420
Qy	6361		
Db	6361	CCGCGCTTCGTGTGAGAGCGAGGGTTCGTACGAAGAAGCGCCACAAGTGGTCAATC	6420
Qy	6361		
Db	6421	ACTCGCATCCGCGAGCATCACGTCCGCGCACGGCGGATGTCTGAGCCAGGCGCTCGCCCC	6480
Qy	6421		
Db	6421	ACTCGCATCCGCGAGCATCACGTCCGCGCACGGCGGATGTCTGAGCCAGGCGCTCGCCCC	6480
Qy	6421		
Db	6481	CCCTCCAAGATGACCGGAGTATTAGCTCTAGA	6513
Qy	6481		
Db	6481	CCCTCCAAGATGACCGGAGTATTAGCTCTAGA	6513
Qy	6481		

RESULT	6	US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
ID	AC	xxxxxx
DT		
DE		Sequence 14, Application US/08232463
CC		Sequence 14, Application US/08232463
CC		Patent No. 5670367
CC		GENERAL INFORMATION:
CC		APPLICANT: DORNER, F.
CC		APPLICANT: SCHEIFLINGER, F.
CC		APPLICANT: FALKNER, F. G.
CC		TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CC		NUMBER OF SEQUENCES: 52
CC		CORRESPONDENCE ADDRESS:
CC		ADDRESSEE: Foley & Lardner
CC		STREET: 1800 Diagonal Road, Suite 500
CC		CITY: Alexandria
CC		STATE: VA
CC		COUNTRY: USA

ZIP: 22313-0299
 COMPUTER TYPE: Floppy disk
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,463
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/935,313
 FILING DATE:
 APPLICATION NUMBER: EP 91 114 300.6
 FILING DATE: 26-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER:
 REFERENCE/DOCKET NUMBER: 50472/114 IMM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)836-9300
 TELEFAX: (703)683-4109
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7218 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 CLONE: pTZgt-F15
 SEQUENCE 7218 BP: 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.

[illegible]

RESULT 7
ID US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
AC xxxxxx
DT
DE Sequence 14, Application US/08232463
CC Sequence 14, Application US/08232463
CC Patent No. 5670367


```

RESULT          9
ID US-08-238-163--5 STANDARD; DNA; UNC; 215 BP.
AC xxxxxx
DT
Sequence 5, Application US/08238163
DE Sequence 5, Application US/08238163
CC Patent No. 5569830
CC GENERAL INFORMATION:
CC APPLICANT: BENNETT, Alan
CC APPLICANT: LABAVITCH, John M.
CC APPLICANT: POWELL, Ann
CC APPLICANT: STOTZ, Henrik
CC TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
CC TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: Steuart Street Tower, One Market Plaza
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: US
CC ZIP: 94105-1493
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/238.163
CC FILING DATE: 03-MAY-1994
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Bastian, Kevin L.
CC REGISTRATION NUMBER: 34,774
CC REFERENCE/DOCKET NUMBER: 2307E-540
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 215 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: misc_feature
CC LOCATION: 1..215
CC OTHER INFORMATION: /standard_name= "Deduced amino acid
CC OTHER INFORMATION: sequence of PGIP from bean."
CC SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER..
SQ
Query Match 0.6%; Score 36; DB 1; Length 215;
Best Local similarity 16.9%; Pred. No. 2.27e-07;
Matches 27; Conservative 61; Mismatches 72; Indels 0; Gaps 0;
Db      1 MTNWMTSSSVSRATSCNDKAKKGNTTSWTTGCCNRTWGVCDDTDFTYRVNDSGHNK 60
Cp      233 ATCTCGTGCTGGTCATCATATCGGAATTCTTTTTGTGTTTCTGCACCATAATCGCG 174
Db      61 YSSANYNGGNVGAKTHTVTVNSVGADSKTVTDYSNASCTSSSSNGTGDGNSGADSY 120
Cp      173 CACCTCTCCCTCGGCTCTCTTTCTTCAGCTCCCTCTGCTTTTCATGTCAGCGGCAAT 114
Db      121 GSKTAMTSRNRGTGTANNVAVDNRNMGDASVSGDKNTKKH 160
Cp      113 GCCTTGTTCGATTGTCACCAATGATTCGGCGGTAAAGGA 74
RESULT        10
ID PCT-US95-11869-1 STANDARD; DNA; UNC; 1809 BP.
AC xxxxxx

```

CC STATE: Illinois
CC COUNTRY: U.S.A.
CC ZIP: 60603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/745,206A
CC FILING DATE: 19910815
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Feder, Scott B
CC REFERENCE/DOCKET NUMBER: 51504
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312-372-7842
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 5904 base pairs
CC TYPE: NUCLEIC ACID
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: DNA (genomic)
CC SEQUENCE 5904 BP; 1353 A; 1717 C; 1544 G; 1260 T; 30 OTHER.
Query Match 0.6%; Score 39; DB 1; Length 5904;
Best Local Similarity 60.3%; Pred. No. 3.54e-09;
Matches 114; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
Db 3759 CATCTGCTCAACACCATCTCCCTGGCCATGCAGCACTACGACGAGCTCCCTGTTCAA 3818
Qy 2504 CATTGTGCTCAACACGATGTTTCATGGCAATGATCACCACGATATGAACAGGAGATGGA 2563
Db 3819 AATGCCATGAACATCTCTCAACATGCTCTTCACTGGCTCTTACCGTGGAGATGATCCT 3878
Qy 2564 ACGGTGCTCAAGATGGCACTATTCTTCACGCCACCTTTCCTATCGAGGCCACCAT 2623
Db 3879 GAAGCTCATTCCTTCAACCCAGGGTACTTTAGTGATCCCTGGGAATGTTTTGACTT 3938
Qy 2624 GAAGTAATGGCCATGATGACCCCAAGTACTATTTCAGAGGGCTGGAACATCTTCGACTT 2683
Db 3939 CCTCATCGT 3947
Qy 2684 CATTATCGT 2692
RESULT 12
ID 5386025-5 STANDARD; DNA; UNC; 6459 BP.
AC xxxxxx
DT 01-JAN-1900
DE Patent No. 5386025.
CC Patent No. 5386025
CC APPLICANT: JAY, SCOTT D.; ELLIS, STEVEN B.; HARPOLD, MICHAEL
CC M.: CAMPBELL, KEVIN P.
CC TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
CC NUMBER OF SEQUENCES: 9
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/482,384
CC FILING DATE: 20-FEB-1990
CC SEQ ID NO.5:
CC LENGTH: 5962
CC Sequence 6459 BP; 1280 A; 1835 C; 1691 G; 1156 T; 497 other;
Query Match 0.6%; Score 37; DB 3; Length 5962;
Best Local Similarity 65.0%; Pred. No. 5.73e-08;
Matches 80; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
Db 3862 CTGCTGAGTGGCGGCGGAGGGCTGGCGACGCTGTGTGGAGCTTCAATCAAGTCTTCAG 3921
Qy 5247 CTGCTGAGGAGGAGCCAGGGGATCGGACACTGTCTCTCGGCTGGGCCATCTCGCTGCCG 5306
Db 3922 GCCCTGCCCTACGTGGCCCTGCTCATCGTCATGCTGTCTTCATCTACGCCGTCATCGGC 3981

QY 5307 GCCTGTCAACATCTGCCCTGCTGCTGCTCTCTGCTCATGTTCATCTTGGCATTTTCGGC 5366
Db 3982 ATG 3984
QY 5367 ATG 5369
RESULT 13
ID US-08-404-354B-1 STANDARD; DNA; UNC; 5975 BP.
AC xxxxxx
DT Sequence 1, Application US/08404354B
DE Sequence 1, Application US/08404354B
CC Patent No. 5618720
CC GENERAL INFORMATION:
CC APPLICANT: Ellis, Steven Bradley
CC APPLICANT: Williams, Mark E.
CC APPLICANT: Harpold, Michael Miller
CC APPLICANT: Schwartz, Arnold
CC APPLICANT: Brenner, Robert
CC TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
CC NUMBER OF SEQUENCES: 3
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Brown, Martin, Haller & McClain
CC STREET: 1660 Union Street
CC CITY: San Diego
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92101-2926
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FastSeq Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/404,354B
CC FILING DATE: 15-FEB-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/314,083
CC FILING DATE: 28-SEP-1994
CC APPLICATION NUMBER: US 07/914,231
CC FILING DATE: 13-JUL-1992
CC APPLICATION NUMBER: US 07/603,751
CC FILING DATE: 08-NOV-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seidman, Stephanie L.
CC REGISTRATION NUMBER: 33,779
CC REFERENCE/DOCKET NUMBER: 6362-53192
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-238-0999
CC TELEFAX: 619-238-0062
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 5975 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC FEATURE:
CC NAME/KEY: Coding Sequence
CC LOCATION: 79..5700
CC OTHER INFORMATION:
CC SEQUENCE 5975 BP; 1291 A; 1832 C; 1695 G; 1157 T; 0 OTHER.
Query Match 0.6%; Score 37; DB 1; Length 5975;
Best Local Similarity 65.0%; Pred. No. 5.73e-08;
Matches 80; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
Db 3814 CTGCTGAGTGGCGGCGGAGGGCTGGCGACGCTGCTGTGGAGTTCATCAAGTCTTCAG 3873

QY 5247 CTGCTGAGGAGGCAAGGCGATTGGACACTGCTCTTCCGGTTGGCCATGCTGCTGCCG 5306
Db 3874 GCCCTGCGCTAGTGGCCCTGCTCATGCTGCTGTTCTTTCATCTAGCGCGTCATCGGC 3933
QY 5307 GCCCTGTTCAACATGCTGCTGCTGTTCTTGGTCATGTTCACTTTGGCATTTTGGC 5366
Db 3934 ATG 3936
QY 5367 ATG 5369
RESULT 14
ID US-08-314-083B-1 STANDARD; DNA; UNC; 5975 BP.
AC xxxxxx
DE Sequence 1, Application US/08314083B
CC Sequence 1, Application US/08314083B
CC Patent No. 5686241
CC GENERAL INFORMATION:
CC APPLICANT: Ellis, Steven Bradley
CC APPLICANT: Williams, Mark E.
CC APPLICANT: Harpold, Michael Miller
CC APPLICANT: Schwartz, Arnold
CC APPLICANT: Brenner, Robert
CC TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
CC NUMBER OF SEQUENCES: 3
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Brown, Martin, Haller & McClain
CC STREET: 1660 Union Street
CC CITY: San Diego
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92101-2926
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FastSeq Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,083B
CC FILING DATE: 28-SEPT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/914,231
CC FILING DATE: 13-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/603,751
CC FILING DATE: 08-NOV-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seidman, Stephanie L
CC REGISTRATION NUMBER: 33,779
CC REFERENCE/DOCKET NUMBER: 6362-53191
CC TELEPHONE: 619-238-0999
CC TELEFAX: 619-238-0062
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 5975 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC FEATURE:
CC NAME/KEY: Coding Sequence
CC LOCATION: 79...5700
CC OTHER INFORMATION:
CC SEQUENCE 5975 BP; 1291 A; 1832 C; 1695 G; 1157 T; 0 OTHER.

Query Match 0.6%; Score 37; DB 1; Length 5975;
Best Local Similarity 65.0%; Pred. No. 5-73e-08;
Matches 80; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Db 3814 CTGCTGAGTGGCGGCGAGGCGTGGCGACGCTGCTGTGAGCGTTTCATCAAGTCCTTCCAG 3873
QY 5247 CTGCTGAGGAGGCAAGGCGATTGGACACTGCTCTTCCGGTTGGCCATGCTGCTGCCG 5306
Db 3874 GCCCTGCGCTAGTGGCCCTGCTCATGCTGCTTCTTTCATCTAGCGCGTCATCGGC 3933
QY 5307 GCCCTGTTCAACATGCTGCTGCTGTTCTTCCCTGGTCACTGTTGCAATTTTCCGC 5366
Db 3934 ATG 3936
QY 5367 ATG 5369
RESULT 15
ID US-08-337-339-1 STANDARD; DNA; UNC; 33 BP.
AC xxxxxx
DE Sequence 1, Application US/08337339
CC Sequence 1, Application US/08337339
CC Patent No. 5593864
CC GENERAL INFORMATION:
CC APPLICANT: Warmke, Jeffrey W.
CC APPLICANT: Hall, Linda
CC APPLICANT: Feng, Gouping
CC APPLICANT: Van Der Ploeg, Leonardus
CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
CC TITLE OF INVENTION: PARA SODIUM CHANNEL
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: John W. Wallen III
CC STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CC CITY: Rahway
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07065-0900
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/337,339
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Wallen III, John W.
CC REGISTRATION NUMBER: 35,403
CC REFERENCE/DOCKET NUMBER: 19332
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (908) 594-3905
CC TELEFAX: (908) 594-4720
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 33 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC SEQUENCE 33 BP; 10 A; 8 C; 9 G; 6 T; 0 OTHER.

Query Match 0.5%; Score 30; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.37e-04;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 TCTAGACGTTGGCGCATAGACAATGACAG 33
QY 1 TCTAGACGTTGGCGCATAGACAATGACAG 30

Search completed: Sun Sep 13 07:25:43 1998
Job time : 321 secs.

Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Db	1	tctagacgttggcgcgatacagaacaatacagaatattccagctcgatatactgagagaac	60
Qy	1	TCTAGACGTTGGCGCATACAGATGACAGAATTCGGACTCGATATCTGAGAGAAC	60
Db	61	gcagttgttccgtcccttaccgcgaatcattggcgcaaatcgaaacacgcattgcg	120
Qy	61	GCAGTTGTTCGTCCTTACCGCGCAATCATTTGGTGCAATCGAAACAACGCAATTGCCG	120
Db	121	ctgaacatgaaacagagagagctggaagaaagagagccgagggagagaggtccgcgat	180
Qy	121	CTGAACATGAACAGCAGAGAGCTGGAAGAAAGAGAGCCGAGGGAGAGGTCCCGCAT	180
Db	181	atggtcgaaagaaacaaagaaatccgatatgatgacgagagcagagatgaaggtc	240
Qy	181	ATGTCGCAAGAAAACAAAAGAAATCCGATATGATGACGAGGACGAGATGAAGTTC	240
Db	241	cacaacggatctctacacttgaaacaggggtgccaatcacctgttcgatgttcagggcagct	300
Qy	241	CACAACGGATCTCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTCGAGGCAGCT	300
Db	301	tccgcgcggaattggctccactcctctcgagatatcgatccctactacagcaatgtac	360
Qy	301	TCCGCGCGGAATTGGCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC	360
Db	361	tgacattcgtagttgtaagcaaaagaaagatatatttcgctttttctgcatcaaaagcaa	420
Qy	361	TGACATTCTGATGTTGAAGCAAAAGAAAGATATTTTCGCTTTTCTGTCATCAAAACCAA	420
Db	421	tgtagtgcgtcgatccatccaatccgataogtgcgtggtggccatttacattctagtgcatc	480
Qy	421	TGTGGATGCTCGATCCATTCATCCGATACGTCGTCGTGTGGCCATTTACATTCTAGTGATC	480
Db	481	cattatttccctattcactcccaaatctcgaatctcgaatccatccatcctaataatgc	540
Qy	481	CATTATTTCCCTATTTCAATCAATCAACCAATCTCGCAACTGCTATCTGATGATAATGC	540
Db	541	cgaaacccacacggttgagtcacactgaggtgatattacccgggaattacacatttgaat	600
Qy	541	CGAAACCCACACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT	600
Db	601	cagctgttaagtgatggcagaggtttcattttatgcccgttacgttatcttagagatg	660
Qy	601	CAGCTGTTTAAAGTGATGGCAGCAGGTTTCATTTTATGCCCGTTTACGTTATCTTAGAGATG	660
Db	661	catggaattggctggaactctgtaaatagctttagcttatgtaccatgggtatagatt	720
Qy	661	CATGGAATTGGCTGGACTTCGTAGTAATAGCTTAGCTTATGTGACCATGGGTATAGATT	720
Db	721	tagtgaatcagcagccctgcgaacgttttaggtgcgtgcgagcgttaaaacccgtagcca	780
Qy	721	TAGTGAATCTAGCAGCCCTGCGAACGTTTAGGTGCTCGAGCGCTTAAAACCCGTAGCCA	780
Db	781	ttgtccaggtctgaagaccatcgtcgcgcgctcatcgaaatcggtgaagaatcgcgc	840
Qy	781	TTGTCCCAAGGTTGAAGACCATCGTCGCGCGCGTCATCGAATCGGTGAAGAATCTGGCGC	840
Db	841	atgtgattactctgaccatgttctccctgcggtggttcgcttgatggcctacagatctt	900
Qy	841	ATGTGATTATCTGACCATGTTCTCCCTGTCCGTTGCGGTTCGATGGCCCTACAGATCT	900
Db	901	atatgggcgtctcaccgagagtgatcaagaagttcccgctggacggttccctggggca	960
Qy	901	ATATGGGCGTCTCACCAGAGTGCATCAAGAAGTTCCCGCTGGACGCTTCTCTGGGCA	960
Db	961	atctacacagagagactgggactatcaaatcgaaatagctccaattggtattccagag	1020
Qy	961	ATCTACACAGAGAGACTGGGACTATCAAAATCGCAATAGCTCCAAATTTGGTATTCGAGG	1020
Db	1021	acgagggcatctcatttccgtttatcgggcaatatatccgggtgcggggaatgcgacgacg	1080
Qy	1021	ACGAGGGCATCTCATTTCGTTATCGGCAATATATCCGGTGCGGGGCAATGCGACGACG	1080

Db	1081	attacgtgtgcctgcaggggtttgtccgaatccgaatttgctacaccagcttcgatt	1140
Qy	1081	ATTACGTGTGCTGCAGGGTTTGTCCGAATCCGAATATGCGTACACCAGCTTCGATT	1140
Db	1141	cgttcggatggccttctcgtccgccttcggctgatgacacaggaacttctgggaggatc	1200
Qy	1141	CGTTCGGATGGCTTCTCCTCCGCTTCCGCTGATACACAGACTTCTGGGAGGATC	1200
Db	1201	tgaccagctggtgtgcgcgcgcgacacatgacacatgctgttctttatagtcaca	1260
Qy	1201	TGTACCAGCTGTTGCGCGCCGCGGACCATGACATGCTGTCTTTATAGTCATCA	1260
Db	1261	tcttcctaggttcattctattgtgaattgttttgccattgttgccattgtcgatg	1320
Qy	1261	TCTTCTAGTTTCACTTCTATCTTGTGAATTTGATTTTGCCATTGTGTCATGCTGATG	1320
Db	1321	agcaattgcaaaaggagccgaagaagaagagctgcggaagaggagcgatcacatgaag	1380
Qy	1321	AGCAATTGCAAAAGGAGCCGAAGAAGAGAGGCTGCCGAAGAGGAGGCGATACGTTGAG	1380
Db	1381	cggaagaactgcgcgcgcgaagcgccaaagctggagagcgggccaatgcagggctc	1440
Qy	1381	CGGAAGAAGCTGCCGCGCCAAAGCGGCCAAGCTGGAGGAGCGGCCAATGCGAGGCTC	1440
Db	1441	aggcagcagcgatgcggtgcgcgcgaagagctgcactgcacatccgcggaatgccaaga	1500
Qy	1441	AGGCAGCAGCGGATGCGGCTGCGCGGAAGAGGCTGCACATCGCAATGCGGAATGCGCAAG	1500
Db	1501	gtccgagctattctgtcatcagctatgactattgttgcgcgagagaagcaacgatg	1560
Qy	1501	GTCGACGTTATTTTCATCAGCTATGAGCTATTTGTTGGCGCGAAGAGGCAACGATG	1560
Db	1561	acaacacaaagagaagatgtccattcggagcgctgcgagtgagtgagtcgggtgagcg	1620
Qy	1561	ACAACAAAGAGAGATGTCATTTCGGAGCGTCGAGGTGGAGTGGAGTCCGTTAGCGG	1620
Db	1621	ttatacaagacaacacagcactaccacagcacaccaagctaccacaaagtctgtaaaagta	1680
Qy	1621	TTATACAAAGACAAACAGCACCTTACACAGCACACCAAGCTACCAAAAGTTCGTAAGTGA	1680
Db	1681	gcacgacatccttactcttaccctggttcaccgtttaacatagcaggggatcacgtagt	1740
Qy	1681	GCACGACATCCTTATCTTACCTGGTTACCGTTTAAACATACGAGGGGATCACGTAGTT	1740
Db	1741	ctcacaaagtacacgaacgcgagcggttgcgcgtttgtataccgcggtagcgatcgta	1800
Qy	1741	CTCACAAGTACAGATACGGAACGGAGCGTGGCGCTTTGTTATACCCGTTAGCGATCGTA	1800
Db	1801	agcattggtattgtcaacatatcagatgccagcagcacttgcctatgcgcgacgt	1860
Qy	1801	AGCATTTGTTTGTCAACATATCAGGATGCCAGCAGCATTGGCCTATGCGCAGCATT	1860
Db	1861	cgaaatgcgltcaccccgatgtccgaagagaattggggccatcatagtgccgtgtactatg	1920
Qy	1861	CGAATGCCGTACCCCGATGTCGAGAGAGATGSGGCCATAGTGCCTGTACTATG	1920
Db	1921	gcaatctaggctccccacactatcgtaacctcgatcagtcagtcgccgaatatcgtaacct	1980
Qy	1921	GCAATCTAGGCTCCGACACTCATCTATACCTCGCATCAGTCCCGAATATCTATACCT	1980
Db	1981	caatggcgatctactcggcggtatggcggtcagtcagtcagcaaatgaccaagaga	2040
Qy	1981	CATATGGCGATCTACTCGGGGATGGCGCTCATGGCGGTACGACCAATGACCAAGGAGA	2040
Db	2041	gcaaatggcgaacccgcaacacacgcgaatacaatcagtgggcgccacaaatggcggaacca	2100
Qy	2041	GCAAAATGGCAACCCGCAACACACGCAATCAATCAGTGGSGGCCACCAATGGCGGACCA	2100
Db	2101	cctgtctggacacaaatcacaagctcgatcgcgactacggaattggcctggagtga	2160
Qy	2101	CTGTCTGGACACCAATCACAAGCTCGATCATCGACTACGAAATTTGGCCTGGAGTGCA	2160

Dbb 2161 cggacgaagctggcaagattaaacatcatgacaatccttttatcgagcccgctcagacac 2220
QY 2161 CGGACGAAGCTGGCAAGATTAAACATCATGACAATCCTTTATTCGAGCCGCTCCAGAC 2220
Dbb 2221 aaacggtgggttgatataaagatgtgagtcctgaatgacatcatcgacaagcgcgctg 2280
QY 2221 AAACGGTGGTGTGATATGAAGAGTGTGATGCTCTGAATGACATCATCGAACAGCCGCTG 2280
Dbb 2281 gtccgacagctcggcgcaagcgatcgcggtgtctccgtttactattttcccaacagagacg 2340
QY 2281 GTCCGACAGCTCGGCGCAAGCGATCGCGGTGTCTCCGTTTACTATTTCCTCAACAGAGACG 2340
Dbb 2341 atgacagagatgggcgcagcttcaaaagacaaggcactcgaagtgcactcctcaaggcaatcg 2400
QY 2341 ATGACAGGATGGGCGCCACGTTTCAAGACAAAGCACGACGTCGAAGTGATCCTCAAAAGGCATCG 2400
Dbb 2401 atgtgtttgtgtggtggaactgtgctgggtttggttgaatttcaggagtggtatcgc 2460
QY 2401 ATGTGTTTTGTGTGGGACTGTGCTGGGTTGGTTGAAATTCAGAGAGTGGGTATCGC 2460
Dbb 2461 tcatcgtcttcgatcccttcgtcgagctcttcacagctgtgcattgtggtcaacacga 2520
QY 2461 TCATCGCTTTCGATCCCTTCGTCAGCTCTTCATCACGCTGTGCTATGTTGCTCAACACGA 2520
Dbb 2521 tgttcattggaattggtatcacacagatagaacaaggagatggaaacggtgtcctcaagagt 2580
QY 2521 TGTTCATGGCAATGGATTCACACAGATAGAACAAGAGATGGAAACGGCGTCTCAAGAGTG 2580
Dbb 2581 gcaactattcttcacgcgcacctttgccatcgagccacatgaagcctaagtgccatga 2640
QY 2581 GCAACTATTCTTCACCGCCACCTTTGCCATCGAGGCCACCATGAAGCTTAATGGCCATGA 2640
Dbb 2641 gcccgaagtactatttccaggaggtggaaacatcttcgcacttcattatcgtggccctat 2700
QY 2641 GCCCAAGTACTATTTCACGAGGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTAT 2700
Dbb 2701 cgtattggaactgggactcgaggtgtccagggtctcgtatgtccgtattccttctcgat 2760
QY 2701 CGCTATTGGAACTGGGACTCGAGGGTCTCCAGGGTCTGTCGGTATTGCGTTCTCTTCGAT 2760
Dbb 2761 tgcctgctgtattcaactggcgaagctcttggccacacttaatttactatttcgatta 2820
QY 2761 TGCTGCTGTATTCAAACCTGGCCAAAGTCTTGGCCACACCTTAATTTACTCATTTTCGAATTA 2820
Dbb 2821 tgggacgcaccatggcgcttgggttaacttgacatttggacttggattcatcatcttca 2880
QY 2821 TGGGACGCACCATGGCGCTTGGGTAACTGTGACATTTGACTTTGGATTAATCATCTCA 2880
Dbb 2881 tctttgcggtatgggaaatgcgaactgttcggaaagaattatcatgatcaaaaggaccgct 2940
QY 2881 TCTTTGCGGTCATGGGAATGCAACTGTTTCGAAAAGAAATTATCATGATCACAAAGGACCGCT 2940
Dbb 2941 ttcggatggcgaactggcgctgggaacttcacggactttatgcagcttcatgatcg 3000
QY 2941 TTCGGATGGCGACTGCCGGCTGGGAACCTTCACCGACTTTATGCACAGCTTCATGATCG 3000
Dbb 3001 tgttccgggtgctctgcggagaaaggatcgatccatctgtgggactgcgtacgtggggcg 3060
QY 3001 TGTTCCGGGTGCTCTGCGGAGAAATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGCG 3060
Dbb 3061 atgtcgtgcattcccttcttcttggccaccggttgcacatcggaacttctgtggaactta 3120
QY 3061 ATGTCGTGTCGATTCCCTTCTTCTTGGCCACCGTGTGCATCGGCAATCTTGTGTACTTA 3120
Dbb 3121 acctttcttagccttcttcttgcgaatttggctcatctagcttatacgccgactg 3180
QY 3121 ACCTTTTCTTAGCCTTCTTGTGTCGAATTTGGCTCATCTAGCTTATCACGCCCGGACTG 3180
Dbb 3181 ccgataacgatacgaataaaatagccgaggtccttcaatgcaattggcggattttaaagtt 3240
QY 3181 CCGATACGATACGAATAAATACCCGAGGCTTCAATCGAATTTGGCCGATTTAAAGTT 3240
Dbb 3241 ggggttaagcgtaatattgtgattgtttcaagtttaacgttaacgttaacaaattgacaaatcaaa 3300

QY 3241 GGTTTAAGCGTAATAATGCTGATTGTTTCAAGTTAATAGCTAAACAAATGACAAATCAAA 3300
Dbb 3301 taagtatcaaccatcaggtgagagacacacacagatcagttgagtttgagcgaagagc 3360
QY 3301 TAAGTGTATCAACCATCAGGTGAGAGACCAACCGAGATCAGTTGGATTTGGAGCGAAGAGC 3360
Dbb 3361 atggtgacaacgaactggagctggggccacgaagagatcctcgcgcagcggcctcatcaaga 3420
QY 3361 ATGGTGACAACGAACCTGGAGCTGGGCCACGACGAGATCTCGCCGACGGCTCATCAAGA 3420
Dbb 3421 aggggatcaaggagcagaacgcaactggaggtggccatcgggggactcggaattcaacga 3480
QY 3421 AGGGGATCAAGGAGCAGACGAACCTGGAGGTGGCCATCGGGGATCGGATGGAATTCACGA 3480
Dbb 3481 tacacggcacatgaaagacaacacgcaagaaatccaaatcttaaaataacgcgaacga 3540
QY 3481 TACACGGCGNATGAAGACAACAGCCGAGAAATCCAAATATCTAANAATACGCAACGA 3540
Dbb 3541 tgattggcaactcaattaaaccaccaagaacaatagactggaacacgagctaaaccatagag 3600
QY 3541 TGATTGSCAACTCAATTAACCAACCAAGACAATAGACTGGAAACACGAGCTAAACCATAGAG 3600
Dbb 3601 gttgttccttaaggagcagacacactgcagcaatttaactcatatggttagcctaagaatc 3660
QY 3601 GTTTGTCTTACAGSACGACGACACTGCCAGCATTAACCTCATATGTTAGCATAAAGAAATC 3660
Dbb 3661 gaccattcaaggagcagacccaagggcagcgcagacgatggagggcgaggaagc 3720
QY 3661 GACCATTCAAGGACGAGAGCCACAGGGCAGCCGAGAGATGGAGGGCGGAGGAAGC 3720
Dbb 3721 ggcaccccgcaaggaggatttaggtctcgacgaggaactggacggagggcggaatgcg 3780
QY 3721 GCACGCCACGAAGGAGGATTTAGGTCTCGACGAGGAACCTGGACGAGGAGGCGAATGCG 3780
Dbb 3781 agagggcccgctcgcagcgtgatcatattcatgcacacgacgaggatatactactgatg 3840
QY 3781 AGGAGGCCCGCTCGACGGTGTATCATTTATTCATGCACACGACGAGGATATCTCGATG 3840
Dbb 3841 aatatccagctgattctcgcgcgattcgtactataagaataattccgactcttagccggtg 3900
QY 3841 AATATCCAGCTGATTTGCTGCCCGATTCGTACTATAGAATAATTTCCGATCTTACGCGGTG 3900
Dbb 3901 acgatgactgcgcttctggcaaggatgggcaatttgcagactgaaacttttcaataa 3960
QY 3901 ACGATGACTGCCGCTTCTGCGAAGGATGGGCAATTTACGACTGAAACTTTTCAATTAA 3960
Dbb 3961 ttgaaaaataatttttgaacacgctgttatcatctatgatttttaagttagctt 4020
QY 3961 TTGAAAAATAAATAATTTTGAACACAGCTGTATCATCTATGATTTTAATAGTAGTAGCTT 4020
Dbb 4021 tggcattagaagatgacatctgcacaagaccatactgcaggatatatttatactata 4080
QY 4021 TGGCATTAGAAGATGATACATCTGCCACAAAGACCCACTACTGACAGGATATTTTATCTATA 4080
Dbb 4081 tggacagaataatttgcggttatattcttcttggaaaattgtaatacaagtggttggcgctcg 4140
QY 4081 TGGACAGAATAATTTACGGTATATTTCTTCTTGGAAATGTTAATCAAGTGGTGGCGCTCG 4140
Dbb 4141 gcttcaagtgacttccacaacgcgtgggttgggtcgatattcgtgatgttcatggtat 4200
QY 4141 GCTTCAAGTGTACTTACCACCAACGCGTGGTGTGGTTCGATTTTCGTATGTCATGGTAT 4200
Dbb 4201 cgtttatcaactcgttgccttactgttggagctgggtggttattcaagccttcaagacta 4260
QY 4201 CGTTTATCAACTTCGTGCTTCACCTTGTGGAGCTGGTGTATTCAGACCTTCAAGACTA 4260
Dbb 4261 tgcgaacggttaagagcactgagaccactacgtgccatgtcccgtatgcagggcatgaggg 4320
QY 4261 TGGACGTTTAAGGACACTGAGACCCTAGTGCCTATGTCCTCCGTATGACAGGGCATGAGGG 4320
Dbb 4321 tctcgttaatgcgctgggttaacagctataccgtccatcttcaattgtctatttgggtgctc 4380

QY 4321 TCGTCGTTAATGCGTGGTACAAAGCTATACCGTCCATCTTCCAATGTGCTAFTTGTGTGTC 4380
Db 4381 Laatatgttgctaaattttgccaataatgggtgtacagcttttggcggaataatttta 4440
QY 4381 TAAATATTTGGCTAAATTTTGGCATAATGGGTGTACAGCTTTTGTCTGGAAATATATTTA 4440
Db 4441 agtgcgagacatgaatggcagaaagctcagccagagatcataccanaatgcgaatgcct 4500
QY 4441 AGTCGGAGGACATGAATGGCAGAAAGCTCAGCCAGAGATCATACCAAAATCGCAATGCCT 4500
Db 4501 gcgagagcgaactacacgcgtgggtgaattcagcaatgaatttcgatactagtgtaacg 4560
QY 4501 GCGAGAGCGAGAACTACACGTGGGTGAATTCAGCAATGAATTCGATCATAGGTAAACG 4560
Db 4561 cgtactgtgctttccaagtggccaccttcaaggctgagatacaaatcatgaacgatg 4620
QY 4561 CGTATCTGTGCTTTTCCAAGTGGCCACCTTCAAGAGCTGGATACAAATCATGAACGATG 4620
Db 4621 ctatcgattcacgagaggtggacaagcaaccaattcgtgaacgaacatctacatgtatt 4680
QY 4621 CTATCGATTACGAGAGGTGGACAAGCAACCAATTCGTGAAACGAACATCTACATGTATT 4680
Db 4681 tatattcgtattcttcatactatttgatcccttttcaactcaatctgttcattggtg 4740
QY 4681 TATATTTGCTATCTTCATCATATTGGATCCTTTTTCACACTCAATCTGTTCATTTGTTG 4740
Db 4741 ttactatgtataatttaatgagcaaaagaaagcaggtggatcattagaaatgttca 4800
QY 4741 TTATCATTTGATTAATTTAATGAGCAAAAGAAAAGCAGGTGGATCATAGAAATGTTCA 4800
Db 4801 tgacagaagatcagaaaaagtactataatgctatgataaaagatgggctctctaaaaaacat 4860
QY 4801 TGACAGAAGATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCAT 4860
Db 4861 taaaagccattccaagaccaaggtggcagcaagcaagcaatgctttcgaatagtaacg 4920
QY 4861 TAAAGCCATTCCAAGCCAAAGTGGCGACCAACAGCAATAGTCTTTGAAATAGTAAACG 4920
Db 4921 ataagaaatcgataatacatattgtattcattgttgctgagactgttcaaccatgacc 4980
QY 4921 ATAGAATAATCGATATAATCAITATTATTATTCTATTGGTCTGAACATGTCACCATGACCC 4980
Db 4981 tccatcgttacgacgctgcggacagctataacgcggtcctagactatctcaatgcgat 5040
QY 4981 TCGATCGTTACGATGCGTCGGACAGCTATACGCGGTCTTAGACTATCTCAATGCGGAT 5040
Db 5041 tccgtattatttcagttccgaatgctctataaaatattcgttcttcagatactactatt 5100
QY 5041 TCGTAGTTATTTTCAGTTCGGAATGCTATTAAAAATATTCGCTTTACGATATCACTATT 5100
Db 5101 ttattgagccatggaatttattgtatgtagtagttgtcattttatccattcttagtcttg 5160
QY 5101 TTATTGAGCCATGGAATTTATTGATGTAGTAGTTGTCTATTATTCATCTTAGTCTTGTG 5160
Db 5161 tacttagcagatatttcgagaagtaactcgtgtcgcgaccctgtcccgagtggtgcgtg 5220
QY 5161 TACTTAGCGATATTATCGAGAAGTACTTCGTGTGCGCGACCCCTGCTCCGAGTGGTGCCTG 5220
Db 5221 tggcgaagtggccgtgtccttcagctgtgaaggagcccaaggcatttcggacactgc 5280
QY 5221 TGCGGAAGTGGCCCGTGTCTTCGACTGGTGAAGGGACCCAAAGGGCATTCGGACACTGC 5280
Db 5281 tcttcgctgtggccatgtcgtgcgcgcctgttcaacatctgcctgctgtcttcctg 5340
QY 5281 TCTTCGCTTGGCCATGTGCTGCGCGCCCTGTTCAACATCTGCCTGCTGCTTCTTCTGG 5340
Db 5341 tcatgttcattcttgccattttcggcatgtcgtttcttcagctgaacgtgaaggagaagcgc 5400
QY 5341 TCATGTTTCATCTTTGCGCATTTTCGGCATGTGCTTCTTCATGACGTTGAAGGAGAGAGCG 5400
Db 5401 gcattaacgactctacaacttcaagacctttggccagagcatgacctgtctttcaga 5460
QY 5401 GCATTAAACGACGCTACAACTTCAAGACCTTTGGCCAGGAGCATGATCCTTGCTTTTCAGA 5460

Db 5461 tgtcagcgtcagccggttggtggtactgtgagccattatcaatgagggaagcatgcg 5520
QY 5461 TGTGACGCTCAGCCGTTGGGATGGTGTACTTGGACCCATTATCAATGAGGAAGCATGCG 5520
Db 5521 atccaccgcagcgcacaaaggctatccgggcaatttgttgcagcgcacgttggaataa 5580
QY 5521 ATCCACCCGACACGCAAAAGGCTATCCGGGCAATTTGGTTACAGCAGCGTTGGAATAA 5580
Db 5581 cgttctcctctcatctacctagttataagctttttgtagttattataatgtacattgctg 5640
QY 5581 CGTTTCTCCTCTCATCTAGTTATTAAGCTTTTGTAGTTATTATAATATGTACATTGCTG 5640
Db 5641 tcattctcgaactactagtcaggccaccagagacgtgcaagggtctaaaccagcagc 5700
QY 5641 TCATTCTCGAAGACTATAGTCAGCCACCGAGGACGTGCAAGAGGCTTAACCCAGCAGC 5700
Db 5701 actacgacatgtactatgagatctgcagcaatttcgacgcgcgcggaggccaccagtaac 5760
QY 5701 ACTACGACATGTACTATGAGATCTGCAGCAATTCGATCCGAGGGCACCCAGTACATAC 5760
Db 5761 gctatgatcagctgtccgaattcctgagcgtactgagccccgcctgcagatccacaac 5820
QY 5761 GCTATGATCAGCTGTCCGAATTCCTGGACGTACTGGAGCCCCGCTGCAGATCCAAAC 5820
Db 5821 cgaaacagtagtaagaatcctatcgtatggacatacccatctgtcgtgacctcatgtact 5880
QY 5821 CGAAACAAGTACAAGATCATATCGATGGACATACCCATCTCTCGCGGTGACCTCATGTACT 5880
Db 5881 gcgtcgacatcctcgcagcccttacgaaagacttcttgcggaagggaacatccgtag 5940
QY 5881 GCGTCGACATCTCCGACGCCCCCTTACGAAAGACTCTTTGCGCGAAGGGCAATCCGATAG 5940
Db 5941 aggagacggtgagattggtgagatagcggccgcgcgcgcgcgcgcgcgcgcgcgcgc 6000
QY 5941 AGGAGACGGGTGAGATTGGTGAGATACGCGCCCGCGGATACGGAGGGCTACGAGCCG 6000
Db 6001 tctcatcaacgctgtgctcagcgtgaggtactggtgcccgcgcgcgcgcgcgcgcgcgcct 6060
QY 6001 TCTCATCAACGCTGTGCGCTCAGCGTGAGGAGTACTGCGCCCGCTAATCCAGCACGCCT 6060
Db 6061 ggcaaaagcaagc 6120
QY 6061 GGCAAAAGCAAGCGCGCGGGAGGAGTGGGTCTTTGAGCCGGATACGGATCATG 6120
Db 6121 gcatggtggtgatacccgatgc 6180
QY 6121 CGGATGGCGGTGATCCGGATCCGGGACCCCGCGCGCGGATGAAGCAACGAGCGCGCATG 6180
Db 6181 cgcccgctgtgtgagatagtgtgttaacggtactgcagaagagcgtgcgcgcgcgcgcgcgc 6240
QY 6181 CGCCCGCTGTGTGAGATGTGTATTAACTGTTACTGCAGAAAGGAGCTGCGCGATGCCGATG 6240
Db 6241 agatgaatgataatagctcccggtgagatcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 6300
QY 6241 AGATTATGTAAATAGTCCGGGTGAGGATCAGCGCGCGCGCGGAGGAGTACGCCGGGACAGA 6300
Db 6301 cggc 6360
QY 6301 CGCGCGCGCGCGGACGACGACGCGCGGAAAGTCCCGGAGCGGGTACGCCGGGCGACAGA 6360
Db 6361 ccgcgcgttctcgttgagagcagc 6420
QY 6361 CCGCGCTTCTCGTGAGAGCAGCGGTTCGTGACGAAGAAGCGGCCACAAGGTGGTCTATCC 6420
Db 6421 actcgc 6480
QY 6421 ACTCGGATCGCCGAGGATACGTCGCGCAGCGCGGATGCTGTAGACCAGGCTCGCCCC 6480
Db 6481 ccctccaagatgcacgc 6513
QY 6481 CCTCCAAGATGCACGCGAGTATTAGTCTTAGA 6513

RESULT 2
 ID T33238 standard; cDNA: 6513 BP.
 DT T33238;
 AC 15-OCT-1996 (first entry)
 DE Drosophila para voltage-activated sodium channel cDNA.
 KW Para voltage-activated sodium channel; cation channel; insecticide;
 KW arachnicide; pesticide; neuroprotective; ischaemia; antagonist;
 OS Drosophila melanogaster.
 PN WO9614860-A1.
 PD 23-MAY-1996.
 PF 06-NOV-1995; U14262.
 PR 10-NOV-1994; US-338702.
 PA (MERI) MERCK & CO INC.
 PI Van Der Ploeg LHT, Warmke JW;
 DR WPI: 96-259563/26.
 PT Mono-specific antibodies to voltage-activated cation channel - also
 PT new cation channel DNA, useful for identifying channel modulators,
 PT potentially useful partic. as insecticide and neuroprotective
 PT agents
 PS Claim 17; Page 39-43; 55pp; English.
 CC A full-length cDNA clone (T33238) codes for the Drosophila para
 CC voltage-activated sodium channel (VASC), a protein responsible for
 CC the fast depolarising phase of the action potential that underlies
 CC electrical signaling in neurons, muscles, etc. The cDNA clone was
 CC obt'd. from 3 overlapping regions of para cDNA isolated by PCR
 CC amplification using primers (see also T33239-44) based on a
 CC published para sequence. Recombinant host cells (E.coli, yeast
 CC mammalian or insect) expressing the Drosophila para VASC can be
 CC used to identify modulators of insect VASCs, useful as insecticides
 CC and arachnicides. VASC antagonists can be used as neuroprotective
 CC agents for treatment of ischaemia in humans.
 SQ Sequence 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T;

Query Match 100.0%; Score 6513; DB 22; Length 6513;
 Best Local Similarity 100.0%; Pred.No. 0.00e+00; Indels 0; Gaps 0;
 Matches 6513; Conservative 0; Mismatches 0;

Db 1 tctagacgttgccgcatacacatgacagaagattccgactcgatatctgaggaagaac 60
 |||||
 QY 1 TCTAGAGTTGGCCGATACACAAATGACAGAGATCCGACTCGATATCTGAGAGAGAC 60
 |||||
 Db 61 gcagttgttccttccttaccgcgaatcattggtgcaatcgacaacgcattgcg 120
 |||||
 QY 61 GCAGTTGTTCCTCCCTTACCGCGCAATCATTTGTCGAATCGAATCGAACGCAATGCGC 120
 |||||
 Db 121 ctgaacatgaaagcagaagagctggaaagaagagccgagggagaggtccgcgat 180
 |||||
 QY 121 CTGAACATGAAAGCAGAGAGCTGGAAAGAGAGAGCCGAGGAGAGGTCCCGCGAT 180
 |||||
 Db 181 atggtcgcagaaacacaaagaaatccgatatgatgacgagggcagggatgaaggtc 240
 |||||
 QY 181 ATGGTCGACAGAAACAAAGAAATCCGATATGATGACGAGGAGAGATGAAGGTC 240
 |||||
 Db 241 cacaacccggaatctacacttgaacaggggtgccaatcacctgttcgattgcagggcagct 300
 |||||
 QY 241 CACAACCCGGATCTACACTTGAACAGGGTGTGCCAATACCTGTTTCGATTTCAGGGCAGCT 300
 |||||
 Db 301 tccgcgcggaattggcctccactcctctcgagatatcgatccctactacagcaatgtac 360
 |||||
 QY 301 TCCGCGCGGAATTGGCCTCCACCTCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360
 |||||
 Db 361 tgacattcgtagtgtgaagcaaaagaaagatatatttctcttttctgcatcaaaagcaa 420
 |||||
 QY 361 TGACATTCGTAGTTGTNAGCAAGGAAAGAAATATTTTCCCTTTCTGCAATCAAGACAA 420
 |||||
 Db 421 tgtggatgctcgatccattcaatccgatacgtcgtgtggccatttatcattctagtcac 480
 |||||
 QY 421 TGTGGATGCTCGATCCATTCAATCCGATACGTCGTGTGGCCATTTACATTTCTAGTGCATC 480
 |||||
 Db 481 cattattttcccttattcatcatcacacaattctcgttcaactgcactcctgatataatgc 540
 |||||

QY 481 CATTATTTTCCCTATTATCATCATCACCAAAATTCCTCGTCAACTGCATCCTGATGATAATGC 540
 |||||
 Db 541 cgacaacgcccacggttgagttccactgaggtgatattaccgcggaatctcacatttgaat 600
 |||||
 QY 541 CGACAACGCCACGGTTGAGTCCACTGAGGTGATATTACCGGAAATCTACACATTTGAAT 600
 |||||
 Db 601 cagctgttaaaagtgtgacagaggtttcatttttatgcccgtttacgatatcttagagatg 660
 |||||
 QY 601 CAGCTGTTTAAAGTGATGGCAGCAGGTTTCATTTTATGCCCGTTTACGTATCTTAGAGATG 660
 |||||
 Db 661 catggaattggctggaacttcgtagtaaatagcttttagcttatgtgaccatggatagatt 720
 |||||
 QY 661 CATGGAATGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT 720
 |||||
 Db 721 taggtaattagcagccctgcgaactgttaggtgctgcgagcgtcttaaaacccgtagcca 780
 |||||
 QY 721 TAGGTAATCTAGCAGCCCTGCGAAGCTTTAGGTTGCTGCGAGCGCTTAAACCCGTAGCCA 780
 |||||
 Db 781 ttgtgccaggttggaaccatcgtggtgcccgtcatcgaatcgttgaaagaatctctgcg 840
 |||||
 QY 781 TTGTGCCAGGCTTGAGACCATCGTCGGCGCGTTCATCGAATCGGTGAAGAATCTCGCG 840
 |||||
 Db 841 atgtgaattatcctgaccatgttctccctcgtcgtgtgttcggttgatggccctacagatct 900
 |||||
 QY 841 ATGTGATTATCTGACCATGTCTCCCTGTCGGTGTTCGGTGTGATGGGCTTACAGATCT 900
 |||||
 Db 901 atatggcgtgctcaccgagaagtgcatacaagaagttcccgcgtgcgacggttctctggggca 960
 |||||
 QY 901 ATATGGCGCTGCTCACCAGAGAGTGCATCAAGAAGTTCCTCGGTGGACGGTTCCTGGGGCA 960
 |||||
 Db 961 atctgaccagagaaactgggactatcaacaatgcgaatagctcccaattggtattccgagg 1020
 |||||
 QY 961 ATCTGACCAGCAGAACTGGGACTATCAACAATCGCAATAGTCCAAATGTGTATTCCGAGG 1020
 |||||
 Db 1021 acgagggaatcatttcctgtatcggaataatataatccggtgcggggcaatgcgacagc 1080
 |||||
 QY 1021 ACAGGGGATCTCATTTCCGTTATGCGCAATATATCCGGTGGGGCAATGCGGACGAGC 1080
 |||||
 Db 1081 attacgtgctgcaggggtttgtccgaatccgaattatggtcacaccagcttcgatt 1140
 |||||
 QY 1081 ATTACGTGTGCTGCAGGGGTTTGTGTCGAATCCGAATTTATGGCTACACCAGCTTCGATT 1140
 |||||
 Db 1141 cgttcgagtggttcttcctgcgcgttcctccgcttgatgacacaggactctctggaggatc 1200
 |||||
 QY 1141 CGTTCGATGGGCTTTCCTGTCGCTTCCGGCTGATGACACAGGACTTCTTGGGAGGATC 1200
 |||||
 Db 1201 tgtaccagctggtgtgctgcgcgcgcgaccatggcaatgctgttctttagtcatca 1260
 |||||
 QY 1201 TGTACCAGCTGTGTGTCGCGCGCGGACCATGGCACATGCTGTGTTCTTTATAGTCATCA 1260
 |||||
 Db 1261 tcttcctaggttcattctctgtgaatttgcatttttgccattgttgcattgtcgtatg 1320
 |||||
 QY 1261 TCTTCTAGTTCATCTATCTGTGAATTTGANTTTTGCCCATTTGTCATGCTCGTATG 1320
 |||||
 Db 1321 acgaattgcaaaaggagggccgaagaagaggtgctccgaagaggaggcgatcgtgaag 1380
 |||||
 QY 1321 ACGAATTGCAAAAGGAGCGCGAAGAAGAGAGGCTGCCGCAAGAGGAGCGATACGTGAAG 1380
 |||||
 Db 1381 cgggaagaactgcccgcgcgcaaaagcgaactggagagcgggccaatgcaggtc 1440
 |||||
 QY 1381 CGGAAGAAGCTGCCGCGCGCAAGCGGCGCAAGCTGGAGGAGCGGCGCAATGCGCAGGCTC 1440
 |||||
 Db 1441 aggcagcagcagatgcgctgcgcgcgaagaggtctcactgcatcgcgaaatggccaaag 1500
 |||||
 QY 1441 AGGCACACGGATGCGGCTGCCGCGAAGAGGCTGCATTCGCAATCGGAAATGGCCAAAG 1500
 |||||
 Db 1501 gtcgcagctatttcttcgcatcagctatgactatttgttggcgcgagaggggcaacgatg 1560
 |||||
 QY 1501 GTCGACGCTATTCTTGCATCAGCTATGAGCTATTTGTTGTCGCGCAGAGAGGCAACGATG 1560
 |||||
 Db 1561 acaacaacaaagagaagatgtccattcgcagcgtcgaggtcgaggtcggtgagcg 1620
 |||||
 QY 1561 ACAACAACAAGAGAAGATGTCATTTCGGAGCGTCGAGGTGGAGTCGGTGGTGAGCG 1620
 |||||

QY 3781 AGGAGGCCGCTCGACGGTGAATCATATTATCATGCACACGACGAGGATATACTCGATG 3840
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 3900
QY 3841 AATATCCAGCTGATTGTCGCCGATTTCGTACTATAGAATAATTCGGATCTTAGCCGGTG 3900
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 3960
QY 3901 ACATGACTCGCCGCTCTGCAAGGATGGGCAATTTACGACTGAAACATTTTCAATTA 3960
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4020
QY 3961 TTGAATAATAATTTTGAACACGCTTATCATGATGATTTAAAGAGTAGCTTAGCTT 4020
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4080
QY 4021 TGGCATTTAGAAAGATGATACATCTGCCACAAAGACCATCTGCAGGATATTTTACTATA 4080
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4140
QY 4081 TGGACAGAAATATTACGGTTATATCTCTTGGAAATGTTAAACAAGTGGTGGCGCTCG 4140
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4200
QY 4141 GCTTCAAGTGTACTTCAACACGCTGGTGGCTTCGATTTGGTGGTGGTGGTGGTGGT 4200
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4260
QY 4261 TGGAAAGCTTAAAGAGCACTAGAGACCACTAGTGGCCATCTGCCGATGTCAGGGCATGAGG 4260
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4320
QY 4321 TCGTCGTTATGCGCTGGTTCACAGCTATACCGTCCATCTTCAATGCTATTTGGTGGT 4320
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4380
QY 4381 TAATATTTTGGCTAAATTTTGGCCATAATGGGTGTACAGCTTTTGGTGGTGGTGGT 4380
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4440
QY 4441 AGTGGAGGACATGAATGGCAGGATGACGACGAGATCATACCAATCGCAATGCCT 4440
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4500
QY 4501 GCGAGCGAGAACTACAGTGGTGAATTCAGCAATGAATTTGATCATGTAGGTAAACG 4500
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4560
QY 4561 CGTATCTGTGCTTTTCCAAAGTGCCACCTTCAAGGCTGGATACAAATCATGACGATG 4560
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4620
QY 4621 CTATCGAATTCACGAGAGGTGGACAAGCAACCAATTCGTAACCAACGACATCTACATGATT 4620
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4680
QY 4681 TATATTTTCGTAATTTTCATCATATTTTGGATCCCTTTTTCACACTCAATCTGTATTGGTG 4680
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4740
QY 4741 TTATCATTTGATAATTTTAAAGGCAAAAGAAAGAAAGCAAGGTGGATCATTTAGAAATGTTC 4740
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4800
QY 4801 TGACAGAAGATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCAT 4800
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4860
QY 4861 TAAAGCCATCCAAAGCCAAAGTGGCGAACCAAGCAATAGTCTTTGAAATGAACCG 4860
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4920

QY 4861 TAAAGCCATTCACAGCAACCAAGGTGGCGACCAACCAATAGTCTTTGAAATAGTAACCG 4920
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 4980
QY 4921 ATAAGAAATTCGATATAATCAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 4980
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 5040
QY 4981 TCGATCGTTACGATGCGTGGACACGTATAACGCGCTCTAGACTATCTCAATTCGATAT 5040
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 5100
QY 5041 TCGTACTATTTTCACTTCGGAATGCTATTAANAATATTCGCTTTACGATACATATT 5100
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 5160
QY 5101 TTATTGAGCCATGGAATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5160
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 5220
QY 5161 TACTTAGCCGATATTATCGAGAACTACTTCTGTCGCCGACCCCTGCTCCGAGTGGTGGTG 5220
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 5280
QY 5221 TGGCGAAAGTGGCCCGTGGCTTCGACTGCTGAAGGGAGCCAAAGGCAATTCGGACACTGC 5280
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 5340
QY 5281 TCFTCGCTTGGCCATGTCGTCGCCGCGCTGTTCAACATCTGCCCTGCTGCTGCTGCTGCTG 5340
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 5400
QY 5341 TCATGTTTATCTTTTGGCATTTTGGCATGCTGCTTCTTCATGTCACGTGAAGGAGAAAGCG 5400
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 5460
QY 5401 GCATTAACGACGCTACAACTTCAAGACCTTTGGCCAGAGCATGATCTCTTTTCAGA 5460
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 5520
QY 5461 TGTGCGAGTCAAGCGGTTGGGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5520
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 5580
QY 5521 ATCCACCCGACAGCAAGGCTATCCGGGCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5580
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 5640
QY 5581 CGTTTCTCTCTCATACCTAGTTATTAAGCTTTTGTATGTTTATTAATATGATGATGATGATG 5640
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 5700
QY 5641 TCATTTCTGAGAACTATAGTCAGGCCACCGAGGACGCTGCAAGAGGGTCTTAACCGACGACG 5700
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 5760
QY 5701 ACTACGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5760
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 5820
QY 5761 GCTATGATCAGCTGTCGGAATTCCTGGACGCTACTGGAGCCCGCTGCGATCCACAAAC 5820
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 5880
QY 5821 CGAACAGTACAAGATCATATCATGATGACATACCCATCTCTCGCGGTGACCTCATGTACT 5880
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 5940
QY 5881 GCGTCGACATCTCGAGCCCTTACGAAGACTTCTTTCGCGGAAGGGCAATCCGATAG 5940
Dbbatccagctgattgtgccccgattcgtactataagaataatccogattcagccggtg 6000
QY 5941 AGGAGACGGGTGAGATTGGTGTAGATAGCGCGCCCGCGGATACGGAGGGGTACGAGCCCG 6000

```
Db 6001 tctcatcaacgctgtggcgtcagcgtgagagtagtactgcgccggcgttaataccagcaacgctt 6060
Qy 6001 TCTCATCAACGCTGTGGCGTCAGCGTGAGGAGTACTGCGCCCGCTAATCCAGCAGCCCT 6060
Db 6061 ggcgaagcaacagcgccgagggagggaggggtggtctctttgagcccgatgacgagcagtg 6120
Qy 6061 GCGCAAGCAACAGCGCGCGAGGAGGGTGGTCTTTGAGCCGATACGATCATG 6120
Db 6121 gcgagtgccggtgatccggatgcccgggagcccgcccgcccgatgaagcaaacgagcgcgatg 6180
Qy 6121 GCGATGGCGGTCATCCGATCCGGGATCCGGGACCGCGCCCGATGAAGCAACGAGCGCGATG 6180
Db 6181 cgcgcgtgggtgagatgtagtgaactgactgcagaagagagctgcgagatcccgatg 6240
Qy 6181 CGCCCGCTGGTGGAGTGTAGTGTAACTGACTGAGAGGAGCTGCCGATGCCGATG 6240
Db 6241 agagttaataatgctcgggtgagatgcagcggcgccggcgagcagcagcagcagcag 6300
Qy 6241 AGAGTAAATGTAATAGTCCGGGTGAGGATGACGGCGCGGCGGACGAGCAGCAGCAG 6300
Db 6301 cggcgccggcgagcagcagcgggaagtcccgagcggcggttagcgcggcgagcagaga 6360
Qy 6301 CGCGCGCGCGGCGACGACGACGCGGGAAGTCCGGAGCGGGTAGCGCGCGGCGAGAGA 6360
Db 6361 cgcgcgttctcgtgagagcagcgggttcgtgacgaagaacgagcgaagtggtcatcc 6420
Qy 6361 CGCGCGCTCTCGTGGAGAGCAGCGGGTCTGTGACGAAGACGGCCACAGGCTGTCATCC 6420
Db 6421 actcgcgatcccgagcatcagctgcgcagcggcggtgtgtgagcagcagcagcagcagc 6480
Qy 6421 ACTCGCATCCCGAGCATCAGCTCGCGCAGCGCGGATGCTGAGCCAGGCGCTCGCCGCC 6480
Db 6481 ccctccaagatgcacgagtagtattagctctaga 6513
Qy 6481 CCCTCCAAGATGCACGCGAGTATTAGCTCTAGA 6513

RESULT 3
ID Q81328 standard; cDNA; 7555 BP.
AC Q81328.
DE Cardiac sodium channel protein coding sequence.
KW Sodium channel protein; ds; therapeutic; diagnostic; prognostic;
KW antiarrhythmic; cardiant; cardioglycoside; pRH3-1; pRH4-23; pRH14-31.
KW Rattus rattus.
FH Key Location/Qualifiers
FT cds 196..6253
FT /*tag= a
PN US5380836-A.
PD 10-JAN-1995.
PF 13-FEB-1989; 331330.
PR 13-FEB-1989; US-331330.
PR 30-SEP-1991; US-768107.
PA (ARCH-) ARCH DEV CORP.
PI Rogart RB;
DR WPI; 95-060381/08.
DR P-PSDB; R67913.
PT Purified DNA's encoding rat and human cardiac sodium channel
PT protein - useful for recombinant expression to produce sodium
PT channel proteins.
PS Claim 8; Fig 1a-1n; 39pp; English.
CC The cDNA is derived from 3 overlapping cDNA clones, designated
CC plasmid pRH3-1 (ATCC 67885), plasmid pRH4-23 (ATCC 67886) and
CC plasmid pRH14-31 (ATCC 67887). A virus/circular DNA plasmid vector
CC comprising the cDNA may be transformed or transfected into a
CC prokaryote/eukaryote host cell, and the resulting recombinant sodium
CC channel protein has various therapeutic, diagnostic and prognostic
CC uses. It may also be used to develop more effective antiarrhythmic,
CC cardiant and cardioglycoside drugs.
SQ Sequence 7555 BP; 1577 A; 2309 C; 2103 G; 1566 T;
Query Match 5.4%; Score 352; DB 14; Length 7555;
```

```
Best Local Similarity 63.5%; Pred. No. 3.93e-221;
Matches 1178; Conservative 0; Mismatches 646; Indels 30; Gaps 19;
Db 3927 ggaacaagatgttcaactacgtcttggtagagatgctgctcaagtgggtgagctacagg 3986
Qy 4082 GGACGAAATATTTACGGTTATATCTCTTGGAATGTTTAATCAAGTGGTGGCGCTCGG 4141
Db 3987 cttcaagaagtacttcaaccaagcctgggtggtggctggacttccgtgattgtggagcgtcc 4046
Qy 4142 CTTCAAGTGTACTTCACCAACGCGTGGTGGCTCGATTTTCGTGATGTGTCATGGTATC 4201
Db 4047 gctgggtcagcctcgtggaacaacaccttagcttcgcgcgaaatgggtcccatcaagtccat 4106
Qy 4202 GCTTATCAACTTCGTTGCTTCACCTTTGGAGCTGGTGTATTCAAGCCTTCAAGACTAT 4261
Db 4107 gaggaacactgcgtgacttcgacctgagggccttgcagactttgagggcagcgtgggt 4166
Qy 4262 GCGAAGCTTAAGAGCACTGAGACCACTACGTGCCATGTCCCTATGACGGCATGAGGT 4321
Db 4167 ggtggtcaatgcgctggtggcgccatccccctcccatgaacgttccctcctcgtctgct 4226
Qy 4322 CGTCGTTAATGCGCTGATACAGCTATACGTCCTCATCTTCAATGTGCTATTGGTGTGCT 4381
Db 4227 catcttctggtcattcttcagcatcatggggtgaaacctcttcgcgcggaagtccgttag 4286
Qy 4382 AATATTTTGGCTAATTTTGCATAATATGGGTGTACAGCTTTTTCGTGGAAAAATATTTTAA 4441
Db 4287 gtcatacaacagagaagaaggagcctgctctgaactacacacatcgtgaacaacaagag 4346
Qy 4442 GTGCGAGGAC- --AT-GAATGGCAGCAAGCTCAGC-C-ACGAGATCATACCAATCGCAA 4495
Db 4347 tgagtgcgagctcttcaacgtgacggagagttgtactggaccaagtggaaggtcaactt 4406
Qy 4496 TGCTGCGAGAGCGAGAAC-T-ACACGTGGGT-GAATTC-AGCAA--TGAATTTGCA--- 4546
Db 4407 tgacaacgtgggagccgggttacctggccctcctgcagggtggcgacatttaagggtcgat 4466
Qy 4547 T--CAT-GTAGGTAACGCGTATCTGTCCCTTTTCCAAGTGGCCACCTTCAAGGCTGGAT 4603
Db 4467 ggaacatcatgtatgcgctgtgactccagaggggtatgaggagcagccgagtggaaga 4526
Qy 4604 ACAATCATGAACGATGCTATCATGATTCAGGAGAGTGGACACACCACTTCGTGNAAC 4563
Db 4527 caacctctacatgatcatctacttctgctcttcattcttccttccttccttccttcctcc 4586
Qy 4664 GAACATCTACATGATTTATTTATTTCTGTTATCTTCATCATATTTGGATCCTTTTTCAC 4723
Db 4587 caacctctcatcgggtgctcatctattgacaacttcaaccagcagagaagaagtaggggg 4646
Qy 4724 CAATCTGTTCAATTGGTGTATCATTTGATAATTTTAATGACCAAAAGAAAACGAGGTGG 4783
Db 4647 c-cag--gatattctcatgcgagagcagagaagaagtactcaatgcctgaagaagct 4703
Qy 4784 ATCAATTAGAAATGTTCAATGACAGAGATCAAGAAAGTACTATATATGCTATGAAAAGAT 4843
Db 4704 gggctccaagaaccccccagaagccccatccccagggcccttgaaacaagtaccaggggttcat 4763
Qy 4844 GGGCTCTAAAAAACCAATTAAGGCCATTTCCAGACCAAGGTGGCGACACACAAGCAATAGT 4903
Db 4764 attgacatgtgaccaagcagccttcgtatgctcaccatcatgttctcctcatctgtttgaa 4823
Qy 4904 CTTTGAATAGTACCAGATAAGAAATTCGATATAAATCATTTATGTTTATTCATGCTGTGAA 4963
Db 4824 catggtgaccatgatggtggagacagatgaccagagccctgagaaggtcaacatcttggc 4883
Qy 4964 CATGTTCAACATGACCCCTCGATCGTTACGATGGCTGGACACGATATAACCGCGTCTAGA 5023
Db 4884 caagatcaacctgctctcgtggccatcttcacagcagcgagtgatgttgcagatggctgc 4943
Qy 5024 CTATCTCAATCGGATATTCGTAGTTATTTTCAGTTCGGAATGCTATTAAAAAATATTCGC 5083
Db 4944 cctgcgcactattacttaccacagcagctgaacatctgcagcttgcgtggtggtcactcct 5003
```


QY 5084 TTTACGATATACATATTTTATTGAGCCATGGAATTTATTGATGTAGTACTGTCATTTT 5143
 Db 5004 ctccattgttggaactgtcctctcccgacataccagaagaattctctctcccgacact 5063
 QY 5144 ATCCATCTTAGGCTTCTGACTAGCGATATATCGAAGTACTTCTGTCGCGCCACT 5203
 Db 5064 ctccgggtcatcgctgcccaggatcgccgcacatcctcagctgatccgcgagccaa 5123
 QY 5204 GCTCCGAGTGGTGGGTGGGAAAGTGGCGGTGCTCTTCGACTGGTGAAGGGAGGCCAA 5263
 Db 5124 ggggttcgacgctgctctcgccctcatgatgctccctcgccgcctctctcaacatcgg 5183
 QY 5264 GGGCATTCGACACTGCTCTTCGGTGGCCATGTCCTCGCGGCCCTGTTCACATCTG 5323
 Db 5184 cctcct 5243
 QY 5324 CCGTCTGCTCTCTGCTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTA 5383
 Db 5244 cgtcaagtggagggcggcggatgacatgcttcaacttccagacattcgcacacagcat 5303
 QY 5384 CGTGAAGGGAAGAGCGGCATTAACGACGCTTCAACTTCAAGACCTTTGCGCAGAGCAT 5443
 Db 5304 gctgctgctgttcagatcaccacatcgccgctgggagcgctcctcagccccatcct 5363
 QY 5444 GATCCTGCTCTTTCAGATGTCGAGCTGAGCGGTGGGATGGTGTACTGGACGCCATAT 5503
 Db 5364 caacacggggcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 5423
 QY 5504 CAAT - GAGGAAGC - -A-TGCGATCC - ACCCGAC - AGCGACAAGGCTATCCGGGCAA 5554
 Db 5424 ctgtggagccggcggtgggagcctctctcctcctcctcctcctcctcctcctcct 5483
 QY 5555 TTGTGGTTCAGCGACCGCTTGGATTAACGTTTCTCTCTCATACCTAGTTATAAGCTTTT 5614
 Db 5484 catcgtgtcaacatgtacacgcatcctcctcctcctcctcctcctcctcctcctcct 5543
 QY 5615 GATAGTTATTAATATGTACATGCTGTCTATCTCGAAGTACTAGTACGCCACCGAGGA 5674
 Db 5544 gagcacagagccctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 5603
 QY 5675 CGTGAAGAGGCTTAACCGACGACGACTACGACATGTACTATGAGATCTGGCAGCAAT 5734
 Db 5604 cgaccggagggcaccagttcattgagatctggtcctcctcctcctcctcctcctcct 5663
 QY 5735 CGATCCGGAGGGACCCAGTACATACCTATGATCACTGTCCGAATTCCTGGACGACT 5794
 Db 5664 gtctgagccctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 5723
 QY 5795 GGAGCCCCCTGTCAGATCCACAAACCGAAGTACAGATCATATCGATGGACATACC 5854
 Db 5724 catggtgagcggagaccgtatccactgtatggacatactgttcgcttccacaa 5777
 QY 5855 CATCTGTCGGGTGACCTCATGTACTCGTCGACATCTCTCGACGCCCTTACGAA 5908

RESULT 4

ID Q05831 standard; cDNA; 7555 BP.
 AC Q05831;
 DE 10-JAN-1991 (first entry)
 DE Cardiac sodium channel gene.
 KW Rat; arrhythmia; ss.
 OS Rattus rattus.
 PN WO009391-A.
 PD 23-AUG-1990.
 PF 09-FEB-1990; U00768.
 PR 13-FEB-1989; US-310330.
 PA (ARCH-) ARCH DEV CORP.
 PI Rogart RB.
 DR WPI; 90-275095/36.
 DR P-PSDB; R06584.
 DR New rat cardiac sodium channel proteins - and associated DNA
 PT sequences, polypeptides and peptides associated with
 PT proteins, useful as antiarrhythmic and cardiotoxic drugs.

PS Claim 7; Fig 1; 65pp; English.
 CC The sequence is derived from 3 overlapping clones, pRH3-1, pRH4-23,
 CC and pRH14-31. (Deposited as ATCC 67885, 67886, and 67887 resp.)
 CC The clones were isolated from a cDNA library in the lambda Zap
 CC vector prep. from mRNA obtd. from newborn rat hearts using rat
 CC brain II cDNA probe. The isolated DNA can be used to screen a
 CC similar human derived cardiac cDNA library for the corresponding
 CC human gene. Proteins produced by expression of the DNA have
 CC diagnostic therapeutic, and prognostic applications.
 SQ Sequence 7555 BP; 1576 A; 2314 C; 1564 T;

Query Match 5.3%; Score 344; DB 1; Length 7555;
 Best Local Similarity 63.3%; Pred. No. 2,00e-215;

Matches 1174; Conservative 0; Mismatches 650; Indels 30; Gaps 19;

Db 3927 ggaacagatgttcaactcctctgtgtgagagctgctcaagtgggtggtcctacgg 3986
 QY 4082 GGACAGATATTTACGGTTATATCTCTTGGAAATGTTAATCAAGTGTGGCGCTCGG 4141
 Db 3987 ctcaagaagtacttccacaaacgctgggtgctgggtggtggtggtggtggtggtggt 4046
 QY 4142 CTTCAAGTGTACTTCAACAAACGCTGGTGTGGCTCGATTTCGTGATTGTCATGTA 4201
 Db 4047 gctgggtcagcctcgtggcacaacaccttagcttcgcgcaaatgggtcccatcaagtcact 4106
 QY 4202 GCTTATCAACTTCGTTGCTTCACTTTGTTGAGCTGGTGTATTCAGACCTTCAAGACTAT 4261
 Db 4107 gagcacatcgctgctcacttcgacccctcgtggcctgctgagatttgagggcctcggt 4166
 QY 4262 GCGAAGTTAAGAGCACTGAGACCACTAGTGCCTATGTCCTGATGCGAGGCAAGGGT 4321
 Db 4167 ggtggtcaatggcgtgggtggcgccatccctccatcatgaacgtcctcctcctcctcct 4226
 QY 4322 CGTCGTTAATGCTGTACAAAGCTATACCGTCCATCTTCAATGTGCTATTGTTGTTCT 4381
 Db 4227 catctctggctcattcagcactcagggcctgctgctgagatttgagggcctcggttag 4286
 QY 4382 AATATTTTGGCTAAATTTTGGCCATAATGGGTGTACAGCTTTTTCGTGGAATATTTTAA 4441
 Db 4287 gtcatcaaccagacagaggggacccctcctcctgaactcacccatcctgtaacacaagag 4346
 QY 4442 GTCCGAGGAC - -AT - GAATGGCAGCAAGCTCAGC - C - ACGAGATCATACCAATCGCAA 4495
 Db 4347 tgagtgcgagtccttcaacgtgaccggagagttgactgaccacaggtgaaggtcaactt 4406
 QY 4496 TGCTTCGAGAGCGAGAAC - T - ACACGTGGGT - GAATTC - AGCAA - -TGAATTTCCA - - 4546
 Db 4407 tgacaacgtgggagccgggtacccctcctcctcctcctcctcctcctcctcctcctcct 4466
 QY 4547 T - -CAT - GTAGGTAAACGCTATCTGTCCCTTTTCCAAGTGGCCACCTTCAAGGCTGGAT 4603
 Db 4467 ggacatcatgtatcgctggtgactccagaggggtatgaggagcagccagtggaaga 4526
 QY 4604 ACAATCATGACGATGCTATCGATTTCAGAGAGGTGGACAACCAACCAATTCGTGAAC 4663
 Db 4527 caacctctacatgtacatcttctcgtcttctcactcctcctcctcctcctcctcctcct 4586
 QY 4664 GAACATCTACATGATTATATTTCTGATCTTTCATCATATTTGGATCCTTTTTCACACT 4723
 Db 4587 caacctctcctcgtgctcactcattgcttctcaccagcagagaagaaagttaggggg 4646
 QY 4724 CAATCTGTTCAATGGTGTATCATTAATTTAATGAGCAAAAGAAAAGACAGGTGG 4783
 Db 4647 c-cag - -gatatctcactcagggagcagaagaagtactacaatgccatgagaagct 4703
 QY 4784 ATCATTAAGAAATGTTTATGACAGAAAGTACTATAATGCTATGATAAAGAT 4843
 Db 4704 gggctccaagaaccccaagaagcccatccacggcctcctgaaacaagtaccagggtttcat 4763
 QY 4844 GGGCTTAATAAACCATTAAGAACCATTCACAGACCAAGGTGGCGACCAACCAATAGT 4903
 Db 4764 attcgacattgtgaccaagcggcctcctcgtcaccatcattgtcctcattctgtttgaa 4823

QY 4904 CTTTGAATAGTACACGATAGAAATTCGATATAATCATATATGTTATTCATGCTCGAA 4963
Db 4824 catgtagacatgatggtggagacagatgaccagagccctgagaaggtcaacatcttggc 4883
QY 4964 CATGTTACCATGACCTCGATCTGATGCTTCAGTATGCTCGGACACGTATACCGCGTCTCTAGA 5023
Db 4884 caagatacaactgtcttctggtgcatcttccacagggagtgattgtcaagatggctgc 4943
QY 5024 CTATCTCAATCGATATTCGTAGTATTTTTCAGTTCGGAATGCTATTAATAATATTCGC 5083
Db 4944 cctggccactatcacttccacacagctggaacatcttggactttgtggtgcatcct 5003
QY 5084 TTTACGATATCACATATTTATTTAGCCATGGAATTTATGATGATAGTGTGTCATTTT 5143
Db 5004 ctccattgttgacactgctctcccgacatcatccagaagtactgtctctcccgacact 5063
QY 5144 ATCCATCTTAGGCTTGTACTTAGCGATATATCGAGAGTACTTCGTGTCGCCGACCT 5203
Db 5064 ctccgggtcatccgtctggcagagatggcgcgcatcctcagggtgatccgcggagccaa 5123
QY 5204 GCTCCGAGTGTGGGTGGGAAAGTGGCGGTGCTCTGACTGGTGAAGGAGGCCAA 5263
Db 5124 gggattcgcagctgctcttcgcccgaatgatctccctcccgccctcttcaacatcgg 5183
QY 5264 GGGATTCGGACACTGCTCTCGGCTGGCCATGTCGTCGCCGCTGTTCACATCTG 5323
Db 5184 cctcctctctcctgctgcttcatctactcctcctcctcctcctcctcctcctcctcct 5243
QY 5324 CCTGCTGCTGTTCTGGTCATGTTTCATCTTTGCGCATTTTCGGCATGCTGTTTCATGCA 5383
Db 5244 cgtcaagtggagcggcgcgcgatgatgatcttcaactccagcctctgcgcaacagcat 5303
QY 5384 CGTGAAGGAGAGAGCGGCATTAACGAGCTCTACAACCTTCAAGACCTTTGGCCAGAGCAT 5443
Db 5304 gctggtcgttccagatcacacatcagcgcgctggagcgcctcctcagcccatcct 5363
QY 5444 GATCTGCTCTTTCAGATGTCGAGTACGCTGACGCGTGGGATGGTGTACTGGACGCCATAT 5503
Db 5364 caacacggggcctcctactcgaccccaacctgcccacagcaacgctcccgggggaa 5423
QY 5504 CAAT--GAGGAAGC--A--TGGATCC--ACCCGAC--AGCGACAAAGGCTATCCGGCAA 5554
Db 5424 ctgtggagccggcgggtgggcatcctcttccacacacatcatcctcctcctcct 5483
QY 5554 TTGTGGTTTCAGCGACCGTGTGAATAACGTTCTCTCTCATACCTAGTATTAACCTTTT 5614
Db 5484 catcgtgtcaacatgcatcgcgcacatcctcgcagaaactcagcgtggccaccgagga 5543
QY 5615 GATAGTTATTAATGATGATGATGCTGTCATTTCTCGAGAACTATAGTCAGGCCACCGAGGA 5674
Db 5544 gagcacagccccctgagcggagcagcttcgacatgttcttatgagatctgggagaagt 5603
QY 5675 CGTGAAGAGGGCTTAACCGACGACGACGACGACGACGACGACGACGACGACGACGACG 5734
Db 5604 cgaacggagccacacagtcattgattgattgattgattgattgattgattgattgattgatt 5663
QY 5735 CGATCGGAGGACCCAGTACATACGCTATGATGATGATGATGATGATGATGATGATGATG 5794
Db 5664 gctcagcgcctccgcatcgcgaacacacacacacacacacacacacacacacacacacac 5723
QY 5795 GGAGCCCCCGCTGAGATCCACAAACCGACAAAGTACAGATCATATCGATGGACATACC 5854
Db 5724 catggtgagcggagacacatcctcctgtagacatactgttgcgttccacaa 5777
QY 5855 CATCTGTGCGGGTACCTCATGTACTGGTGGACATCTCCTCGACGCGCTTACGAA 5908

RESULT 5
ID T30192 standard; cDNA; 3033 BP.
AC T30192;
DT 25-OCT-1996 (first entry)
DE Peripheral nervous system sodium channel peptide-1 alpha-subunit gene.
KW Rat; peripheral nervous system; sodium channel; PN1; PC12; PKI-4;

KW sodium-agonist; sodium-antagonist; drug screening; analgesic;
KW hypertensive; antiinflammatory; trauma; pain; neurological disorder;
KW antisense; gene therapy; ss.
OS Rattus rattus.
FH Key Location/Qualifiers
FT conflict 1
FT /tag= a
FT /note= "T30193 contains G at this position"
FT 697..1665
FT /tag= b
FT /note= "Probe used in differential tissue
FT expression studies"
FT primer_bind complement (1132..1151)
FT /tag= c
FT /note= "Binds primer T30196"
FT primer_bind 1495..1518
FT /tag= d
FT /note= "Binds primer T30197"
FT WO9614077-A1.
PN 17-MAY-1996.
PD 02-NOV-1995; U14251.
PF 02-NOV-1994; US-334029.
PR 07-JUN-1995; US-482401.
PA (TROP-) TROPHIX PHARM INC.
PI (OIN) UNIV NEW YORK STATE RES FOUND.
PI Borden LA, Halegoua S, Mandel G;
DR WPI; 96-251547/25.
PT P-PSDB; R99638.
PT Nucleic acid encoding peripheral nervous system specific sodium
PT channel peptide - useful for sodium channel-associated disease or
PT trauma.
PT Claim 2; Fig 7; 80pp; English.
PS The sequence encodes repeat domain-II of a rat peripheral nervous
CC system sodium channel peptide-1 alpha-subunit (PN1), with sodium
CC channel activity, and has been isolated from a rat PC12 subclone
CC PKI-4 cell culture, expressing high levels of cAMP-dependent
CC protein-kinase-inhibitor. A cDNA library has been screened with
CC primers T30196-97, and the product has been used as a probe to
CC re-screen the library to isolate this sequence. The full-length
CC gene is given in T30193. A probe derived from the sequence may be
CC used in differential tissue expression studies. The peptide may be
CC used to isolate sodium-agonists and sodium-antagonists for use as
CC analgesics, hypotensives, antiinflammatories, and in therapy of
CC sodium channel-associated pathology or trauma, e.g. neurological
CC disorders. The DNA (in sense or antisense orientation) may be used
CC in gene therapy.
SQ Sequence 3033 BP; 860 A; 689 C; 687 G; 797 T;

Query Match 4.88; Score 312; DB 22; Length 3033;
Best Local Similarity 62.38; Pred. No. 1.22e-192;
Matches 1210; Conservative 0; Mismatches 700; Indels 33; Gaps 21;

Db 736 atgactcgtcagcagtgagctcgtggttttgaagatatctatattgaaagaaaaag 795
QY 3996 ATGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4055
Db 796 accattaagattatcctcgtgagtgatgctgacagatatcaccatcattcctcgttggaa 855
QY 4056 ATACTGCAGGATATTTTATACTATATGACAGAAATATTTACGGTTATATTTCTTCTGGAA 4115
Db 856 atgcttctaaatgggtcgcacatgggtataaacaatttccactaatcctcgttgg 915
QY 4116 ATGTTTAAATCAAGTGGTGGCGCTCGCGCTTCAAAAGTGTACTTCAACACGGGTGTGG 4175
Db 916 ctggactcttaattgttgatgctgctccttagttactttagtagcacaacacatttggctac 975
QY 4176 CTCGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4235
Db 976 tcagaccttggcccccataaattcctcagacactgagggccctcagaccctccttaagacc 1035
QY 4236 GGTGGTATTCAAGCCTTCAAGACTATGCGAACGTTAAGAGCACTAGACCACTACGTGCC 4295
Db 1036 ttgcttagattgaaggaatgagggtagtggtcgaagcactcatagagcaatcccttcc 1095

4296 ATGTCGGTATGAGGCGATGAGGTCGCTTAAGTCGCTGTACAAAGCTATACCGTCC 4355
1096 atcatgaacgtgtcttcgtgtgcttataatctgtgtaataattagcatgtggagtc 1155
4356 ATCTTCAATGCTATATGGTGTCTAAATATTTGGCTAATTTTGGCATAATGGGTGA 4415
1156 aatctgtttgctggaagtctctatgagtgtcaacacaccagatgggtcacgatttcc 1215
4416 CAGCTTTTCTGCGAAATAATTTAAGTCGAGAGACATGA---ATGG--CACGAAGCTCA 4470
1216 acatctcaagtgtgcaaaccttctgagtggtttgcccctgatgaacgttagtggaaatgtg 1275
4471 GC--CAGGAGATCATACCAATCGAATGCCT-GC---GA-GAGCGAGAACT-ACAGCTG 4522
1276 cgatggaaaaacctgaaagtaaaccttcgacacagctgggtgttacctgtgcgtctt 1335
4523 GG-TG---AATTGAGCAA-TGAATTTCCGATCATGTAGGTAAACGGTATCTGTGCCCTTTC 4577
1336 caagtgtcaacattcaaggctggatgatatattatgatcagcaggttgactctgttaat 1395
4578 CAAGTGGCCACCTTCAAGGCTGGATCAACAAATCATGAACGATGCTATCGAATCAGGAG 4637
1396 gtaaatgaacagcgaaatcacgaatcagtcctctacatgtacatttacttctgcatcttc 1455
4638 GTGGACAAAGCAACAATTCGTGAACGAACATCTACATGTATTATTATTTTCGTATTCTTC 4697
1456 atcatcttcggtctcatcttcacgttgaacctgttcattggtgtcatcatagataatttc 1515
4698 ATCATATTTGGATCCTTTTTCACATCAATCTGTTCAATGGTGTATCATTTGATAATTTT 4757
1516 aaccacacagaa-aaaaagctttggaggtca--agatatcttttatgacagaagacgaag 1572
4758 AATGAGCAAAAGAAAAAGCAGGTGGATCATTTAGAAATGTTTCATGACAGAAGATCAGAAA 4817
1573 aaatactataatcaatgaagaagcttgggtcccaaaaaacacacaaaacaaattccaagg 1632
4818 AAGTACTATATGCTATGAAAAAGATGGGCTCTAAAAAACCATTAAGAGCCATTCCCAAGA 4877
1633 ccaggggaacaaatccagagtgatatattgacttagtgacaaaccaagctttttgatc 1692
4878 CCAAGGTGGCGACCAACGAATAGTCTTTGAAATAGTACCAGTAAGAAATTCGATATA 4937
1693 accatcagttcttataatgcctcaacatggttaaccatgagtgtgtagaaaaaggggcaa 1752
4938 ATCATTTATTTATTTATTTGCTGAGACATGTTCAACATGACCCCTCGATCGTTACGATGCG 4997
1753 actgagtacatgattatgttttacactggatcaacatggttcttcattatccgtttcaact 1812
4998 TCGGACACGTATAACGGCGTCTAGACTATCTCAATGCGATATTCGTAGTTATTTTCAGT 5057
1813 ggggagtggtgtgagagctaaatccctccctcagacattactactcactgtggtgtggaac 1872
5058 TCCGAATGCTATTAAAAATATTCGGCTTTACGATATACATATTTTATTGAGCCATGGAAT 5117
1873 attttgattttgtggtgtagtgatectcctcattgtaggaatgtttctcgtgagatgata 1932
5118 TTAATTCATGTAGTAGTGTGTCATTTTATCCATCTTAGTCTTGTAATAGCGATATATTC 5177
1933 gagaagtatttgttccctcactcctcctcctcctcctcctcctcctcctcctcctcctcctc 1992
5178 GAGAAGTACTTCGTTGTCGGCGACCCCTCTCCGAGTGGTGGCGTGGCGGAAAGTGGCCGT 5237
1993 atctacgctgtatcaaggcgcaagggtatccgcaactctgctctttgtttgtgatg 2052
5238 GTCCCTTCGAGTGGTGAAGGAGCGCAAGGGCATTCGGACACTGCTCTTCGGGTGGCCATG 5297
2053 tcccttcctgctgtttcaacatcgcttgcctgtcttcttctggttcattgttcactacgcc 2112
5298 TCGTGGCGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5357
2113 atctttggagtgatccaaactttgctacgttataaaagaggtggaattaatgacatgttc 2172

5358 ATTTTCGGCATGTCGTTCTTCATGCACGTGAAGGAGAAGAGCGGCATTAAACGACGTCTAC 5417
2173 aactttgagacttttgcaacagcatgatctgtctgtttccaaatcaccacctctgcggc 2232
5418 AACTTCAAGACCTTTTGGCAGAGCATGATCCTGCTCTTTTCAGATGTCGAGCTCAGCCGGT 5477
2233 tgggacgagactgtggtcccccattcctcaacagcgcaacctcccgactgtgacctataaaaa 2292
5478 TGGGATGGTGTACTTGACGCCATTATCAATAGGAAGCATGCGA-TCC-ACCCGACAGC- 5534
2293 gttcccccaggaagtccagtggaaaggggactgtgggaacccatccctgggggattttttac 2352
5535 GA-CAA--AGGCTATCCGG-GCAATTG---TG-GTTACGGA-CCGTTGGAATAACGTTT 5585
2353 ttgtcagttacatcatcatctctctctgtgtgtgtggtggaacatgtacatcgtctgctc 2412
5586 CTCCTCTCATACCTAGTATTAAAGCTTTTGTAGTATTGATATTAAATATTGATTTGCTGTCATT 5645
2413 ctggagaaccttcagctcgccaccgaagagcactgagcctctgagtgagtgagcacttt 2472
5646 CTCGAAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGGGTCTAACCGACGACGACTAC 5705
2473 gagatgttctacgaggtctctgggagaaggttcgaccctgagcgcactcagttcatagagttc 2532
5706 GACATGTACTATGAGATCTGGCAGCAATTTCGATCCGGAGGGCACCAGTACATACGCTAT 5765
2533 tgcaagctctctgacttgcagctgcccgtggatccctccctcctcctcctcctcctcctcctc 2592
5766 GATCAGCTGTCCGAATTCCTGGAGCTGAGGAGCCCGCTGCAGATCCACAAACCGAAC 5825
2593 aaagtccagctcattccatggtgacctgcccattggtgagtgagagcgcactcctcactgctg 2652
5826 AAGTACAAGATCATATCGATGGACATACCATCTGTGCGGGTGACCTCATGTACTGCGTTC 5885
2653 gacatctgtttgtcttttcaaa 2675
5886 GACATCTCGACGCCCTTACGAA 5908

RESULT 6
ID T30193 standard; DNA; 6452 BP.
AC T30193;
DT 25-OCT-1996 (first entry)
DE Peripheral nervous system sodium channel peptide-1 alpha-subunit gene.
KW Rat; peripheral nervous system; sodium channel; PNI; PC12; PKI-4;
KW sodium-agonist; sodium-antagonist; drug screening; analgesic;
KW hypotensive; antiinflammatory; trauma; pain; neurological disorder;
KW antisense; gene therapy; ss.
OS Rattus rattus.
FH Key
FT cds
FT 326..6280
FT /tag= a
FT /product= Full-length PNI protein
FT 3185
FT conflict
FT /tag= b
FT /note= "T30192 contains A at this position"
FT 3185..6217
FT misc_feature
FT /tag= c
FT /note= "Fragment T30192 (claim 2)"
FT 3881..4847
FT misc_feature
FT /tag= d
FT /note= "Probe used in differential tissue
expression studies"
FT complement (4316..4335)
FT /tag= e
FT /note= "Binds primer T30196"
FT 4679..4702
FT primer_bind
FT /tag= f
FT /note= "Binds primer T30197"
FT W09614077-A1.
PD 17-MAY-1996.
PR 02-NOV-1995; U14251.
PR 02-NOV-1994; US-334029.

PR	07-JUN-1995; US-482401.
PA	(TROP-) TROPHIX PHARM INC.
PI	(UINY) UNIV NEW YORK STATE RES FOUND.
PI	Borden LA, Halegoua S, Mandel G;
WPI:	96-251547/25.
P-PSDB:	R99639.
DR	Nucleic acid encoding peripheral nervous system specific sodium
PT	channel peptide - useful for sodium channel-associated disease or
PS	trauma.
PS	Example 1; Fig 9; 80pp; English.
CC	The sequence encodes a rat peripheral nervous system sodium channel
CC	peptide-1 alpha-subunit (PNI) with sodium channel activity, and
CC	has been isolated from a rat PC12 subclone PKI-4 cell culture,
CC	expressing high levels of CAMP-dependent protein-kinase-inhibitor.
CC	A cDNA library has been screened with primers T30196-97, and the
CC	product has been used as a probe to re-screen the library to
CC	isolate the fragment given in T30192. This has been used to isolate
CC	the full-length gene. A probe derived from the sequence may be
CC	used in differential tissue expression studies. The peptide may be
CC	used to isolate sodium-agonists and sodium-antagonists for use as
CC	analgesics, hypotensives, antiinflammatories, and in therapy of
CC	sodium channel-associated pathology or trauma, e.g. neurological
CC	disorders. The DNA (in sense or antisense orientation) may be used
CC	in gene therapy.
SQ	. Sequence 6452 BP; 1816 A; 1454 C; 1550 G; 1632 T;
	Query Match 4.8%; Score 312; DB 22; Length 6452;
	Best Local Similarity 62.3%; Pred. No. 1,22e-192;
	Matches 1210; Conservative 0; Mismatches 700; Indels 33; Gaps 2
Db	3920 atgatctgtcgcagcagtggagcttggcgtttgaagatatctatttgaaagaaaaag 3979
QY	
	3996 ATGATTTTAATGAGTAGCTTAGCTTTGGCATTAGAAGATGTACATCTGCCACAAGACC 4055
Db	3980 accattaagaatattcctggagtatcgtacaaagatatcacactacatttcattctgaa 4039
QY	
	4056 ATACTGCAGGATATTTTATACATATATGGACAGAAATATTACGGTTATATTCCTTGAA 4115
Db	4040 atgcttctaataatgggtcgcatatgggtataaacatatcttaacctaatgccctgtgttg 4099
QY	
	4116 ATGTTAATCAAGTGGTTGGCGCTCGGCTTCAAAGTGTACTTCAACACGCGTGTGTGG 4175
Db	4100 ctggacattcttaattgttgtatgtctcttagttaaccttagtagccaaacctcttggctac 4159
QY	
	4176 CTGGAFTTCGTATGTTCATGTGTATCGTATTCAACTTCGTTGCTTCACTTGTGGAGCT 4235
Db	4160 tcagaccttggccccataaatactctacggacactgaaggccctaaagaccctaaagacc 4219
QY	
	4236 GGTGGTATTTCAGCCCTTCAAGSACTATGCCAACGTTTAAGAGCACATGAGACCATTACGTGCC 4295
Db	4220 ttgtctagatttgaaggaatgaggttagtgggtcaacgcaactcagaggaatccctccc 4279
QY	
	4296 ATGTCCCGTATGCAGGGCATGAGGTCGTGCTTANTGCGCTGGTTACAGCTATACCGTCC 4355
Db	4280 atcatgaacgtgtctctcgttgccttattctctggcttaatttagcatcatcattggagtc 4339
QY	
	4356 ATCTTCAATGTCTATTGTGTGTCTAATAATTTTGGCTAAATTTTGCCATAATGGGTGA 4415
Db	4340 aaatcgtttgtgccaagtctcatagtggttcaaacaccacggtgggtcagcatcttccct 4399
QY	
	4416 CAGCTTTTTTCGTGGAAAATAATTTTAAAGTCGAGGACATGA---ATGG--CACGAAGCTCA 4470
Db	4400 acatctcaagttgcaaacogttcctgagtgtttccctcgtatgaacgttagtggaatgtg 4459
QY	
	4471 GC--CACGAGATCATCCAANAATGCCAATGCCCT-GC--GA-GAGCGAGAAGCT-ACACGTG 4522
Db	4460 cgatggaaaacacctgaaagtaaacttcgacaacgttgggttggcttacctgtcgtcctt 4519
QY	
	4523 GG-TG--AATTCAGCAA-TGAATTTCCATCATGTAGGTACGCGTATCTGTGCGCTTTTC 4577
Db	4520 caagttgcaacattcaaaggtcgtggatgatatattgtatgcagcagttgacctctgttaat 4579
QY	
	4578 CAAAGTGGCCACCTTCAAAGGCTGGATACAAATCATGAACGATGCTATCGATTACAGAGAG 4637


```
QY 4543 TCGATCATGTAGGTAACCGCGTATCTGTGCCCTTTTCCAAAGTGGCCACCTTCAAAAGCGCTGGA 4602
Db 4274 cgattatatgtatgcagcagtggtattctgttgaatgtagacaagcagcccaaatatgaat 4333
QY 4603 TACAATATCATCAAGCATGCTATCGATTCACAGAGGTGGACAAGCAACCAATTCGTGAAA 4662
Db 4334 atagcctctacatgatattattttatttgcctttatcatctcttgggtcattcttcactt 4393
QY 4663 CGAACATCTACATGATTTATTTTCGTATTCCTTCATCATATTTGGATTCCTTTTTCACAC 4722
Db 4394 tgaacttgcttggtgtcatcagataaatttcaaccacacagaa-aagaagacttggga 4452
QY 4723 TCAATCTGTTTCATTTGGTGTATCATTTATGATATTTTATGAGCAAAAGAAAACACGAGTG 4782
Db 4453 ggtea--agacatctttatgcagagaagacagagaataactataatgcgaatgaaaaagc 4510
QY 4783 GATCATTAGAAATGTTTCATGACAGAAGATCAGAAAAAGTACTATAATGCTATGAAAAAGA 4842
Db 4511 tggggtccaagaagccacaaaagccaattcctcgaccagggagacaaaatccaaggaatgta 4570
QY 4843 TGGGCTCTTAAAAAACCATTAAGAGCCATTCCAAGACCAAGGTGGCGACCAAGCAATAG 4902
Db 4571 tatttgacctagtacaaaatacaagcctttgatattagtatcatgtgttcttatctgtctca 4630
QY 4903 TCTTTGAAATAGTAACCGATAAGAAATTCGATATAATCATTTATGTTATTCATTGGTCTGA 4962
Db 4631 acatggttaacctatgatgtagaagaggggt-caaaagtcacacatagactgaagtttta 4689
QY 4963 ACATGTTTACCATGACCTCGATCGTTACGATGCGTCGGACACGTATAAC-GCGGTCTCTA 5021
Db 4690 tattggataaatggtgtttttataatccttttctactcgaggaatggtgctaaactgactc 4749
QY 5022 GACTATCTCAATGCGATATTCGTAGTTATTTTCAGTTTCCGAATGCTATTAAAAAATATTC 5081
Db 4750 tccctcgacacactactctcactgtaggagtggaatatctttgtattgttggttgat 4809
QY 5082 GCTTTAGATATACATATTTTATGAGCCATGGAATTTATTTGATGATAGTAGTTGTCAAT 5141
Db 4810 atctccattgtagtgatttctagctgattgattgaaacgtattttgtgctccctacc 4869
QY 5142 TTATCCATCTTTAGGTTGTGTTACTTAGCGATATTATCGAGAAGTACTTCGTGTCGCCGACC 5201
Db 4870 ctgttcgagtgatccgtcttgccaggaattggccgaatccctactgtagtcaaaaggagca 4929
QY 5202 CTGCTCCGAGTGGTGCGTGGCGGAAAGTGGGCGCGTGTCTTCGACTGGTGAAGGAGACC 5261
Db 4930 aaggggatcccgacgctctcttgcttgatgatgtgcccttctcgtggtgtttaaactc 4989
QY 5262 AAGGCAATTCGGACACTGCTCTTCGCGTTGGCCATGTGCGTGGCGGCCCTGTTCAACATC 5321
Db 4990 ggctctgctcttctctggtcatgttcatctacgccatctttggaatgccaactttggc 5049
QY 5322 TGCCTGCTGCTGTTCCGTGTCATGTTTCATCTTTGCCATTTTCGCGATGCTGTTCTTCATG 5381
Db 5050 tatgttaaaagggaagtggaaatgaatgacatgttcaatttttggaacctttggcaacagt 5109
QY 5382 CACGTGAAGGAGAAGAGCGGCATTAAACGACGCTACAACTTCAAGACCTTTGGCCAGAGC 5441
Db 5110 atgatttgctcttccaaataacacctctgctggctggagtgattgctgacacctatt 5169
QY 5442 ATGATCTGCTCTTTTCAGATGTCAGCTGACGCTACGCGGTTGGGATGTGTACTGGACGCCATT 5501
Db 5170 cttaacagtaagccacccgactgtgacccaaaaaaagtctcatctcggaagttcagttgaa 5229
QY 5502 ATCAATGAGGAAGCATGCGA-TCC-ACCCGACAGC-GA-CAAG-GCTA--TCCG--G-- 5550
Db 5230 ggagactgtgtgaacccaatctgttggaaattcttactttgttagttatcatcatatcc 5289
QY 5551 GCA-ATTGTGTTTACGACCGCTTGGAAATAACGTTTCTCCCTCTCATACCTAGTTATAAGC 5609
Db 5290 ttctgtggttggtggaacatgatactgcagtcatactggaagaatttttagtgttgcact 5349
QY 5610 TTTTGTAGTATTATAATATGATCTGCTGCTATCTTCGAGAACTATAGTCAGGCCACC 5669
```

```
Db 5350 gaagaaagtactgaacctctagtgaggatgactttgagatgttctatgaggtttggag 5409
QY 5670 GAGGACGTGCAAGAGGTCTTAACCGACGACGACTACGACATGTACTATGAGATCTGGCAG 5729
Db 5410 aagtttgatcccaatcgaccagttttatagattctctaaactctctgattttgcagct 5469
QY 5730 CAATTCGATCGGAGGCCACCCAGTACATACGCTATGATCAGCTGTCCGAATTCCTGGAC 5789
Db 5470 gccctggatcctctctctctcatagcaaaaccccaaaagctccagctcattgcccagat 5529
QY 5790 GTACTGGAGCCCCGCTGCAGATCCACAACCCGAACGATACAAGATCATATCGATGGAC 5849
Db 5530 ctgccatggtttagtggtgaccggatccattgtcttgtagactcttattgtttttacaaa 5588
QY 5850 ATACCATCTGTGCGGTGACCTCATGTACTGTGGTGCACATCCTCGACGCCCTTACGAA 5908
```

RESULT 9

ID T77803 standard; cDNA; 6524 BP.

AC T77803;

DT 09-OCT-1997 (first entry)

DE cDNA encoding wild type rat DRG (SNS-B).

KW Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin;

KW modulator; impulse; sensory neuron; acute pain; chronic pain;

KW neuropathic pain; glia; muscle; parasympathetic nervous system;

KW enteric nervous system; central nervous system; dorsal root ganglia;

KW cranial ganglia; ss.

OS Rattus rattus.

PH Key Location/Qualifiers

FT cds 204..6077

FT /*tag= a

FT /product= Rat_DRG (SNS-B)

PN WO9701577-A1.

PD 16-JAN-1997.

PF 25-JUN-1996; G01523.

PR 28-JUN-1995; GB-013180.

PA (UNLO) UNIV COLLEGE LONDON.

PI Akopian AN, Wood JN;

DR WPI: 97-100165/09.

DR P-PSDB; W21737.

PT New isolated mammalian sensory neuron sodium channel protein - used

PT to identify modulators of the sodium channel, partic. for the

PT treatment of pain

PS Claim 9; Page 50-58; 128pp; English.

CC The sequences given in T77803-06 encode the wild type and three

CC variant forms of a rat sensory neuron sodium channel protein which

CC is insensitive to tetrodotoxin. The proteins can be used for

CC identifying modulators of the sodium channel. Blockers of the

CC sodium channel will block or prevent the transmission of impulses

CC along sensory neurons and thereby be useful in the treatment of acute,

CC chronic or neuropathic pain. The novel protein is found only in sensory

CC neurons and not in glia, muscle or the neurons of the (para)sympathetic,

CC enteric or central nervous system. The protein is found preferably in

CC the neurons of the dorsal root ganglia or cranial ganglia.

SQ Sequence 6524 BP; 1540 A; 1866 C; 1662 G; 1456 T;

Query Match 4.5%;

Best Local Similarity 63.8%; Pred. No. 2.83e-181;

Matches 890; Conservative 0; Mismatches 486; Indels 18; Gaps 11;

Db 4254 aactcgacaacgtcgctatgggtacctcgacattcttcaggtggcaaccttcaaaaggc 4313

QY 4539 AATTTGCATCATGTAGTAAAGCGGTATCTGCTTTCCAAGTGGCCACCTTCAAGGC 4598

Db 4314 tggatgacataatgtatgcagctgttgatctccggagagatcaacagtcagcctaactgg 4373

QY 4599 TGGATACAAATCATGAACGATGCTATCGATTTCACGAGGTTGGACAAGCAACCAATTCGT 4658

Db 4374 gagaacaactgtacatgtacctgtactctgtgttcttcattcttcggtggtctcttc 4433

QY 4659 GAAACGAACATCTACATGTATTTATATTTCTGATTTCTTCATCATATTTGGATCCTTTTC 4718

FT FT /*tag= n
 PN /note= "Addition of AAA"
 PD WO9701577-A1.
 PF 16-JAN-1997.
 PR 25-JUN-1996; G01523.
 PA 28-JUN-1995; GB-013180.
 PI (UNLO) UNIV COLLEGE LONDON.
 PI AKopian AN, Wood JN;
 DR WPI; 97-100165/09.
 DR P-PSDB; W21740.
 PT New isolated mammalian sensory neuron sodium channel protein - used
 PT to identify modulators of the sodium channel, partic. for the
 PT treatment of pain
 PS Claim 9; Page 85-93; 128pp; English.
 CC The sequences given in T77803-06 encode the wild type and three
 CC variant forms of a rat sensory neuron sodium channel protein which
 CC is insensitive to tetrodotoxin. The proteins can be used for
 CC identifying modulators of the sodium channel. Blockers of the
 CC sodium channel will block or prevent the transmission of impulses
 CC along sensory neurons and thereby be useful in the treatment of acute,
 CC chronic or neuropathic pain. The novel protein is found only in sensory
 CC neurons and not in glia, muscle or the neurons of the (para)sympathetic,
 CC enteric or central nervous system. The protein is found preferably in
 CC the neurons of the dorsal root ganglia or cranial ganglia. This
 CC sequence contains 12 nucleotide differences to the wildtype rat
 CC DRG(SNS-B) (see also T77803) causing nine amino acid changes.
 SQ Sequence 6527 BP; 1542 A; 1863 G; 1459 T;
 SQ Sequence 6527 BP; 1542 A; 1863 G; 1459 T;
 Query Match 4.5%; Score 296; DB 32; Length 6527;
 Best Local Similarity 63.8%; Pred. No. 2.83e-181;
 Matches 890; Conservative 0; Mismatches 486; Indels 18; Gaps 11;
 Db 4254 aacttcgacacgtcgctatgggttaactcgcactcttcaggtggcaacctccaaagc 4313
 QY 4539 AATTTCGATCATGTAGTAAAGCGTATCTGTCCTTTTCCAAGTGGCCACCTTCAAGGC 4598
 Db 4314 tggatgacataatgatcgagctgttgatcccgagagatcaacagtcgcctaaatgg 4373
 QY 4599 TGGATACAAATCATGACGATGCTATCGATTTCACGAGGTGGACAAACCAATTCGT 4658
 Db 4374 gagaaacttgatcatctactctactctctctctctctctctctctctctctctctctc 4433
 QY 4659 GAAACGAACATCATATGATTTATATTCGTATTCATCATATTTGGATCCTTTTC 4718
 Db 4434 acgtgaatctcttgggtggtcataatgcacacttcaacacacagaaaaagccta 4493
 QY 4719 ACATCAATCTGTTTCATGTTGTTATCATGATTAATTTATGACAAAGAAAGCA 4778
 Db 4494 ggagggc-cag--gacatcttcacagagagagcagagaagtactacaatgccatgaag 4550
 QY 4779 GGTGGATCATTTAGAAATGTTTCATGACAGAGATCAGAAAAAAGTACTATATGCTATGAAA 4838
 Db 4551 aagctgggtcccaagaaccccaagccatccacgcccctgaataagtaaccaagc 4610
 QY 4839 AAGATGGGCTCTAAAAACCATTTAAAGCCATTCAGACCAAGTGGCGACCAACAGCA 4898
 Db 4611 ttcgtgttgatcatgtagcaggaagcctttgacatcatcatcaggttctctatcgc 4670
 QY 4899 ATAGTCTTTGAATAGTAAACCGATAGAAATTCGATATATATGATTTATTCATTTGGT 4958
 Db 4671 ctoacatgatcaccatgatggtggagaccgagcagggcgaggaagaaaggtt 4730
 QY 4959 CTGAACATGTTTCACCATGACCTCGATCGTTTACGATGGTGGACACATATAACGGGTC 5018
 Db 4731 ctgggcagaatacaaccagttcttggccgtcttcacggcgagtggtgatgaagatg 4790
 QY 5019 CTAGACTATATCAATGCGATATTCGATTTATTTTCAGTTCGGAATGCTATTAAAAATA 5078
 Db 4791 ttgcgcctgcacagtgactacttaccacacggctggagcgtgttcgcacttcattggtg 4850
 QY 5079 TTCGCTTTACGATATCACTATTTATTCAGGCATGGAATTTATTTGATGATGATGTC 5138
 Db 4851 atctgtccattggagtgctgttttctgcaatccttaagtcactggaaactacttc 4910

QY 5139 ATTTTATCCATCTTAGGTCT--TGTACTTAGCGATA-TTA--TCGA-GAAGTACTTCGTG 5192
 Db 4911 tccccgacgctcttcggggtcattccgtctggccagagatggccgcatccaggctgac 4970
 QY 5193 TCGCCGACCTGCTCCGAGTGGTGGTGGCGAAAGTGGCGTGTCTCTCCACTGGTG 5252
 Db 4971 cgagcgcaaggggattgcacgctgtcttctgcctcatgatgtcctgcgcgcctc 5030
 QY 5253 AAGGGAGCCAAAGGCATTCGGACACTGCTCTCGCGTTGGCCATGCTGCTGCGGCCGTG 5312
 Db 5031 ttcaacatggcctc 5090
 QY 5313 TTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5372
 Db 5091 agttcgtctaaactcgtggagcggcggcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 5150
 QY 5373 TTCTTCATGACCTGAAGGAGAGAGCGGATTAACGACGCTTACAACATTCAGACCTTT 5432
 Db 5151 ggcaacagcatgctgtgctgttctccagatcaacacctcggcggcggcggcggcggcggc 5210
 QY 5433 GGCAGAGCATGATCTGCTCTTTTTCAGATGTCGACGTCAGCGGTTGGGATGTTGACTG 5492
 Db 5211 agcccatcctcaacacgggctcctcctcctcctcctcctcctcctcctcctcctcctc 5270
 QY 5493 GACGCCATTATCAAT--GAGGAAGC---A-TGGGATCC--ACCCGAC-AGCGACAAAGGC 5543
 Db 5271 tcccgggggaactcgggagcccgcggtgggcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 5330
 QY 5544 TATCCGGGCAATTTGGTTTCAGGACCGGTTGGAAATACGTTTCTCTCTCATACCTAGTT 5603
 Db 5331 atctctctctcctcgtggttcaacatgtacatcgagtgatctctgagaaactcaacgta 5390
 QY 5604 ATAAAGCTTTTGTAGTTATTAATATGTACATTTGCTGCTCATTTCTCGAGAACTATAGTCAG 5663
 Db 5391 gcacagagagagacagcggagccctcctcctcctcctcctcctcctcctcctcctcctc 5450
 QY 5664 GCCACCGAGACGCTGCAAGAGGGTTAAACGACGACGACTACGACATGTTACTATGATC 5723
 Db 5451 tgggagaagtctgacccggagccacccagttcattgctcttctcctcctcctcctcctc 5510
 QY 5724 TGCAGCAATTCGATCCGAGGAGGCCCCGATACATGCTATGATCAGCTGTCCGAATTC 5783
 Db 5511 gcggacacgctctccggcctcttagaattcccaaccccaacccagaaatattatcaaccag 5570
 QY 5784 CTGGACGTTACTGGAGCCCCCGCTGCAGATCCACAAACCGAAGTACAGATCATATCG 5843
 Db 5571 atggacctcgcgttgggtcccccgggataagaatccactgtctgacatcctctttgcttc 5630
 QY 5844 ATGGACATACCATCTGTCGCGGTGACCTCATGCTACTGCTGCAGCATCTCCGCGCCTT 5903
 Db 5631 acaaaagacgtctt 5644
 -QY 5904 ACGAAGACCTTCTT 5917
 RESULT 11
 ID T77805 standard; cDNA; 7052 BP.
 AC T77805;
 DT 09-OCT-1997 (first entry)
 DE cDNA encoding variant rat DRG (SNS-B) #2.
 KW Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin;
 KW modulator; impulse; sensory neuron; acute pain; chronic pain;
 KW neuropathic pain; glia; muscle; parasympathetic nervous system;
 KW enteric nervous system; central nervous system; dorsal root ganglia;
 KW cranial ganglia; ss.
 OS Rattus rattus.
 FH key Location/Qualifiers
 FT cds 204..6602
 FT /*tag= a
 FT /product= variant_Rat_DRG(SNS-B)
 PN WO9701577-A1.
 PD 16-JAN-1997.

PF 25-JUN-1996; G01523.
PR 28-JUN-1995; GB-013180.
PA (UNLO) UNIV COLLEGE LONDON.
PI Akopian AN, Wood JN;
DR WPI; 97-100165/09.
PT P-PSDB; W21739.
PT New isolated mammalian sensory neuron sodium channel protein - used
PT to identify modulators of the sodium channel, partic. for the
PT treatment of pain
PS Claim 9; Page 69-78; 128pp; English.
CC The sequences given in T77803-06 encode the wild type and three
CC variant forms of a rat sensory neuron sodium channel protein which
CC is insensitive to tetrodotoxin. The proteins can be used for
CC identifying modulators of the sodium channel. Blockers of the
CC sodium channel will block or prevent the transmission of impulses
CC along sensory neurons and thereby be useful in the treatment of acute,
CC chronic or neuropathic pain. The novel protein is found only in sensory
CC neurons and not in glia, muscle or the neurons of the (para)sympathetic,
CC the neurons of the dorsal root ganglia or cranial ganglia. This
CC sequence encodes a 2132 amino acid protein that contains a 176 amino
CC acid repeat inserted after amino acid 585 of wildtype rat DRG(SNS-B)
CC (see also W21737).
SQ Sequence 7052 BP; 1655 A; 2009 C; 1795 G; 1593 T;

Query Match 4.5%; Score 296; DB 32; Length 7052;
Best Local Similarity 63.8%; Pred. No. 2.83e-181;
Matches 890; Conservative 0; Mismatches 486; Indels 18; Gaps 11;

Db 4779 aacttcgacaaagtcgctatggctacacgcacacttcctcaggtgggaacattcaaaaggc 4838
QY 4539 AATTTTCGATCATGTAGTAAACGCGTATCTGTCGCTTTTCCAAGTGGCCACCTTCAAGGC 4598
Db 4839 tggatggacataatgatcgactgttgattccggagagatcaacagtcagcctaactgg 4898
QY 4599 TGGATACAAATCATCAGACGATCTATCGATTCACGAGAGGTGGCAAGCAACCAATTCGT 4658
Db 4899 gagaacaactgtacatgacgttaacttcgttcgttttcacatatttgggtggtcttctc 4958
QY 4659 GAAACGAACATCTACATGATTAATTAATTCGTATTTCTTCATCATATTTGGATCCTTTTC 4718
Db 4959 acgctgaactctcttgggtgggtcataatcgacaacttcacacccaacagaaaaaagcta 5018
QY 4719 ACACTCATCTCTTCATTTGGTGTATATTTATGATTAATTTTATGACAAAGAAAGCA 4778
Db 5019 ggagggc-cag--gacatctcatgacagaagacagaagaagtactacaatgccaatgaag 5075
QY 4779 GGTGATCATTTAGAATGTTTCATGACAGAGATCAGAAAGATCTAATGCTATGAAA 4838
Db 5076 aagctgggtcccaagaacccccagagcccatccacgcccctgaataaagtaccacagc 5135
QY 4839 AAGATGGGCTTAAAAAACCATTAAGAGCCATTCCAAGACCAAGGTGGCGACCACAAGCA 4898
Db 5136 ttcggtttgacatgtagacagggcaagcccttgacatcactatcatatggtttctcctgc 5195
QY 4899 ATAGTCTTTTGAATAAGTAAACCATTAAGAAATTCGATATAATCATTTATGTTATTCGT 4958
Db 5196 ctcaacatgatcaccatgatggtgagaccgagcagggcgagggagagaagcagaagttt 5255
QY 4959 CTGACATGTTTACCATGACCTCCATCGTACGATGCGTGGACACATATAACCCGGTTC 5018
Db 5256 ctggggcagaatacaacagttcttttggccgtcttcacagggcgagtggtgatgaagatg 5315
QY 5019 CTAGACTATCTCAATGCGATATTCGTAGTTATTTTCAGTTCCGAATGCTATTAAAAATA 5078
Db 5316 ttcgcccctgcagactactacttaccacagcggctggaacgtgttcgaacttcattagtg 5375
QY 5079 TTCGCTTTACGATATCACTATTTTATTGAGCCATGGAATTTATTGATGTAGTATTCCTC 5138
Db 5376 atcctgtccattggagctctgctgttttctgcaatcccttaagtcactggaactacttc 5435
QY 5139 ATTTTATCCATCTTAGGCT--TGTACTTAGCGATA-TTA--TCCA-GAAGTACTTCGTG 5192

Db 5436 tccccgacgctctctccggggtccatccgctctggccaggatccggccgcacatccctcaggtc 5495
QY 5193 TCGCCGACCCCTGCTCCGAGTGGTGGCGAAAGTGGCGTGTCTTCGAGTGGTG 5252
Db 5496 cgacagcgaaggggattcgacgctgctcttgcctcctcctcctcctcctcctcctc 5555
QY 5253 AAGGAGCCCAAGGCGATTCGACACTGCTCTTCGCGTGGCCATGTCGCTCGCGCCCTG 5312
Db 5556 ttcaacatcgccctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5615
QY 5313 TTCAACATCTGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5372
Db 5616 agcttcgtaacgtcgctggagagggcgccgcacatcgacacatggttcaacttcaaaccttt 5675
QY 5373 TTCTTCATGACGTGAAGGAGAGAGCGGATTAACGACGCTTACAACTTCAAGACCTTT 5432
Db 5676 ggaacagcatgctgctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5735
QY 5433 GGCCAGACATGATCTGCTCTTTTCAGATGTCGACGTCAGCGGTTGGGATGGTGTACTG 5492
Db 5736 agccccatctcacaacggggccctcctcctcctcctcctcctcctcctcctcctcctc 5795
QY 5493 GACCCCATTTCAAT--GAGGAAGC---A-TGCCATCC--ACCCGAC-AGCGACAAGGC 5543
Db 5796 tccccggggaactcggggagccggcggtggggaactcctcttccaccacactacatcctc 5855
QY 5544 TATCCGGCAATTTGTTGTTGAGCAGCGTTGGAATAACGTTTCTCTCTCATACCTAGTT 5603
Db 5856 atctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5915
QY 5604 ATAAGCTTTTGTAGTATTAATAATATGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 5663
Db 5916 gccaccgagagagacggagccctcctcctcctcctcctcctcctcctcctcctcctcctc 5975
QY 5664 GCCACCGGAGGAGTGCAGAGAGGTCTAACCCGACGACGACGACGACGACGACGACG 5723
Db 5976 tgggagaagttcgaccgggagggccacccagttccttcttctcctcctcctcctcctcctc 6035
QY 5724 TGGCAGCAATTCGATCGGAGGCGACCCAGTACATACGCTATGATCAGTGTCCGAATTC 5783
Db 6036 gcgagacgctctccggccctcttagaatacccccaaccccaaccccaaccccaacccca 6095
QY 5784 CTGACGCTACTGGAGCCCGCTCGACATCCACAAACCGAACAAAGTACAAGATCATATCG 5843
Db 6096 atggacctcgccgttgggtcccggggataaagatccactgctggacatcctcttcttgccttc 6155
QY 5844 ATGGACATACCCATCTGTCGGGTGACCTCATGCTGCTGCTGCTGCTGCTGCTGCTG 5903
Db 6156 acaagaacgtctt 6169
QY 5904 ACGAAGACTTCTT 5917

RESULT 12
ID T77804 standard; cDNA; 2573 BP.
AC T77804;
DT 09-OCT-1997 (first entry)
DE cDNA encoding variant rat DRG (SNS-B) #1.
KW Rat; sensory neuron sodium channel protein; Insensitive; tetrodotoxin;
KW modulator; impulse; sensory neuron; acute pain; chronic pain;
KW neuropathic pain; glia; muscle; parasympathetic nervous system;
KW enteric nervous system; central nervous system; dorsal root ganglia;
KW cranial ganglia; ss.
OS Rattus rattus.
FH Key Location/Qualifiers
FT CDS 561..2126
FT /*tag= a
FT /product= Variant_Rat_DRG(SNS-B)
FT
FT
FT
PD WO9701577-A1.
PF 16-JAN-1997.
PF 25-JUN-1996; G01523.
PF 28-JUN-1995; GB-013180.
PA (UNLO) UNIV COLLEGE LONDON.

THIS PAGE BLANK (USPTO)

Result	No.	Score	Query		Length	DB	ID	Description	Pred. No.
			Match	Match					
c	1	124	1.9	343	21	HSC2HD061	H. sapiens partial cDN	1.16e-19	
	2	121	1.9	529	24	AA18390	m53602.r1 Life Tech m	4.89e-19	
	3	99	1.5	594	25	AA272867	v09f10.r1 Soares mous	4.27e-14	
	4	91	1.4	619	26	FR0002753	F. rubripes GSS sequenc	5.18e-12	
	5	77	1.2	413	20	AA4227267	ve83f11.r1 Soares mous	1.01e-97	
	6	76	1.2	706	18	AA984063	am76b09.s1 Stratagene	1.15e-95	
	7	70	1.1	252	13	AA754459	97SN1787 Rice Immature	1.93e-83	
	8	62	1.0	214	4	AA360938	EST70140 T-cell Lympho	1.68e-67	
	9	64	1.0	252	13	AA754459	97SN1787 Rice Immature	1.92e-71	
	10	67	1.0	328	16	AA914778	v209a09.r1 Stratagene	2.07e-77	
	11	65	1.0	573	11	AA692527	HL08049.5prime HL Dros	2.00e-73	
	12	59	0.9	247	13	AA754458	97SN1784 Rice Immature	1.19e-61	
	13	60	0.9	247	13	AA754458	97SN1784 Rice Immature	1.36e-63	

Putative full length read
vector to vector length is
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 354.
Location/qualifiers

FEATURES	SOURCE
1. Geographical Location: The study area is located in the northern part of the state, covering a total area of 1,200 square kilometers.	State Geographical Information System (GIS) data.
2. Population Density: The population density is relatively low, with an average of 150 inhabitants per square kilometer.	Census Bureau data.
3. Climate: The climate is semi-arid, with annual rainfall ranging from 400 to 600 millimeters.	Local meteorological station records.
4. Topography: The terrain is mostly flat, with some low hills and valleys.	Aerial photography and topographic maps.
5. Vegetation: The vegetation is primarily dry grassland and shrubs.	Field observations and satellite imagery.
6. Water Resources: There are several small rivers and streams in the area.	Hydrological survey data.
7. Land Use: The land is primarily used for agriculture and grazing.	Land use maps and local government records.
8. Infrastructure: The area has a network of roads and a few small towns.	Infrastructure planning documents.
9. Environmental Concerns: There are concerns about soil erosion and water pollution.	Environmental impact assessment reports.
10. Historical Context: The area has a long history of human settlement.	Historical records and archaeological findings.

FEATURES source

```

/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 5' strand cDNA
was primed with a Not I - oligo(dT) primer [5,
TCTTACCATCGAAGTGGGAGCGCGCGAAGTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Minoru Ku, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
/db_xref="taxon:10090"
/clone="832845"
/clone_lib="Soares mouse NbMH"
/sex="male"
/tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"

```

BASE COUNT	117 a	92 c	110 g	94 t
ORIGIN				

Query Match 1.2%; Score 77; DB 10; Length 413;
Best Local Similarity 69.2%; Pred. No. 1.01e-97;
Matches 139; Conservative 0; Mismatches 62; Indels

Db	1	TACACAGCTTTGACACAGTCGGCTGGGCGCTTCTTGGCGCTTGTTCGGCTAATGACTCAG	60
QY	1125	TACACCAGCTTCGATTCGATCGGCTTCCCTGTCGGCTTCGGGCTGATGACACAG	1184
Db	61	GACTACTGGGAGAACCTTTATCAACAGACACACTGCCTGCTGCTGGCAAAACCTACATGATT	120
QY	1185	GACTTCTGGGAGGATCTGTACCAGCTGGTGTTCGCGCGCGGACCATGGCAGATCGTG	1244
Db	121	TTCTTTTGCCTGGTGATATTTCTCGGATCCCTTTTACCTGTATAAACTTGTATCCTGGCTGTG	180
QY	1245	TTCTTTTATGATCATCATCTCTCAGGTTCATCTCATCTGTGAAATTTGATTTTGGCCATT	1304
Db	181	GTAGCCATGGCGTACAGGAA	201
QY	1305	GTGGCCATGTCGTATGACGAA	1325

RESULT	6				
LOCUS	AA984063	706 bp	mrna	EST	27-MAY-1998
DEFINITION	am76b09.s1 Strateqene schizo brain s11 Homo sapiens cDNA clone IMAGE:1616345 3' similar to gb:M94055 SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT (HUMAN);; mRNA sequence.				

ACCESSION	AA984063
NID	Q3162588

KEYWORDS EST.
SOURCE human.

ORGANISM	Homo sapiens	Eukaryotes
1	100	100
2	100	100
3	100	100
4	100	100
5	100	100
6	100	100
7	100	100
8	100	100
9	100	100
10	100	100
11	100	100
12	100	100
13	100	100
14	100	100
15	100	100
16	100	100
17	100	100
18	100	100
19	100	100
20	100	100
21	100	100
22	100	100
23	100	100
24	100	100
25	100	100
26	100	100
27	100	100
28	100	100
29	100	100
30	100	100
31	100	100
32	100	100
33	100	100
34	100	100
35	100	100
36	100	100
37	100	100
38	100	100
39	100	100
40	100	100
41	100	100
42	100	100
43	100	100
44	100	100
45	100	100
46	100	100
47	100	100
48	100	100
49	100	100
50	100	100
51	100	100
52	100	100
53	100	100
54	100	100
55	100	100
56	100	100
57	100	100
58	100	100
59	100	100
60	100	100
61	100	100
62	100	100
63	100	100
64	100	100
65	100	100
66	100	100
67	100	100
68	100	100
69	100	100
70	100	100
71	100	100
72	100	100
73	100	100
74	100	100
75	100	100
76	100	100
77	100	100
78	100	100
79	100	100
80	100	100
81	100	100
82	100	100
83	100	100
84	100	100
85	100	100
86	100	100
87	100	100
88	100	100
89	100	100
90	100	100
91	100	100
92	100	100
93	100	100
94	100	100
95	100	100
96	100	100
97	100	100
98	100	100
99	100	100
100	100	100

REFERENCE

AUTHORS Hillier, D.
Krizman, D.

Martin, J.
Theising,

WashU-NCJ
Unpublished

COMMENT

Washington
4444 Foreign
Tel. 314

TEL: 314

;

Fax: 314 286 1810
Email: est@watson

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information..
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 425

FEATURES	SOURCE
1. Feature 1	Source 1
2. Feature 2	Source 2
3. Feature 3	Source 3
4. Feature 4	Source 4
5. Feature 5	Source 5
6. Feature 6	Source 6
7. Feature 7	Source 7
8. Feature 8	Source 8
9. Feature 9	Source 9
10. Feature 10	Source 10

```

i.: 700
/organism="Homo sapiens"
/note=Vector: Bluescript SK-; Site_1: EcoRI; Library
constructed from S-11 frontal lobe, male, 34 years old,
50% caucasian, 50% Aleutian. Schizophrenic suicide.
Random primed into EcoRI site of ZAP II Vector. Mass
excised. Custom library. Avg insert length 1.4kb.
Material obtained by Johnston N., Torrey, E.F., Yolken R.,
and the Stanley Neuropathology Consortium - Analysis of
RNAs from the Brains of Individuals with Psychiatric
Diseases (Unpublished) Stanley Neurovirology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."
/db_xref="taxon:9606"
/clone="IMAGE:l616345"
/clone_lib="Stratagene schizo brain S11"
/sex="male"
/tissue_type="schizophrenic brain S-11 frontal lobe"
/dev_stage="34 years old"
/lab_host="SOLR (kanamycin resistant)"
232 a 135 c 135 q 184 t
BASE COUNT

```

Query Match 1.2%; Score 76; DB 18; Length 705;
Best Local Similarity 66.0%; Pred. No. 1.15e-95;
Matches 177; Conservative 0; Mismatches 89; Indels

431	GCCCATGAACAACTGCAATCTATTACGCGAAACACACGCTTAGACAGAACACAGTCAAGAT	490
432		
433		
434		
435		
436		
437		
438		
439		
440		
441		
442		
443		
444		
445		
446		
447		
448		
449		
450		
451		
452		
453		
454		
455		
456		
457		
458		
459		
460		
461		
462		
463		
464		
465		
466		
467		
468		
469		
470		
471		
472		
473		
474		
475		
476		
477		
478		
479		
480		
481		
482		
483		
484		
485		
486		
487		
488		
489		
490		
491	CATGACATCAGAAAGCTTCTTCTACTGACTGATCAGGCAGGCACC-ACAAATGGTCTTCAGGCC	549
492		
493		
494		
495		
496		
497		
498		
499		
500		
501		
502		
503		
504		
505		
506		
507		
508		
509		
510		
511		
512		
513		
514		
515		
516		
517		
518		
519		
520		
521		
522		
523		
524		
525		
526		
527		
528		
529		
530		
531		
532		
533		
534		
535		
536		
537		
538		
539		
540		
541		
542		
543		
544		
545		
546		
547		
548		
549		
550	TGGAATGACTGAAATGTGTTTTTCAATGCTCGGAGAAGCTTGAATGTCTCAAGCTTGAGA	609
551		
552		
553		
554		
555		
556		
557		
558		
559		
560		
561		
562		
563		
564		
565		
566		
567		
568		
569		
570		
571		
572		
573		
574		
575		
576		
577		
578		
579		
580		
581		
582		
583		
584		
585		
586		
587		
588		
589		
590		

RESULT

FOCUS DEFINITION

ACCESSION

KEYWORDS

SOURCE	ORGANISM
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14
15	15
16	16
17	17
18	18
19	19
20	20
21	21
22	22
23	23
24	24
25	25
26	26
27	27
28	28
29	29
30	30
31	31
32	32
33	33
34	34
35	35
36	36
37	37
38	38
39	39
40	40
41	41
42	42
43	43
44	44
45	45
46	46
47	47
48	48
49	49
50	50
51	51
52	52
53	53
54	54
55	55
56	56
57	57
58	58
59	59
60	60
61	61
62	62
63	63
64	64
65	65
66	66
67	67
68	68
69	69
70	70
71	71
72	72
73	73
74	74
75	75
76	76
77	77
78	78
79	79
80	80
81	81
82	82
83	83
84	84
85	85
86	86
87	87
88	88
89	89
90	90
91	91
92	92
93	93
94	94
95	95
96	96
97	97
98	98
99	99
100	100

REFERENCE

AUTHORS

TITLE
TOURNAMENT

JOURNAL
COMMENT

Contact: Eun M. Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeungsun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahe@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.

```

FEATURES
source
Location/Qualifiers
1. .252
/organism="Oryza sativa"
/cultivar="Milkyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional CDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/clone="97SN1787"
/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
5 a 21 c 12 g 35 t 179 others
BASE COUNT
ORIGIN

```

[illegible]

RESULT	8
LOCUS	AA360938 214 bp mRNA EST
DEFINITION	EST70140 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to sodium channel 1, mRNA sequence.
ACCESSION	AA360938
NID	Q2013258
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
	Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae;
	Homo.

REFERENCE
AUTHORS

1 (bases 1 to 214)

Adams, M.D., Kurlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Well, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fritchum, W.M., Fritchum, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Patantes, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudke, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,

Kozak, D. L., Kneisler, C., Hunglun, J., Li, H., Meissner, P. S., Olsen, H., Raymond, L., Wei, F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M., Dillion, P. J., and Venter, J. C., 1993. Rosen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M., and Venter, J. C. Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence. *Nature* 377 (6547 Suppl), 3-174 (1995) 96026280

Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

```

FEATURES
source
1. 214
Location/Qualifiers
/organism="Homo sapiens"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
seq primer: fwd reverse.

```

IN	COUNT	mRNA	57 a	50 c	57 g	47 t	3 others
			57 a	50 c	57 g	47 t	3 others

	Query Match	1.0%	Score 62;	DB 4;	Length 214;
	Best Local Similarity	75.4%;	Pred. No. 1.68e-67;		
	Matches	95; Conservative	0; Mismatches 30;	Indels 1;	Gaps 1;
b	89	AAGTTTGACATCCCAAGCATGCATAGATAAACAATGCCAGGAGACGACGAGCGCCGATG	148		
p	5377	AAGAACGACATGCCGGAATGGCAAGATGAACATACCAGGAAACAGCAGCGACGACATG	5318		
b	149	TTAAACAACGAGGAGGACATCATCANAGCAAGAGCAGCGTTGGCGATTCCCCTTTGC	208		
p	5317	TTGACAGGGCGGACGACATGCCAACGCGAGAGCAGTGTG-CGATATGCCCTTTGC	5259		
b	209	TCCTTTT 214			
	5258	TCCTTT 5253			

	9	
RESULT		
OCUS	AA754459	252 bp mRNA EST
DEFINITION	97SNL787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SNL787, mRNA sequence.	
<hr/>		

SOURCE ORGANISM
 Rice.
Oryza sativa
 Eukaryotae: Viridiplantae; Charophyta/Embryophyta group;
 Eukaryotae: Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
 Poales; Poaceae: *Oryza*.
 1 (bases 1 to 252)

REFERENCE AUTHORS
 Nahn, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R., Moon, E.P.,
 Kim, W.Y., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, O.I., Kang, K.Y.,
 Lee, M.C. and Eun, M.Y.

TITLE
 Large-scale Sequencing Analysis of ESTs from Rice Immature Seed

JOURNAL
 Unpublished (1998)

Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea

Tel: 82 331 290 0301

Fax: 82 331 290 0307

Email: myeun@sun20.astl.re.kr

Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji University, Yongin, Korea. 449-728 bnhnm@bioserver.myongji.ac.kr

Seq primer: M13 Reverse Primer.

Location/Qualifiers

FEATURES

source
1..252
/organism="Oryza sativa"
/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; Directional cDNA library inserted into lambda ZAPII vector at 5' end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/clone="9/SNI787"
/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
BASE COUNT 5 a 21 c 12 g 35 t 179 others
ORIGIN

Query Match 1.0%; Score 64; DB 13; Length 252;
Best Local Similarity 11.6%; Pred. No. 1.92e-71;
Matches 26; Conservative 115; Mismatches 82; Indels 2; Gaps 2;

Db 22 SYBCHGNBVVVCVASHGNYMVHNCBTRGTHCDCKNNWMTWGTWNBNVSGDWHYWB 81

Qy 303 CCGCGGAATGGGCTCCACTCCCTCAGGATATCGATCCCTACTACAGCAATGTACTG 362

Db 82 VBNTKVDVGNTRCSRWBRVEMAHYHDYTNCBYNNNDYHWHBMYBFBGCMTCMWC 141

Qy 363 ACATTCTGAGTGTGAAGCAAGGAAAGATATTTTCGCTTTTCGATCAAAAAGCAATG 422

Db 142 WBHYNTKCTASGWHSTNTYDKSNTWGTBSYDKSMHGYWCBBVYKHVKTTRATR 201

Qy 423 TGG-ATGCTCGATCATTCATCCGATACGTCGTGTGCGCATTTACATTCI-ATGTCATC 480

Db 202 SYTCVRKVCVMMYKVKVYHVBBGCHBDSCKTMWMTNKHV 246

Qy 481 CATTATTTTCCTATTTCATCATCACCACAATTCGTCACATGCA 525

RESULT 10
LOCUS AA914778 328 bp mRNA EST 14-APR-1998
DEFINITION v209a09.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone 1315192 5', similar to gb:M81758 SODIUM CHANNEL PROTEIN, SKELETAL MUSCLE ALPHA-SUBUNIT (HUMAN); gb:U26707 Mus musculus voltage-gated sodium channel alpha subunit SCN8A (MOUSE);, mRNA sequence.
ACCESSION AA914778
NID 93054170
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sclurognath; Muridae; Murinae; Mus.
1 (bases 1 to 328)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)

Contact: Marra M/Mouse EST Project
WASHU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:865488
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 262.
Location/Qualifiers

FEATURES

source
1..328
/organism="Mus musculus"
/strain="NIH/Swiss"
/note="Organ: heart; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts. Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"/db_xref="taxon:10090"
/clone="1315192"
/clone_lib="Stratagene mouse heart (#937316)"
/sex="pooled"
/tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
BASE COUNT 72 a 107 c 79 g . 70 t
ORIGIN

Query Match 1.0%; Score 67; DB 16; Length 328;
Best Local Similarity 70.7%; Pred. No. 2.07e-77;
Matches 123; Conservative 0; Mismatches 50; Indels 1; Gaps 1;

Db 145 CTTCCTCATCGTGGTCAACATGTACATTCGATCCTCGAGACCTTCAGTCAGTGGCCAC 204

Qy 5609 CTTTTGATGATTATATATATGATGATGCTGCTCAATTCGAGAACTATAGTCAGGCCAC 5668

Db 205 AGAAGAGCAGCAGACCCCTCGAGGAGATGACTTCGACATGTTCTATGAGATCTCGGA 264

Qy 5669 CGAGGACGTCCAAGAGGGTCTAACCGACGACGACTACGACATGACTATGAGATCTGCA 5728

Db 265 GAAGTTGACCCCGAGC-CACCAGTTCATGAGTATGGGCCCTGTCGCACTT 317

Qy 5729 GCAATTCGATCCGAGGGGCCACCCAGTACATACGCTATGATCAGCTGTCGCAAT 5782

RESULT 11
LOCUS AA699257 573 bp mRNA EST 18-DEC-1997
DEFINITION HL08049.5prime HL Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone HL08049 5prime similar to X14398: Drosophila put. sodium channel gene part 5 (AA 1320-1680), mRNA sequence.
ACCESSION AA699257
NID 92702186
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
REFERENCE Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 573)
AUTHORS Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C., Brokstein,P., Lewis,S. and Rubin,G.M.
TITLE BDGP/HMI Drosophila EST Project
JOURNAL Unpublished (1997)
COMMENT

Contact: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://fruitfly.berkeley.edu/EST, est@fruitfly.berkeley.edu
Plate: 80 row: E column: 1
High quality sequence stop: 426.
Location/Qualifiers

FEATURES

source
1..573
/organism="Drosophila melanogaster"
/note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:

XhoI: Sized fractionated cDNAs were directly ligated into
 pOT2." /db_xref="taxon:7227"
 /clone="HL08049"
 /clone_lib="HL Drosophila melanogaster head pOT2"
 /sex="male and female"
 /dev_stage="head--brain & sensory organ"
 /lab_host="XLI Blue"

BASE COUNT 129 a 147 c 145 g 152 t
 ORIGIN

Query Match 1.0%; Score 65; DB 11; Length 573;
 Best Local Similarity 62.9%; Pred. No. 2,00e-73;
 Matches 171; Conservative 0; Mismatches 100; Indels 1; Gaps 1;

Db 23 GGGCGTATTCGGGTGATCAAGCGCCCAAGGGGATCAGAAAGTTGCTATTCGCTC 82

QY 5232 GCGCGTGTCTTCGACTGTGGAAGGAGCAAGGCACTTCGCGGTTG 5291

Db 83 GTAGTGTCTCCCGCCCTATTACATCGGAGCTCTCTAGGACTGATCACCCTTATC 142

QY 5292 GCGATGTCTCGCGCCCTGTTCACATCTGCCCTGCTCTGCTGATGTTTCATC 5351

Db 143 TAGCGAATCTCGGCATGCTGCTGTTTCGAAATGTCAAGCTCCAGGCTCTCGATGAC 202

QY 5352 TTGCGCATTTTGGCATGTCGTTCTTATCGACGTGAAGAGCGGCATTAACGAC 5411

Db 203 ATGGTGAACCTCCAGACCTTCGCGGCA-CATGCACTTACTGTCGGTTGATGACCTCA 261

QY 5412 GTCTACAACCTCAAGACCTTTGGCCAGAGCATGATCCTCTTTCAGATGTCGAGTCA 5471

Db 262 GCGGGTGAATGACGTACTTGAGTCCCTGAT 293

QY 5472 GCGGGTGGATGGTGTGCTACTGGACGCCATTAT 5503

RESULT 12 AA754458 247 bp mRNA EST 20-JAN-1998
 LOCUS 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
 DEFINITION CDNA clone 97SN1784, mRNA sequence.
 ACCESSION AA754458
 NID 92801164
 KEYWORDS EST.
 SOURCE rice.

ORGANISM Oryza sativa
 Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
 Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
 Poales; Poaceae; Oryza.

REFERENCE 1 (bases 1 to 247)
 AUTHORS Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
 Lee,M.C. and Eun,M.Y.

TITLE Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
 JOURNAL Unpublished (1998)
 COMMENT

Contact: Eun M.Y.
 Department of Cytogenetics
 National Inst. of Agri. Sci. and Tech, RDA
 Suwon, Kyunggido, Korea
 Tel: 82 331 290 0301
 Fax: 82 331 290 0307
 Email: myeun@sun20.asti.re.kr

Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
 University, Yongin, Korea. 449-728 bnhahm@bioserver.myongji.ac.kr
 Seq primer: M13 Reverse Primer.

FEATURES
 Location/Qualifiers
 1..247
 /organism="Oryza sativa"
 /cultivar="Milyang23"

/note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2:
 XhoI: Directional cDNA library inserted into lambda ZAPII
 vector at 5' end with EcoRI and 3' end with Xho I site."

/db_xref="taxon:4530"

/clone="97SN1784"

/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"

/tissue_type="Immature Seed"

/clone="97SN1784"
 /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
 /tissue_type="Immature Seed"
 /dev_stage="5 days after pollination"
 /lab_host="E. coli SOLR"
 BASE COUNT 7 a 16 c 21 g 34 t 169 others
 ORIGIN

Query Match 0.9%; Score 59; DB 13; Length 247;
 Best Local Similarity 16.1%; Pred. No. 1.19e-61;
 Matches 40; Conservative 119; Mismatches 83; Indels 6; Gaps 6;

Db 1 HWDCTMTNTVWRCCCBAMNKHHTHMTBWCVRVGTNTNNGKHNGRTTWNDCSDNA 50

QY 2605 TTGCCATCGAGGCCACCATGAAGCTAATGGCCATGAGCCCACTACTATTCCA-GG-A 2662

Db 61 HCRYTVBMYARSKYGYGTBYYSNVNDTNTGGTGVGKTTVNVHSGNNRCSNVVYVBT 120

QY 2663 GGGCTGGACATCTT-CGATTCATATTCGTGGCCCTATCGCTATTTGAACCTGGACTCG 2721

Db 121 AYCDYBHYEDRANHVDYDTRCTNDRGYCNYTASDNGTSATKRVTYGDK-TDSDGGGCGWRK 179

QY 2722 AGGGTGTCCAGGTCTGTCGGTATTCGCTCTCTTCGATTCGCTGCTATTTCAAACCTGG 2781

Db 180 VTIGSSBYRCCVNVVTTTSMWTKSTKMS-MDMSRR-SRVHYGRWMBNKKRMSRW 237

QY 2782 CCAAGTCTTGGCCACACTTAATTTACTCATTTGATTTGGAGCCACCATGGCGCTT 2841

Db 238 TDTKTWRT 245

QY 2842 TGGGTAAT 2849

RESULT 13 AA754458 247 bp mRNA EST 20-JAN-1998
 LOCUS 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
 DEFINITION CDNA clone 97SN1784, mRNA sequence.
 ACCESSION AA754458
 NID 92801164
 KEYWORDS EST.
 SOURCE rice.

ORGANISM Oryza sativa
 Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
 Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
 Poales; Poaceae; Oryza.

REFERENCE 1 (bases 1 to 247)
 AUTHORS Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
 Lee,M.C. and Eun,M.Y.

TITLE Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
 JOURNAL Unpublished (1998)
 COMMENT

Contact: Eun M.Y.
 Department of Cytogenetics
 National Inst. of Agri. Sci. and Tech, RDA
 Suwon, Kyunggido, Korea
 Tel: 82 331 290 0301
 Fax: 82 331 290 0307
 Email: myeun@sun20.asti.re.kr

Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
 University, Yongin, Korea. 449-728 bnhahm@bioserver.myongji.ac.kr
 Seq primer: M13 Reverse Primer.

FEATURES
 Location/Qualifiers
 1..247
 /organism="Oryza sativa"
 /cultivar="Milyang23"

/note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2:
 XhoI: Directional cDNA library inserted into lambda ZAPII
 vector at 5' end with EcoRI and 3' end with Xho I site."

/db_xref="taxon:4530"

/clone="97SN1784"

/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"

/tissue_type="Immature Seed"

```
/dev stage="5 days after pollination"
/lab_host="E. coli SOLR"
7 a 16 c 21 g 34 t 169 others

BASE COUNT
ORIGIN

Query Match 0.8%; Score 60; DB 13; Length 247;
Best Local Similarity 15.8%; Pred. No. 1.36e-63;
Matches 34; Conservative 102; Mismatches 76; Indels 3; Gaps 3;

Db 5 TMNTVVRGCCBAMNKH-THMTBWCVRVRVGTNTNNGKNGRTTWNDCSDNAHCR 63
Cp 3657 TCATATGCTACCATAGACTTAATCGTCGACGTGCTGCTCTGTAAGGACAACCTC 3598
Db 64 Y-TVNTYASKYGYBPYYSWNVDNTWGTGKKTIVNVHSGWNNRCSNVVYVWBTAY 122
Cp 3597 TATGGTTTAGCTGCTTCAGTCTATTGCTTGGTGGTAAATGAGTTGCCA-ATCATC 3539
Db 123 CDVBHBDRAHHVDDTRCTNDRUCYNVTASDNGTSATKRVGTGDKVDSDCGGCGRKVYI 182
Cp 3538 GTTGGCTATTAGATATTGGATTCTTCGGCTTGTGTCTTCATGCGCGGTATC 3479
Db 183 GSBYBRGVNVVVRTSMWTDKSTKMSMDMSRR 217
Cp 3478 GTGAATTCATCCGATCCCGATGCCACCTCCAG 3444

RESULT 14
LOCUS AA913881 330 bp mRNA EST 14-APR-1998
DEFINITION Om21h12.s2 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1541735 3' similar to TR:P70276 P70276 SODIUM CHANNEL, TYPE
X, ALPHA POLYPEPTIDE ;, mRNA sequence.
ACCESSION AA913881
NID 93053273
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 330)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 322.
Location/Qualifiers
1. .330
/organism="Homo sapiens"
/note="Organ: pooled; Vector: p7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI-CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="IMAGE:1541735"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"

BASE COUNT 99 a 69 c 59 g 103 t
ORIGIN

Query Match 0.8%; Score 49; DB 16; Length 330;
Best Local Similarity 59.5%; Pred. No. 8.90e-43;
Matches 153; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Db 16 CRAAGTCTCGTTCGACATAGTCACAGCCAGATCTTTGACATCATCATATAGTCTC 75
QY 4893 CAAGCAATAGTCTTTGAATAGTAACCGATAAGAAATTCGATATAATCATATTATTC 4952
Db 76 ATTATCTAAACATGATTAGCATGCTGAATCATACCAACCAACCCAAAGCCATGAA 135
QY 4953 ATGGTCTGAACATGTTCCACATGACCCCTCGATGCTGTAGATGCGGACACGATATAAC 5012
Db 136 TCCATCCTTGACCATCTCAACTCGGTCTTTGTGGTCATCTTTACGTAGAAATGCTCATC 195
QY 5013 GCGGCTCTAGACTATCTCAATCGGATATTCGAGTAGTATTTTCAGTTCGGAATGCTATTA 5072
Db 196 AAATCTTTGCTTTGAGGCAATACTACTTCCACCAATGCTGGAATTTATTTGACTGTGTG 255
QY 5073 AAAATATTGCTTTAGCATATCATCTATTTATTGAGCCATGGAATTTATTGATGTAGTA 5132
Db 256 GTCGTGCTTCTTTCCAT 272
QY 5133 GTTGCAATTTATCCAT 5149

RESULT 15
LOCUS AA885211 435 bp mRNA EST 27-MAR-1998
DEFINITION am34c11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1468724 3' similar to TR:P70276 P70276 SODIUM CHANNEL, TYPE
X, ALPHA POLYPEPTIDE ;, mRNA sequence.
ACCESSION AA885211
NID 92994288
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 390.
Location/Qualifiers
1. 435
/organism="Homo sapiens"
/note="Organ: pooled; Vector: p7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI-CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="IMAGE:1468724"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"

BASE COUNT 132 a 89 c 78 g 136 t
ORIGIN
```

Query Match 0.8%; Score 49; DB 16; Length 435;
Best Local Similarity 59.5%; Pred. No. 8.90e-43;
Matches 153; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Db 16 CAAGGTCTCGTTCGACATAGTCACAGCCGAGATCTTTGACATCATCATCAATAGTCTC 75
Qy 4893 CAAGCAATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATAATCATTTATGTTATTC 4952

Db 76 ATTATCCTAAACATGATTAGCATGATGGCTGAATCATACACCAACCCAAAGCCCATGAAA 135
Qy 4953 ATTGGTCTGAACATGTTTCACCATGACCCCTCGATCGTTACGATGCGTCGGACACGTATAAC 5012

Db 136 TCCATCCTTGACCATCTCAACTGGGTCTTTTGGTGCATCTTTACGTTAGATGTCTCATC 195
Qy 5013 GCGGCTCTAGACTATCTCAATGCGATATTCGTAGTATTTTCAGTTCGGAATGTCTATTA 5072

Db 196 AAAATCTTTGCTTTGAGGCAATACTTTCACCAATGGCTGGAATTTATTGACTGTGTG 255
Qy 5073 AAAATATTCGCTTTACGATATCACTATTTTATTGAGCCATGGAATTTATTGATGTAGTA 5132

Db 256 GTCGTGCTTCTTTCCAT 272
Qy 5133 GTTGTCAATTTTATCCAT 5149

Search completed: Sun Sep 13 07:01:11 1998
Job time : 9067 secs.

THIS PAGE BLANK (USPTO)